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FIGURE 1

GTTACTCGGTGGTGGCGGAGTCTACGGAAGCCGTTTTTCGCTTCACTTTTCCTGGCTGTAGAGC
GCTTTCCCCCTGGCGGGTGAGAGTGCAGAGACGAAGGTGCGAGATGAGCACTATGTTTCGCGGA
CACTCTCCTCATCGTTTTTTATCTCTGTGTGCACGGCTCTGCTCGCAGAGGGCATAACCTGGGT
CCTGGTTTACAGGACAGACAAGTACAAGAGACTGAAGGCAGAAGTGGAACAGAGTAAAAA
ATTGGAAGAAGAAGGAAACAATAACAGAGTCAGCTGGTCGACAACAGAAAAAGAAAATAGA
GAGACAAGAAGAGAACTGAAGAATAACAACAGAGATCTATCAATGGTTCGAATGAAATCCAT
GTTTGCTATTGGCTTTTGTTTTACTGCCCTAATGGGAATGTTCAATTCCATATTTGATGGTAG
AGTGGTGGCAAAGCTTCCTTTTACCCCTCTTTCTTACATCCAAGGACTGTCTCATCGAAATCT
GCTGGGAGATGACACCACAGACTGTTTCCTTCATTTTCCTGTATATTCTCTGTACTATGTCGAT
TCGACAGAACATTGAGAAGATTCTCGGCCTTGCCCTTCACGAGCCGCCACCAAGCAGGCAGG
TGGATTTCTTGGCCCACCACCTCCTTCTGGGAAGTTCTCTTGAACTCAAGAACTCTTTATTTT
CTATCATTCTTTCTAGACACACACACATCAGACTGGCAACTGTTTTGTAGCAAGAGCCATAGG
TAGCCTTACTACTTGGGCCTCTTTCTAGTTTTGAATTATTTCTAAGCCTTTTGGGTATGATTA
GAGTGAAAATGGCAGCCAGCAAACCTGATAGTGCTTTTGGTCCTAGATGATTTTTATCAAATA
AGTGGATTGATTAGTTAAGTTCAGGTAATGTTTATGTAATGAAAAACAAATAGCATCCTTCTT
GTTTCATTTACATAAGTATTTTCTGTGGGACCGACTCTCAAGGCACTGTGTATGCCCTGCAAG
TTGGCTGTCTATGAGCATTTAGAGATTTAGAAGAAAAATTTAGTTTGTTTAACCCTTGTAAC
GTTTGTTTTGTTGTTGTTTTTTTTTCAAGCCAAATACATGACATAAGATCAATAAAGAGGCCA
AATTTTATAGCTGTTTTATGTACAAGGAGAGATCTGTTTCATTTTGTGTTTGCCGTATTTCTAGA
TATAAGTTTTAGCATGGGCCAGGAAGGACTAAAATAAAAGTTTTTAAGGTACAAAAA
AAAA

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FIGURE 2

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGR
QQKKKIERQEEKLKNNNRDLMSVRMKSMFAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSYIQ
GLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

Important features:**Signal peptide:**

amino acids 1-22

N-myristoylation sites..

amino acids 103-109, 163-169

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 53-57

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FIGURE 3

AGCCGGGGGCGGGTTTGAAGACGCGTCGTTGGGTTTTGGAGGCCGTGAAACAGCCGTTTGAGT
TTGGCTGCGGGTGGAGAACGTTTGT CAGGGGCCCCGGCCAAGAAGGAGGCCCGCCTGTTACGAT
GGTGTCCATGAGTTTCAAGCGGAACCGCAGTGACCGGTTCTACAGCACCCGGTGCTGCGGCTG
TTGCCATGTCCGCACCGGGACGATCATCCTGGGGACCTGGTACATGGTAGTAAACCTATTGAT
GGCAATTTTGCTGACTGTGGAAGTGACTCATCAAACCTCCATGCCAGCTGTCAACATTCAGTA
TGAAGTCATCGGTAATTACTATTCTGCTGAGAGAATGGCTGATAATGCCTGTGTTCTTTTTGC
CGTCTCTGTTCTTATGTTTATAATCAGTTCAATGCTGGTTTATGGAGCAATTTCTTATCAAGT
GGGTTGGCTGATTCCATTCTTCTGTTACCGACTTTTTGACTTCGTCCCTCAGTTGCCTGGTTGC
TATTAGTTCTCTCACCTATTTGCCAAGAATCAAAGAATATCTGGATCAACTACCTGATTTTCC
CTACAAAGATGACCTCCTGGCCTTGGACTCCAGCTGCCTCCTGTTCAATTGTTCTTGTGTTCTT
TGCCTTATTCATCATTTTTTAAGGCTTATCTAATTAACGTGTTTTGGAACGTCTATAAATACAT
CAACAACCGAAACGTGCCGGAGATTGCTGTGTACCCTGCCTTTGAAAGCACCTCCTCAGTACG
TTTTGCCAACCTATGAAATGGCCGTGAAAATGCCTGAAAAAGAACCACCACCTCCTTACTTAC
CTGCCTGAAGAAATTCTGCCTTTGACAATAAATCCTATAACCAGCTTTTTGTTTGTTTATGTTA
CAGAATGCTGCAATTCAGGGCTCTTCAAACCTGTTTGATATAAAATATGTTGTCTTTTGTTTA
AGCATTTATTTCAAACACTAAGGAGCTTTTTGACATCTGTTAAACGTCTTTTTGTTTTTTG
TTAAGTCTTTTACATTTTAATAGTTTTTGAAGACAATCTAGGTTAAGCAAGAGCAAAGTGCCA
TTGTTTGCCTTTAATTGGGGGTGGGAAGGGAAAGAGGGTACTTGCCACATAGTTTCCTTTTT
AACTGCACTTCTTTTATATAATCGTTTGCATTTTGTTACTTGCTACCCTGAGTACTTTCAGGA
AGACTGACTTAAATATTCGGGGTGAGTAAGTAGTTGGGTATAAGATCTGAACTTTTCATCTGC
AGAGGCAAGAAAAATATTTGACATTGTGACTTGACTGTGGAAGATGATGGTTGCATGTTTCTA
GTTTGTATATGTTTCCATCTTTGTGATAAGATGATTTAATAAATCTCTTTAAATACTAAAAAA
AAAAAAA

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FIGURE 4

MVSMSEFKRNRSDRFYSTRCCGCCHVRTGTIIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQ
YEVIGNYYSSERMADNACVLFAVSVLMFIISSMLVYGAIQVGVLPFFCYRLFDFVLSCLV
AISSLTYLPRIKEYLDQLPDFPYKDDLLALDSSCLLFIVLVFFALFIIFKAYLINCWNCYKY
INNRRNVPEIAVYPAFESTSSVRFANL

Important features of the protein:

Transmembrane domain (Possible type II transmembrane protein):

amino acids 30-49, 81-100, 111-131, 158-175

N-glycosylation site.

amino acids 9-13

Tyrosine kinase phosphorylation sites.

amino acids 8-16, 193-202

N-myristoylation site.

amino acids 68-74

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FIGURE 5

CCCGCTGGCCCGTCAGTGCTCTCCCCGTCGTTTGCCCTCTCCAGTTCCCCCAGTGCCTGCCCT
ACGCACCCCGATGGCGGAGCTGCGGCCTAGCGGCGCCCCCGGCCCCACCGCGCCCCCGGCCCC
TGGCCCGACTGCCCCCCCCGGCCTTCGCTTCGCTCTTTCCCCCGGGACTGCACGCCATCTACGG
AGAGTGCCGCCGCCTTTACCCTGACCAGCCGAACCCGCTCCAGGTTACCGCTATCGTCAAGTA
CTGGTTGGGTGGCCCAGACCCCTTGACTATGTTAGCATGTACAGGAATGTGGGGAGCCCTTC
TGCTAACATCCCCGAGCACTGGCACTACATCAGCTTCGGCCTGAGTGATCTCTATGGTGACAA
CAGAGTCCATGAGTTTACAGGAACAGATGGACCTAGTGTTTGGCTTTGAGTTGACCTTTCG
TCTGAAGAGAGAACTGGGGAGTCTGCCCCACCAACATGGCCCGCAGAGTTAATGCAGGGCTT
GGCAGGATACGTGTTCCAGTCAGAGAACACCTTCTGCAGTGGGGACCATGTGTCTTGGCACAG
CCCTTTGGATAACAGTGAGTCAAGAATTACGACATGCTGCTGACAGAGGACCCACAGATGCA
GCCCGTGCAGACACCCTTTGGGGTAGTTACCTTCCTCCAGATCGTTGGTGTCTGCACTGAAGA
GCTACACTCAGCCCAGCAGTGGAACGGGCAGGGCATCCTGGAGCTGCTGCGGACAGTGCCTAT
TGCTGGCGGCCCTGGCTGATAACTGACATGCGGAGGGGAGAGACCATATTTGAGATCGATCC
ACACCTGCAAGAGAGAGTTGACAAAGGCATCGAGACAGATGGCTCCAACCTGAGTGGTGTGAG
TGCCAAGTGTGCCTGGGATGACCTGAGCCGGCCCCCGAGGATGACGAGGACAGCCGGAGCAT
CTGCATCGGCACACAGCCCCGGCGACTCTCTGGCAAAGACACAGAGCAGATCCGGGAGACCCT
GAGGAGAGGACTCGAGATCAACAGCAAACCTGTCCTTCCACCAATCAACCCTCAGCGGCAGAA
TGGCCTCGCCCACGACCGGGCCCCGAGCCGCAAAGACAGCCTGGAAAGTGACAGCTCCACGGC
CATCATTCCCCATGAGCTGATTTCGCACGCGGCAGCTTGAGAGCGTACATCTGAAATTCAACCA
GGAGTCCGGAGCCCTCATTCCTCTCTGCCTAAGGGGCAGGCTCCTGCATGGACGGCACTTTAC
ATATAAAAGTATCACAGGTGACATGGCCATCACGTTTGTCTCCACGGGAGTGGAAGGCGCCTT
TGCCACTGAGGAGCATCCTTACGCGGCTCATGGACCCTGGTTACAACTCTGAACCTATCCTCG
GAGCTCTGCCCTCCCGTCCTGGAACGTCTTTCTGCCCTGAGGAGAGGGTAGTCAGCATCTCCA
ATTTTCAGCAGCTCAAGAACCTTGGCCCCCAGGACTTCGCAGATGTCACATTGCCCTCAG
TCCCCTGAATGCCCTTCGGACCCAACCCCAATTCCCCAAGCCCCTGACCCCTAGCTGCCGGG
GTTCCCCTCCAGTGCCACAAACCCCTCACCTCCCCTGGCAGCCCCCTCAGCGAGCCTGAGGC
CCAGCACCCGCTGGCTCCCCAGCACATGGTCCCCTCCCATGGGCTGTTGCCAGGGGAACCGGG
GCGCGGTGGGAACGAGCTGCTGGCCTCGGCATGTTTCAATAAAGTTGCTGTGCTGGGAG

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FIGURE 6

MAELRPSGAPGPTAPPAPGPTAPPAFASLFPPGLHAIYGECRRLYPDQPNPLQVTAIVKYWLG
GPDPLDYVSMYRNVGSPSANIPEHWHYISFGLSDLYGDNRVHEFTGTDGPGSGFGFELTFRLKR
ETGESAPPTWPAELMQGLARYVFQSENTFCSGDHVSWHSPLDNSESRIQHMLLTEDPQMOPVQ
TPFGVVTFLQIVGVCTEELHSAQQWNGQGILELLRTVPIAGGPWLITDMRRGETIFEIDPHLQ
ERVDKGIETDGSNLSGVSAKCAWDDLSPPEDEDSRSICIGTQPRRLSGKDTEQIRETLRRG
LEINSKPVLPPINPQRQNGLAHDRAPSRKDSLESSTAIIPHELIRTRQLESVHLKFNQESG
ALIPLCLRGRLHGRHFTYKSITGDMAITFVSTGVEGAFATEEHPYAAHGPWLQL

Important features:**N-glycosylation site.**

amino acids 265-268

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FIGURE 7

CGCGAATGAAGTTTGCATTTTCCTCTGTTCTTGAGCCCAGCTTCTTCTCGTCTCCCACCCCAG
CTTCCCGGCATTGGAAGAAGGGACCGTCCTCTTCCTTGTCTTGGCCACCCAAATCCTGGTATC
GAAAGGGTTGAACGGACCGGAAGTGTGCAGCAGCGACGGGTCCCCAGCTAATCGACGCCGGAA
GTAGCAATTACTAGACAAGCATTCCGCCGCCGGCTTCGCTATGGCGGCAATTCCCCCAGATTC
CTGGCAGCCACCCAACGTTTACTTGGAGACCAGCATGGGAATCATTGTGCTGGAGCTGTACTG
GAAGCATGCTCCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCGAGGTTACTACAATGG
CACAAAATTCACAGAATTATCAAAGACTTCATGATCCAAGGAGGTGACCCAACAGGGACAGG
TCGAGGTGGTGCATCTATCTATGGCAAACAATTTGAAGATGAACTTCATCCAGACTTGAAATT
CACGGGGGCTGGAATTCTCGCAATGGCCAATGCGGGGCCAGATACCAATGGCAGCCAGTTCTT
TGTGACCCCTCGCCCCACCCAGTGGCTTGACGGCAAACACACCATTTTTTGGCCGAGTGTGTCA
GGGCATAGGAATGGTGAATCGCGTGGGAATGGTAGAAACAACTCCCAGGACCGCCCTGTGGA
CGACGTGAAGATCATTAAGGCATACCCTTCTGGGTAGACTTGCTACCCTCTTGAGCAGCTCTT
CTGAGATGGCCCCAGTGAACCAGCTTCTAGATGACATAGAATGACATGTAATGCTAAATTTCA
TTTTGGCTTTGCAAGTCATGAAGCTTAGGAGGCCTGGCATCTTGGGTGAGTTAGAGATGGAAG
TACATTTTAATAGGATGCTTCTTTTCTCTTCCCCAGTGCCTAGGTTGCCAGAGCATTTCAC
AAATGCCCCCTGTTTATCAATAGGTGACTACTTACTACACATGAACCATAATGCTGCTTCTTGT
GCATGTCTGCTCTGATATACGTGCAACAATGTAGCAGCCACTGTCATTTCTCAGTGGTTTTGC
CTAACCAAACCTTCTTCCTAAGGAGATTTATATTCTGGCCTACACAGCAGTCCTTGATGGCTGA
CAGCCACAGAATTCCAAACCAAGTAGTGTCTGTGAGCCCTCTTAACCTCTGTGCACGCCCTATT
TCAGTCTTTTACATTTGTTCTTCTAGGGAATGTATGCATCTCTATATATATTTTCCCTCTCAA
AACCAGAACATCAACAGTGTGTTTCTGACACTTCAGACATCCACGCAAAGCCACATTGAAT
TTTTGCCAAATGAAAAACACATCCAACAATCAAGTTTCTAAGAAGGTGTCAAGTGGGGAATAA
TAATAATGTATAATAATCAAGAAATTAGTTTATTTAAAGGAAGCAGAAGCATTGACCATTTTT
TCCCAGAGAAGAGGAGAAATCTGTAGTGAGCAAAGGACAGACCATGAATCCTCCTTGAGAAGT
AGTACTCTCAGAAAGGAGAAGCGCCACTCAAGTTCTTTTAACCCAAGACTTTAGAGAAATTAG
GTCCAAGATTTTTATATGTTTCAGTTGTTTATGTATAAAAATAACTTTCTGGATTTTGTGGGGA
GGAGCAGGAGAGGAAGGAAGTTAATACCTATGTAATACATAGAACTTCCACAATAAAATGCC
ATTGATGGTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 8

MAAIPDSWQPPNVYLETSMGIIIVLELYWKHAPKTCKNFAELARRGYNGTKFHRIKDFMIQ
GGDPTGTGRGGASIYGKQFEDELHPDLKFTGAGILAMANAGPDTNGSQFFVTLAPTQWLDGKH
TIFGRVCQGIGMVNRVGMVETNSQDRPVDDVKIIKAYPSG

Important features:**N-glycosylation sites:**

amino acids 49-52, 108-111

N-myristoylation sites:

amino acids 64-69, 69-74, 143-148

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature:

amino acids 48-65

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FIGURE 10

MWHEARKHERKLRGMMVDYKKRAERRREYYEKIKKDPAQFLQVHGRACKVHLDSAVALAAESP
VNMMPWQGDNTNMIDRFDVRAHLDPDYTPPLTTISPEQESDERKCNERYRGLVQNDFA
ISEEQCLYQIYIDELYGGLQRPSEDEKKKLAEEKKASIGYTYEDSTVAEVEKAAEKPEEEESAA
EEESNSDEDEVIPDIDVEVDVDELNQEQVADLNKQATTYGMADGDFVRMLRKDKKEAEAIKHA
KALEEEKAMYSGRRSRRQRREFREKRLRGRKISPPSYARRDSPTYDPYKRSPSESSSESRSRS
RSPTPGREEKITFITSFGGSDEEAAAAAAAAAASGVTTGKPPAPPQPGGPAPGRNASARRRSS
SSSSSSASRTSSSRSSSRSSSRSGGGYYRSGRHARSRSRSWSRSRSRSTRYSRSRSRGRR
HSGGSRDGHRYSRSPARRGGYGPRRRSRSRSHSGDRYRRGGRGLRHHSSSRSSWSLSPSR
SRLTRSRSHSPSPSQSRSRSRSSQSPSPSPAREKLTRPAASPAVGEKLLKTEPAAGKETGA
AKVTQADASGEAETEDAEGAEQAVQGG

Important features:**N-glycosylation site:**

amino acids 370-373

Glycosaminoglycan attachment site:

amino acids 443-446

cAMP- and cGMP-dependent protein kinase phosphorylation site:amino acids 159-162, 282-285, 291-294, 374-377, 375-378, 430-433,
440-443, 466-469**Casein kinase II phosphorylation site:**amino acids 149-152, 166-169, 171-174, 187-190, 193-196, 195-198,
303-306, 307-310, 335-338, 571-574**N-myristoylation sites:**

amino acids 118-123, 229-234, 350-355, 446-451, 586-591

Amidation sites:

amino acids 263-266, 280-283, 438-441

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FIGURE 11

GGTAGGCGCGCCAGACCTGAGACGGGTTGGGACTGGGCTGCGTCACGCGCGGGCTCTAAGCG
CCCCGGGCCCCGCCAGTGGCCGGCACAGCCAATCGCAGCGCGGGAAGGCGGTGGGGGCGGGG
AAGGCCGCGCTGGAACTTAAATCCCGAGGCGGGCGAACCTGCACCAGACCGCGGACGTCTGTA
ATCTCAGAGGCTTGTTTGCTGAGGGTGCCTGCGCAGCTGCGACGGCTGCTGGTTTTGAAACAT
GAATCTTTCGCTCGTCCCTGGCTGCCTTTTGCTTGGAATAGCCTCCGCTGTTCCAAAATTTGA
CCAAAATTTGGATACAAAGTGGTACCAGTGGAAAGCAACACACAGAAGATTATATGGCGCGAA
TGAAGAAGGATGGAGGAGAGCAGTGTGGGAAAAGAATATGAAAATGATTGAACTGCACAATGG
GGAATACAGCCAAGGGAAACATGGCTTCACAATGGCCATGAATGCTTTTGGTGACATGACCAA
TGAAGAATTCAGGCAGATGATGGGTGCTTTCGAAACCAGAAATTCAGGAAGGGGAAAGTGT
CCGTGAGCCTCTGTTTCTTGATCTTCCCAAATCTGTGGATTGGAGAAAGAAAGGCTACGTGAC
GCCAGTGAAGAATCAGAAACAGTGTGGTTCTTGTTGGGCTTTTAGTGCGACTGGTGCTCTTGA
AGGACAGATGTTCCGGAAAACCTGGGAACTTGTCTCACTGAGCGAGCAGAATCTGGTGGACTG
TTCGCGTCCTCAAGGCAATCAGGGCTGCAATGGTGGCTTCATGGCTAGGGCCTTCCAGTATGT
CAAGGAGAACGGAGGCCTGGACTCTGAGGAATCCTATCCATATGTAGCAGTGGATGAAATCTG
TAAGTACAGACCTGAGAATTCTGTTGCTAATGACACTGGCTTCACAGTGGTCGCACCTGGAAA
GGAGAAGGCCCTGATGAAAGCAGTCGCAACTGTGGGGCCCATCTCCGTTGCTATGGATGCAGG
CCATTCGTCCCTCCAGTTCTACAAATCAGGCATTTATTTTGAACCAGACTGCAGCAGCAAAAA
CCTGGATCATGGTGTTCTGGTGGTTGGCTACGGCTTTGAAGGAGCAAATTCGAATAACAGCAA
GTATTGGCTCGTCAAAAACAGCTGGGGTCCAGAATGGGGCTCGAATGGCTATGTAAAAATAGC
CAAAGACAAGAACAACCACTGTGGAATCGCCACAGCAGCCAGCTACCCCAATGTGTGAGCTGA
TGGATGGTGAGGAGGAAGGACTTAAGGACAGCATGTCTGGGGAAATTTTATCTTGAAACTGAC
CAAACGCTTATTGTGTAAGATAAACCAGTTGAATCATGGAGGATCCAAGTTGAGATTTTAATT
CTGTGACATTTTTTACAAGGGTAAAATGTTACCACTACTTTAATTATTGTTATACACAGCTTTA
TGATATCAAAGACTCATTGCTTAATTCTAAGACTTTTGAATTTTCATTTTTTAAAAAGATGTA
CAAAACAGTTTGAAATAAATTTTAATTCGTATATA

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FIGURE 12

MNLSLVLA AFCLGIASAVPKFDQNLDTKWYQWKATHRRLYGANEEGWRRRAVWEKNMKMIELHN
GEYSQGKHGFTMAMNAFGDMTNEEFRQMMGCERNQKFRKGKVFREPLFLDLPKSVDWRKKGYV
TPVKNQKQCGSCWAFSATGALEGQMFRKTGKLVSLSEQNLVDCSRPOGNQGCNGGFMARAFQY
VKENGGLDSEESYPYVAVDEICKYRPENSVANDTGFTVVAPGKEKALMKAVATVGPISVAMDA
GHSSFQFYKSGIYFEPDCSSKNLDHGVLVVGYGFEGANSNNISKYWLVKNSWGP EWGSNGYVKI
AKDKNNHCGIATAASYPNV

Important features:**Signal sequence**

amino acids 1-17

N-glycosylation sites.

amino acids 2-6, 221-225, 292-296

N-myristoylation sites.amino acids 13-19, 93-99, 136-142, 145-151, 174-180, 177-183,
180-186, 194-200, 288-294, 324-330**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 132-144

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 275-286

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FIGURE 13

GGCGGCGTCATGTGATCCGCTTCCCTGCTCCTTTAAGCGTCCACAGGCGGCGGAGCGGCCACA
ATCACAGCTCCGGGCATTGGGGGAACCCGAGCCGGCTGCGCCGGGGGAATCCGTGCGGGCGCC
TTCCGTCCCGGTCCCATCCTCGCCGCGCTCCAGCACCTCTGAAGTTTTGCAGCGCCCAGAAAG
GAGGCGAGGAAGGAGGGAGTGTGTGAGAGGAGGGAGCAAAAAGCTCACCCCTAAAACATTTATT
TCAAGGAGAAAAGAAAAAGGGGGGGCGCAAAAATGCTGGGGCAATTATAGAAAACATGAGCA
CCAAGAAGCTGTGCATTGTTGGTGGGATTCTGCTCGTGTTCCAAATCATCGCCTTTCTGGTGG
GAGGCTTGATTGCTCCAGGGCCACAACGGCAGTGTCTACATGTCTGGTGAATGTGTGGATG
CCCGTAAGAACCATCACAAGACAAAATGGTTCGTGCCTTGGGGACCCAATCATTGTGACAAGA
TCCGAGACATTGAAGAGGCAATTCCAAGGGAAATTGAAGCCAATGACATCGTGTTCCTGTTC
ACATTCCCCCTCCCCACATGGAGATGAGTCTTGGTTCCAATTCATGCTGTTTATCCTGCAGC
TGGACATTGCCTTCAAGCTAAACAACCAAATCAGAGAAAATGCAGAAGTCTCCATGGACGTTT
CCCTGGCTTACCGTGATGACGCATTTGCTGAGTGGACTGAAATGGCCCATGAAAGAGTACCAC
GGAAACTCAAATGCACCTTCACATCTCCCAAGACTCCAGAGCATGAGGGCCGTTACTATGAAT
GTGATGTCCTTCCTTTCATGGAAATTGGGTCTGTGGCCCATAGTTTTACCTTTTAAACATCC
GGCTGCCTGTGAATGAGAAGAAGAAAATCAATGTGGGAATTGGGGAGATAAAGGATATCCGGT
TGGTGGGGATCCACCAAAATGGAGGCTTACCAAGGTGTGGTTTGCCATGAAGACCTTCCTTA
CGCCAGCATCTTCATCATTATGGTGTGGTATTGGAGGAGGATCACCATGATGTCCCAGCCCC
CAGTGCTTCTGGAAAAAGTCATCTTGGCCTTGGGATTTCCATGACCTTTATCAATATCCCAG
TGGAATGGTTTTTCATCGGGTTTGACTGGACCTGGATGCTGCTGTTTGGTGACATCCGACAGG
GCATCTTCTATGCGATGCTTCTGTCTTCTGGATCATCTTCTGTGGCGAGCACATGATGGATC
AGCACGAGCGGAACCACATCGCAGGGTATTGGAAGCAAGTCGGACCCATTGCCGTTGGCTCCT
TCTGCCTCTTCATATTTGACATGTGTGAGAGAGGGGTACAACCTCACGAATCCCTTCTACAGTA
TCTGGACTACAGACATTGGAACAGAGCTGGCCATGGCCTTCATCATCGTGGCTGGAATCTGCC
TCTGCCTCTACTTCTGTCTTCTATGCTTCATGGTATTTTCAGGTGTTTCGGAACATCAGTGGGA
AGCAGTCCAGCCTGCCAGCTATGAGCAAAGTCCGGCGGCTACACTATGAGGGGCTAATTTTTTA
GGTTCAAGTTCCTCATGCTTATCACCTTGGCCTGCGCTGCCATGACTGTATCTTCTTCATCG
TTAGTCAGGTAACGGAAGGCCATTGGAAATGGGGCGGCGTCACAGTCCAAGTGAACAGTGCCT
TTTTTCACAGGCATCTATGGGATGTGGAATCTGTATGTCTTTGCTCTGATGTTCTTGTATGCAC
CATCCCATAAAAACATATGGAGAAGACCAGTCCAATGGCGATCTGGGTGTCCATAGTGGGGAAG
AACTCCAGCTCACCACCACTATCACCCATGTGGACGGACCCACTGAGATCTACAAGTTGACCC
GCAAGGAGGCCCAGGAGTAGGAGGCTGCAGCGCCCGGCTGGGACGGTCTCTCCATACCCAGC
CCCTCTAACTAGAGTGGGGAGCATGCCAGAGAGAGCTCAATGTACAAATGAATGCCTCATGGC
TCTTAGCTGTGGTTTTCTTGGACCAGCGGCATGGACATTTGTCAGTTTGCCTTCTGACGGTAGC
TTTTGGAGGAAGATTCTTGCAGCCACTAATGCATTGTGTATGATAACAAAACTCTGGTATGA
CACATTTTCTGTGATCATTGTTAATTAGTGACATAGTAACATCTGTAGCAGCTGGTTAGTAAA
CCTCATGTGGGGGTGGGGTGGGGGTGTATTCCTTGGGGGATGGTTTGGGCCGAATGGGGAGTG
GAATATTTGACATTTTTCCTGTTTTAAATTCTAGGATAGATTTTAAACATCCTTTGCGGTCCCA
GTCCAAGGTAGGCTGGTGTATAGTCTTCTCACTCCTAATCCATGACCACTGTTTTTTTCTTA
TTTATATCACCAGGTAGCCTACTGAGTTAATATTTAAGTTGTCAATAGATAAGTGTCCCTGTT
TTGTGGCATAATATAACTGAATTTTCATGAGAAGATTTATTCACCAGGGGTATTTTCAGCTTTG
AAACCAAACTGTGTATCTAATACTAACCAATCTGTTGGATGTGGATTTTAAAAAATGTTTGC
TAACTACCCAAGTAAGATTTACTGTATTAATGGCCTTCGGGTCTGAAAAGCTTTTTTAAACC
TCTTGCTTAAATGCGTTTTATTTTGATAAGATACTTCAAATAGCCTCCAAAAGTGATAGATCC
AATCACTTAAATAAACCTGTATGTATATGCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 14

MAGAI IENMSTKKLCIVGGILLVFQIIAFLVGGLIAPGPTTAVSYMSVKCVDARKNHHKTKWF
VPWGNHCDKIRDIEEAIPREIEANDIVFSVHIPLPHMEMSPWFQFMLFILQLDIAFKLNNQI
RENAEVSM DVSLAYRDDAFAEWTEMAHERVPRKLKCTFTSPKTPEHEGRYYECDVLPFMEIGS
VAHKFYLLNIRLPVNEKKKINVGIGEIKDIRLVGIHQNGGFTKVWFAMKTFLTPSIFIIMVWY
WRRITMMSRPPVLLKLVIFALGISMTFINIPVEWFSIGFDWTWMLLFGDIRQGIFYAMLLSFW
IIFCGEHMMDQHERNHIAGYWKQVGPIAVGSFCLFIFDMCERGVQLTNPFYSIWTTDIGTELA
MAFIIVAGICLCLYFLFLCFMVVFQVFRNISGKQSSLPAMSKVRRRLHYEGLIFRFKFLMLITLA
CAAMTVIFFIVSQVTEGHWKWGGVTVQVNSAFFGTGIYGMWNLYVFALMFLYAPSHKNYGEDQS
NGDLGVHSGEELQLTTTITHVDGPTEIYKLTTRKEAQE

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:amino acids 239-253, 269-284, 302-318, 338-352, 377-399, 434-452,
471-488**N-glycosylation sites.**

amino acids 8-12, 406-410

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 254-258

N-myristoylation sites.amino acids 223-229, 274-280, 305-311, 358-364, 374-380, 386-392,
509-515

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FIGURE 15

GTGAGGGGAACAGCTGATCCGTCTGTTGGGAGGACAGATATCTCAAGGCCAGG**ATG**GGAAGAAT
CACCAC TAAGCCGGGCACCATCCCGTGGTGGAGTCAACTTTCTCAATGTAGCCCGGACCTACA
TCCCCAACACCAAGGTGGAATGTCACTACACCCTTCCCCCAGGCACCATGCCAGTGCCAGTG
ACTGGATTGGCATCTTCAAGGTGGAGGCTGCCTGTGTTCCGGGATTACCACACATTTGTGTGGT
CTTCCGTGCCTGAAAGTACAAGTATGATGGTTCCCCCATTCACACCAGTGTCAGTTCCAAGCCA
GCTACCTGCCCAAACCAGGAGCTCAGCTCTACCAGTTCCGATATGTGAACCGCCAGGGCCAGG
TGTGTGGGCAGAGCCCCCTTTCCAGTTCCGAGAGCCAAGGCCCATGGATGAACTGGTGACCC
TGGAGGAGGCTGATGGGGGCTCTGACATCCTGCTGGTTGTCCCAAGGCAACTGTGTTACAGA
ACCAGCTCGATGAGAGCCAGCAAGAACGGAATGACCTGATGCAGCTGAAGCTACAGCTGGAGG
GACAGGTGACAGAGCTGAGGAGCCGAGTGCAGGAGCTCGAGAGGGCTCTGGCAACTGCCAGGC
AGGAGCACACGGAGCTGATGGAACAGTACAAGGGGATTTCCCGGTCCCATGGGGAGATCACAG
AAGAGAGGGACATCCTGAGCCGGCAACAGGGAGACCATGTGGCACGCATCCTGGAGCTAGAGG
ATGACATCCAGACCATCAGTGAGAAAGTGCTGACGAAGGAAGTGGAGCTGGACAGGCTTAGAG
ACACAGTGAAGGCCCTGACTCGGGAACAAGAGAAGCTCCTTGGGCAACTGAAAGAAGTACAAG
CAGACAAGGAGCAAAGTGAGGCTGAGCTCCAAGTGGCACAACAGGAGAACCATCACTTAAATT
TGGACCTGAAGGAGGCGAAGAGCTGGCAAGAGGAGCAGAGTGCTCAGGCTCAGCGACTGAAAG
ACAAGGTGGCCAGATGAAGGACACCCTAGGCCAGGCCAGCAGCGGGTGGCCGAGCTGGAGC
CCTTGAAGGAGCAGCTTCGAGGGGCCCAGGAGCTTGACAGCCTCAAGCCAGCAGAAAGCCACCC
TTCTTGGGGAGGAGTTGGCCAGTGACAGCAGCAGCCAGGGACCGCACCATAGCCGAACTACACC
GCAGCCGCCTGGAAGTGGCTGAAGTTAACGGCAGGCTGGCTGAGCTCGGTTTGCACCTGAAAG
AAGAAAAATGCCAATGGAGCAAGGAGCGGGCAGGGCTGCTGCAGAGTGTGGAGGCAGAGAAGG
ACAAGATCCTGAAGCTGAGTGCAGAGATACTTCGATTGGAGAAGGCAGTTCAGGAGGAGAGGA
CCCAAACCAAGTGTTCAAGACTGAGCTGGCCCCGGGAGAAGGATTCTAGCCTGGTACAGTTGT
CAGAAAGTAAGCGGGAGCTGACAGAGCTGCGGTCAGCCCTGCGTGTGCTCCAGAAGGAAAAGG
AGCAGTTACAGGAGGAGAAACAGGAATTGCTAGAGTACATGAGAAAGCTAGAGGCCCGCCTGG
AGAAGGTGGCAGATGAGAAGTGGAATGAGGATGCCACCACAGAGGATGAGGAGGCCGCTGTGG
GGCTGAGCTGCCCGGCAGCTCTGACAGACTCAGAGGACGAGTCCCCAGAAGACATGAGGCTCC
CACCCTATGGCCTTTGTGAGCGTGGAGACCCAGGCTCCTCTCCTGCTGGGCCTCGAGAGGCTT
CTCCCCTTGTTGTATCAGCCAGCCGGCTCCCATTTCTCCTCACCTCTCTGGGCCAGCTGAGG
ACAGTAGCTCTGACTCGGAGGCTGAAGATGAGAAGTCAGTCCTGATGGCAGCTGTGCAGAGTG
GGGTGAGGAGGCCAACTTACTGCTTCTGAACTGGGCAGTGCCTTCTATGACATGGCCAGTG
GCTTTACAGTGGGTACCCTGTGAGAAACCAGCACTGGGGGCCCTGCCACCCCCACATGGAAGG
AGTGTCTATCTGTAAGGAGCGCTTTCCTGCTGAGAGTGACAAGGATGCCCTGGAGGACCACA
TGGATGGACACTTCTTTTTCAGCACCCAGGACCCCTTACCTTTGAG**TGA**TCTTACTCCCTCG
TACATGCACAAATACACACTCATGCACACACACACTCACACACATGCATACACTTAGGTTTCA
TGCCCATTTTCTATCACACTGGGCTCCATGATATTCTGTTCCCTAAGAACTGCTTCTGTGTGC
CCTGTTTTTCATCCCAAGATTTCTCACTTCATCCTCTCCTACCTGGCTCTTTTGTCCAGGGAG
GGGTCCTGTTTCGGAAGCAGTGGCTGAATTTATCCCCTGAAAGTGGTTTGGAGGAACCGGGAT
GGAGGAGGCCCTTCCCCTGTGGGAATAGAATCGTCCACTCCTAGCCCTGGTTGCTTCTGATACA
CAGCCACTGCACACACACACTCACACTCACACTCCCTTGTCTGATGCCCCAAAGCCAATTCTCT
GGGGCACCCCTACCCTCTCTTATTTGGAGTTTCCGTTGGTTTACCTGAGTTTCTCTGGGGTCT
GCACAGAGGCAGCAGCATGGACATCATGGCCTCTCAGGTCCCTTTTGGTTCTCAGTTTCATTG
GTTCTCTTTCTGTTCCCCCATTTGACTTCTGTGCCCCACCCTAGCCTTTTCCATAACCTTAGG
TATTCAGTTTGGAGGGGTTTTTTGTATTTTTGAGGATTCTGTATTCTGTATCCTCTCCTCGC
ATCTCCTCACATGGAAAGAAATAATGTATTTGTGCCTTCTGTGAGGAATGGGGGGAACAAGTG
GTCCCAGGTATCCCCATTTCCAAGGCCCCCTCCCTCTCCAGGTCCCCCACAGCAATAAAAG
CTTCCCCCTGATATCCATCCCTTTGTAGTTTGAACAAATATATTTATATGATATGTAA

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FIGURE 16

MEESPLSRAPSRGGVNFLNVARTYIPNTKVECHYTLPPGTMPASDWDWIGIFKVEAACVRDYHT
FVWSSVPESTTDGSPIHSTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPFPQFREPRPMDE
LVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLMQLKLQLEGQVTELRSRVQELERALA
TARQEHTELMEQYKGISRSHGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKVELD
RLRDTVKALTREQEKLKGQLKEVQADKEQSEAEQVAQQENHHLNLDLKEAKSWQEEQSAQAQ
RLKDKVAQMKDTLGQAQQRVAELEPLKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIA
ELHRSRLEVAEVNGRLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILKLSAEILRLEKAVQ
EERTQNQVFKTELAREKDSSLVQLSESKRELTELSALRVLQKEKEQLQEEKQELLEMYMRKLE
ARLEKVADEKWNEDATTEDEEAAGVGLSCPAALTDSEDESPEDMRLPPYGLCERGDGSSPAGP
REASPLVVISQPAPISPHLSGPAEDSSSDSEAEDEKSVLMAAVQSGGEEANLLLPELGSAFYD
MASGFTVGTLSSETSTGGPATPTWKECPICKERFPAESDKDALEDHMDGHFFSTQDPFTFE

Important features:**Casein kinase II phosphorylation sites:**

amino acids 28-31, 43-46, 68-71, 72-75, 129-132, 156-159, 208-
211, 239-242, 282-285, 305-308, 376-379, 383-383, 468-471, 520-
523, 521-524, 537-540, 539-542, 543-546, 593-596, 595-598, 597-
600, 612-615, 639-642, 652-655, 667-670, 683-686

N-myristoylation sites:

amino acids 39-44, 107-112, 204-209, 414-419, 561-566, 613-618

Cell attachment sequence:

amino acids 557-559

Leucine zipper pattern sequence:

amino acids 163-184, 475-496, 482-503

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FIGURE 17

GCAAGTTGGGAATTTTAGACTGTCACTGCACATGGACCTCTGGGAAGACGTCTGGCGAGAGCT
AGGCCCCTGGCCCTACAGACGGATCTTGCTGGCTCACCTGTCCCTGTGGAGGTTCCCCTGGG
AAGGCAAGATGCCCAACAACAGCACTGCTCTGTCAATTGGCCAATGTTACCTACATCACCATGG
AAATTTTCATTGGACTCTGCGCCATAGTGGGCAACGTGCTGGTCATCTGCGTGGTCAAGCTGA
ACCCAGCCTGCAGACCACCACCTTCTATTTTCATTGTCTCTCTAGCCCTGGCTGACATTGCTG
TTGGGGTGCTGGTCATGCCTTTGGCCATTGTTGTCAGCCTGGGCATCACAATCCACTTCTACA
GCTGCCTTTTTATGACTTGCCTACTGCTTATCTTTACCCACGCCTCCATCATGTCCCTTGCTGG
CCATCGCTGTGGACCGATACTTGCGGGTCAAGCTTACCGTCAGATTCAGAATTCCTGGGCTCC
CTGGGTGCATTCTATCATTCCAGTTGAAAGTTTGCTTCCTTCCAGTCATGTGGCTCTTCATTC
TACTCTCCTTGCTCTCATTTTCAGATGCCATGGTCATGGATGAAAAGGTCAAGAGAAGCTTTG
TGCTGGACACGGCTTCTGCCATCTGCAACTACAATGCCCACTACAAGAATCACCCCAAATACT
GGTGCCGAGGCTATTTCCGTGACTACTGCAACATCATCGCCTTCTCCCTAACAGCACCAATC
ATGTGGCCCTGAGGGACACAGGGAACCAGCTCATTGTCACTATGTCTCTGCCTGACCAAAGAGG
ACACGGGCTGGTACTGGTGTGGCATCCAGCGGGACTTTGCCAGGGATGACATGGATTTTACAG
AGCTGATTGTAAGTACGACAAAGGAACCCTGGCCAATGACTTTTGGTCTGGGAAAGACCTAT
CAGGCAACAAAACCAGAAGCTGCAAGGCTCCCAAAGTTGTCCGCAAGGCTGACCGCTCCAGGA
CGTCCATTCTCATCATTTCGATACTGATCACGGGTTTGGGAATCATCTCTGTAATCAGTCATT
TGACCAAAGGAGGAGAAGTCAAAGGAATAGAAGGGTAGGCAACACTTTGAAGCCCTTCTCGC
GTGTCCTGACTCCAAAGGAAATGGCTCCTACTGAACAGATGTGACTGAAGATTTTTTTAATTT
AGTTCATAAAGTGATGCTACAACAGAATAATCACCATGACAACCTGGCCCACACCTCAGAGACT
GATTCTGATCTCCAGGAATTCTGAAGGACCTCTATCCTTGACAACAATCATTTCAGCCAG
GTAGCAACGGCGGTAGTCAGAGGAGCTATGATAGACCACACCCAAGCAAGGCTGCCCTCAAAT
AACATCTCAAGATCTTAGTTCTTATGCATTCCATCAGTCAGAAGTGAAGAAGAGGTGGAGAAT
CTGGATTGGGGACCAGGAAATCACTTGTATTTTGTAGCCAATAAATTCCTAGCCAGTGTTGA
ATGAAAAAAAAAAAAA

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FIGURE 18

MPNNSTALSLANVTYITMEIFIGLCAIVGNVLVICVVKLNPSLQTTTFYFIVSLALADIAVGV
LVMP LAIVVSLGITIHFYSCLFMTCLLLIFTHASIMSL LAIVDRYL RVKLT VRFRIPGLPGC
ILSFQLKVCFLPVMWLFILLSLALISDAMVMDEKVKRSFVLDTASAICNYN AHYKNHPKYWCR
GYFRDYCNIIAFSPNSTNHVALRDTGNQLIVTMSCLTKEDTGWYWCGIQRDFARDDMDFT ELI
VTDDKGT LANDFWSGKDL SGNKTR SCKAPKVVRKADRSRTS ILIICILITGLGIISVISHLTK
RRRSQRNRRVGNTLKPFSRVLTPKEMAPTEQM

Important features of the protein:**Transmembrane domains:**

amino acids 16-35, 62-80, 89-101, 134-152, 292-311

N-glycosylation sites.

amino acids 3-7, 4-8, 12-16, 204-208, 273-277

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 316-320

N-myristoylation sites.

amino acids 122-128, 125-131, 258-264

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 214-225

G-protein coupled receptors proteins.

amino acids 29-59, 76-116

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FIGURE 19

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTGCGATTGAGCTGCGGGTCGCGGCCGGCGCCGGCCTCTCCAATG
GCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTTCGGCAAAGGCAGTCGAGTGTTTGCAGACCGGGGCGAGTC
CTGTGAAAGCAGATAAAAGAAAACATTTATTAACGTGTCATTACGAGGGGAGCGCCCGGGGCTGTGCGACT
CCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTACAGTCG
TTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTATTAGCGATGCCCCCTG
GTTTGTGTGTTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCCTGGGCG
AATCCACATCTGTTTCAACTCTCCGCCGAGGGCGAGCAGGAGCGAGAGTGTGTGGAATCTGCGAGTGAAGAGGG
ACGAGGGGAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAGAAGCACCAGATCAGCAAAA
AAAGAAGATGGGCCCCCCGAGCCTCGTGCTGTGCTTGCTGTCCGCAACTGTGTTCTCCCTGCTGGGTGGAAGCTC
GGCCTTCTGTGCGACCACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCAACATCATCCT
GGTGTGACGGACGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATCATGGAGCA
GGGCGGGGCGCACTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCTCAGCTCCTCCATCCTCACTGG
CAAGTACGTCCACAACCACAACACCTACACCAACAATGAGAACTGCTCCTCGCCCTCCTGGCAGGCACAGCACGA
GAGCGCACCTTTGCGGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAGTATCTTAATGAATA
CAACGGCTCCTACCTGCTGACCCCGGCTGGAAGGAGTGGGTGCGACTCCTTAAAAACTCCCGCTTTTATAACTACAC
GCTGTGTGCGAACGGGGTGAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCACAGACCTCATCACCAA
TGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCTCATGGTCATCAGCCATGC
AGCCCCCAGCGCCCTGAGGATTACGCCCCACAATATTCACGCCTCTTCCCAAACGCATCTCAGCACATCACGCC
GAGCTACAACCTACGCGCCCAACCCGGACAACACTGGATCATGCGCTACACGGGGCCCATGAAGCCCATCCACAT
GGAATTCACCAACATGCTCCAGCGGAAGCGCTTGACAGCCCTCATGTGCGGTGGACGACTCCATGGAGACGATTTA
CAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGCCGACCACGGTTACCACATCGG
CCAGTTTGGCCTGGTGAAGGGAAATCCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGGCC
CAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCTCAACATTGACCTGGCCCCCACCATCCTGGACATTGC
AGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCTGGACACGGAGCGGCGCGTGAATCG
GTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGACTCCTTCTTGGTGAGAGAGGCAAGCTGTACACAAGAG
AGACAATGACAAGGTGGACGCCAGGAGGAGAACTTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTAGCG
TGCTGAGTACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTGTGTGGAGGACGCCACGGGGAAGCTGAA
GCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCCTCTCCAACCTCGTGCCCAAGTACTACGG
GCAGGGCAGCGAGGCTGACCTGTGACAGCGGGGACTACAAGCTCAGCCTGGCCGGACGCCGGAAGAACTCTT
CAAGAAGAAGTACAAGGCCAGCTATGTCCGCAGTGCCTCCATCCGCTCAGTGGCCATCGAGGTGGACGGCAGGCT
GTACCAGTAGGCTGGGTGATGCGGCCAGCCCGAAACCTCAACAGCGGCACTGGCCAGGGCCCCCTAGGA
CCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGCCTTCCGACTACTCAGCCGCCAACCCCATTA
AGTGACACATCGGTGCTACATCCTAGAGAACGACACAGTCCAGTGTGACCTGGACCTGTACAAGTCCCTGCAGGC
CTGGAAAGACCACAAGCTGCACATCGACCACGAGATTGAAACCCTGCAGAACAAATTAAGAACCCTGAGGGAAAGT
CCGAGGTACCTGAAGAAAAAGCGGCCAGAAGATGTGACTGTACAAAATCAGCTACCACACCCAGCACAAAGG
CCGCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAGGAAGGGCCTGCAAGAGAAGGACAAGGTGTGGCTGT
GCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGCTCAAGCGCCTGCAGAACACGACAGTGCAGCATGCC
AGGCCTCACGTGCTTCACCCACGACAACCAGCACTGGCAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGC
CTGCACCAGCGCCAACAATAACACGTACTGGTGCATGAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGA
ATTTGCAACTGGCTTCTAGAGTACTTTGATCTCAACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACT
GGACAGGGATGTCTCAACCAGCTACAGTACAGCTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAA
CCCCGGACTCGAAACATGGACCTGGATGGAGGAAGCTATGAGCAATACAGGCAGTTTCAGCGTCAAAAGTGGCC
AGAAATGAAGAGACCTTCTTCCAAATCACTGGGACAACCTGTGGGAAGGCTGGGAAGGTTAAGAAACAACAGAGGT
GGACCTCCAAAAACATAGAGGCATCACCTGACTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACC
TGTGCTATTGGCCAGGAGGCTGAGAAAGCAAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCA
GCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTGGCCCTGCTTTTGTCTTGGATTATACCTCACCAGCTGCAC
AAAATGCATTTTTCGTATCAAAAAGTCACCACTAACCTCCCCAGAAGCTCACAAGGAAAACGGAGAGAGCG
AGCGAGAGAGATTCTTGGAAATTTCTCCCAAGGGCGAAAGTCATTGGAATTTTAAATCATAGGGGAAAAGCA
GTCCTGTTCTAAATCCTCTTATTCTTTTGGTTTGTACAAAAGGAACTAAGAAAGCAGGACAGAGGGCAACGTGG
AGAGGCTGAAAACAGTGCAGAGACGTTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTAT
AAACCCTGGTTGCCTCTGAAGAACTGCCTTCAATGTATATATGTGACTATTTACATGTAATCAACATGGGAACT
TTTAGGGGAACCTAATAAGAAATCCCAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAA
GAAAAA

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FIGURE 20

MGPPSLVLCCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQV
MNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHESTR
FAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSDYSK
DYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITPSYNY
APNPDKHWIMRYTGPMKPIHMEFTNMLQKRQLQTLMSVDDSMETIYNMLVETGELDNTYIVYT
ADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDIAGLDIP
ADMKGKSLKLLDTERPVRNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQR
VKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALS NLVPKYYGQGSEAC
TCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAAQPRNLTKRHW
PGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLH
IDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGLQEKD
KVWLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNNT
YWCMTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGY
KQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

Important features:**Signal peptide:**

amino acids 1-17

Sulfatases signature 1.

amino acids 86-99

Homologous region to sulfatase:

amino acids 87-106, 133-146, 216-229, 291-320, 365-375

N-glycosylation sites.amino acids 65-69, 112-116, 132-136, 149-153, 171-175, 198-202,
241-245, 561-565, 608-612, 717-721, 754-758, 764-768

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FIGURE 21

GGGCGCGGAGAGCTGCTAGGGCGGTTTCTCTGCCTCGGGCCTGTTGGGCAGGGCCGGCT
AAGGTGCGCGTGCTCGCTGGTTCTAACCCTTCTGTTGGGCGTTTCTGCTGAGAGGCGGGA
GGCGCTGAGAGTCTGTGCGGAGGTCCGTGGACAGACTGCTTTGCTCGTTGTTGCTCTTCG
GAGGCGGCGATCCCCGAAGGCGAGCTGAAATACGGCTGCAGGCTACAATTTGCAGCCGAC
GATTATGGAAGACGGAAGCGGGAGAGGTGGCCCCACCCTCATGGAGCGCTTGTGCTCGGAT
GGCTTCGCATTTCCCCAATACCCCATTAACCGTATCATCTGAAGAGGATCCACAGAGCT
GTCTTACATGGTAATCTAGAGAACTGAAGTACCTTCTGCTCACGTATTATGACGCCAAT
AAGAGAGACAGGAAGGAAAGGACCGCCCTACATTTGGCCTGTGCCACTGGCCAACCGGAA
ATGGTACATCTCCTGGTGTCCAGAAGATGTGAGCTTAACCTCTGCGACCGTGAAGACAGG
ACACCTCTGATCAAGGCTGTACAACCTGAGGCAGGAGGCTTGTGCAACTCTTCTGCTGCAA
AATGGCGCCAATCCAAATATTACGGATTTCTTTGGAAGGACTGCTCTGCACTACGCTGTG
TATAATGAAGATACATCCATGATAGAAAACTTCTTTCACATGGTACAAATATTGAAGAA
TGCAGCAAGGTATAGGTCAACCAATGTTATTTTCAAACCTATCTGAAATGAATTTATTTTA
ACATTGACACATGTAAGGGTCAATTTTTCATATTTGGAAGCTCAACATTCCTTGAATGA
AAATATTTTGAAATGCCTTAACCTGTCTAAGATTTTACTTTAAATATTGGAACCTTTTAAAG
AAGCATTATAGGGAACAGCCTTTTTTTCATGCACTTATGGTAAATAACTATAAAAACAAAT
GAATTACAATAAATTTTATAATTCATGACAACCTGAATTTGGGAAAGGTAATAGTTAAGTGT
TTTTCCACTAAATTACTTTTT

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FIGURE 22

MERLCSDGFAFPQYPIKPYHLKRIHRAVLHGNLEKLYLLTTYDANKRDRKERTALHLACAT
GQPEMVHLLVSRRCENLDCREDRTPLIKAVQLRQEACATLLLQNGANPNITDFFGRTALHYA
VYNEDTSMIEKLLSHGTNIEECSKV

Important features of the protein:**N-glycosylation site.**

amino acids 113-117

N-myristoylation site.

amino acids 109-115

Microbodies C-terminal targeting signal.

amino acids 149-153

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FIGURE 23

GAGGCAGAAAGGCAGAAAGGAGAAAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTG
CCATGTAGTGCACGCAGGACATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGT
CACTTATTCTAAAGGCCCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAG
GGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAACTGAAGGAGTGTGT
TTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGC
TGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGC
CGCCCTGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCT
GCCAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACT
GAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG
TGCCGTTTCAAGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAGTGA
AACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGG
AAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTTATATA
TGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGT
CCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAATATGCCTGA
AACACTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACT
CCAATTGCAATACCAAGAGAAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTTGG
TGCATTGAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTCTCTGT
ACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAA

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FIGURE 24

MDDSTEREQSRLTSCCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLLALLSCCLTV
VSFYQVAALQGD LASLRAELQGHHA EKLPAGAGAPKAGLEEAPAVTAGLKIFEP PAPGEGNSS
QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL EEEKENKILVKE
TGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFR CIQNMPETLPNNSCYSAGIAK
LEEGDELQLAIPRENAQISLDGDVTFFGALKLL

Transmembrane domain:

amino acids 47-72

N-glycosylation site.

amino acids 124-127, 242-245

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36, 173-176

N-myristoylation site.

amino acids 96-101

TNF family proteins.

amino acids 172-206

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FIGURE 25

CTGCTTGGATACCTCCAGTCCCCAACTGTGTTCCAGGAGTTTTCTTGGCCGAAGCTGCCCCGA
TGTTTGGAGCCTTTTCTTCCCAGAGAAGAAGATGGACTGAAAGCTGCCAGTTGGGGACTTTTTG
TGATCACGGCGTTGCAGCGTTTTAAAGGAGGTGATGGGGCTTGCGCTGGCTTGTCTTCCCACC
CAAGTGAAGAGTTGATGTTCACTGGTTATGCTTAGACAATGTGCAGTTTGTGTTAATTTAAAA
TTTTGGGTGGGATAGGGGCATAGGCTTGTGAAGGGCAGTCCGGATCCGGAGGAACTCGTCTTT
GTCCCTGGTAGGAGAGACACCCCCAGTCTATCCTCGATGCCGTGAGCCTTGGCCATCTTCACT
TGCCGCCCCGAAGCTCGCACCCGTTTCAGGAGCGTCATGTCTACCTGGACGAGCCCATCAAATC
GGCCGCTCAGTGGCCCGCTGTGACACCAGCGCAGAATAATGCCACTTTTGATTGCAAAGTGCTA
TCAAGGAACACGCTCTCGTCTGGTTGATCACAAAGACGGGCAAGTTTTATCTTCAAGACACT
AAAAGTAGTAATGGTACTTTTATAAATAGCCAGAGATTGAGTCGAGGCTCTGAAGAAAGTCCA
CCATGTGAAATTTCTTCCGGTGACATTATCCAGTTTGGAGTAGACGTGACAGAGAATACACGG
AAAGTTACCCATGGGTGTATTGTTTCCACAATAAACTTTTTCTACCAGATGGTATGGAAGCC
CGGCTCCGCTCAGATGTCTATCCATGCACCATTACCAAGTCCTGTTGACAAAGTTGCTGCTAAC
ACTCCAAGTATGTACTCTCAGGAAGTATTCCAGCTTTTCTCAGTATCTACAGGAGGCCTTACAT
CGGGAACAAATGTTGGAACAGAAGTTAGCCACGCTTCAGCGGCTACTAGCCATCACCCAAGAG
GCTTCAGATACCAGTTGGCAGGCTTTAATAGATGAAGATAGACTCTTATCACGGTTAGAAGTT
ATGGGAAACCAATTACAGGCATGCTCCAAAAATCAAACAGAAGATAGTTTACGAAAGGAACTT
ATAGCATTACAAGAGGATAAACATAACTATGAGACAACAGCCAAAGAGTCCCTGAGGCGGGTT
CTTCAGGAGAAAATTGAAGTGGTTAGAAAACCTTTCAGAAGTTGAGCGAAGTCTGAGTAATACT
GAAGATGAATGTACCCATCTGAAAGAAATGAATGAAAGGACTCAGGAAGAATTAAGAGAATTA
GCCAACAAATATAATGGAGCAGTTAATGAGATTAAAGATTTATCTGATAAATTAAGGTAGCA
GAGGGAAAACAAGAGGAAATCCAACAGAAGGGACAGGCTGAGAAAAAAGAATTACAACATAAA
ATAGATGAAATGGAAGAAAAAGAACAGGAGCTCCAGGCAAAAATAGAAGCTTTGCAAGCTGAT
AATGATTTTACCAATGAAAGGCTAACAGCTTTACAAGTACGGTTAGAACATCTTCAGGAGAAA
ACTCTTAAAGAAATGCAGCAGCTTGGCTGATCGTCAAGGGCATCTAACCAAAGCGGTAGAAGA
AACAAAGCTTTCAAAGGTTTGTCTTCTGTTTTCTATGTTTTTTGACAGTTCTTTTGGATAA
TGAAGGTTAGTGTATATTTTCAAGGTTATAGTATTTTAAACCATCAGTTTACTTCTTATAGCTC
ACAAAATAGCAAGCCAGTAACAGTATCAGATAATATATAAAATAATCAGACTTCTGTTTTAAG
AAGGGTATCGTAAGTGAATGTGTCTTTTTAAGTGGATGTATATTTATGGTTTTTTGAATGTT
AGTACTTGATATAGGTTTCTTTAGGTATTAAAGATTTGTTGCAATCTCTGTCAATCCCAGCAT
TAATTTTCAGCTTTGATCTCAAATTTTAAATCAAACACAATGTAAGTCGTTTGTGATACAACCTA
AGTGAAACATGCTTGCACTTCTATTTTGGGGGTACAGTACCTTTAAATCTCTTATGATGTT
TAATATTTCCCTAATTTTTTGGCATCTCAGTTTGATTTAAACAAAATTAATGACTTTTGTGAAT
GTAGAATCTTCTTATATTTTATGAGTAGTCCAGTAATTGCCCAAAGTAGTTTATTGTGTTAAT
TCTGTTACAGTTGTCAGAGAAGAAAAGTGAGTTTAAAGCACCATATTGTCAAGTCACTTTTA
TACATAGGGAAATTAGGCAAATAAATTTGGTGGCATGTGTTTATCATAGTAGAACTTTCATTA
GACTATACCAGTATAAAATTTAAACTAGATTACAGTCCTTTTGGCCAATTAACAACTTGAG
TTACAAAAGTTTGAGATACTTAATTTTAGTACATTCTATTTTATTAAAGTAACTGGATTCAAT
TGACTTTTTTAACCATGTAAGAGGATGGTGTATTTCAAATATCTCGTGGTTTCCATTCTGAA
TTTTGTGCACGGCAGATGCCATATTTGGGGAAAAAATGCATAGAATATGCATCATTAAATATTG
TTTTGGCAAACAGGCATTGAGTTTCAGAACAGTGAAGTATTTTATGATACATATGGCAATTTTT
TTCACCTTATTAAAGTGAGATGAGAACAGACCTTAAATAGCTTTTACCTCACCATCCAAATA
CCTATTCAGATTAGTTGGTTGAATAGCCAGCACTTTGAAGTAGAGCCTTAGG

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FIGURE 26

MEARLRSDVIHAPLPSPVDKVAANTPSMYSQELFQLSQYLQEALHREQMLEQKLATLQRLAI
TQEASDTSWQALIDEDRLLSRLEVGMGNQLQACSKNQTEDSLRKELIALQEDKHNYETTAKESL
RRVLQEKIEVVRKLSEVERSLSNTEDECTHLKEMNERTQEELRELANKYNGAVNEIKDLSDKL
KVAEGKQEEIQQKGQAEKKELQHKIDEMEEKEQELQAKIEALQADNDFTNERLTALQVRLEHL
QEKTLEKCSSLADRRRASNQSGRRNKAFKRFVFCFSMFFDSSFG

Important features of the protein:**N-glycosylation sites.**

amino acids 98-102, 271-275

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 138-142, 267-271

Amidation site.

amino acids 273-277

Tropomyosins proteins.

amino acids 169-217

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FIGURE 27

GAACCTGGCGCCGCCGGAACCTGATCGCGGCCTAGTCCCGACGCGTGTGTGCTAGTGAGCCGGA
GCCGGCGACGGCGGCAGTGGCGGCCCGGCCTGCAGGAGCCCGACGGGGTCTCTGCCATGGGGG
AGTGACGCGCCTGCACCCGCTGTTCCGCGGCAGCGGCGAGACATGAGGAGACCCCGCGACAGG
GGCAGCGGCGGCGGCTCGTGAGCCCCGGG**GATGG**AGGAGAAATACGGCGGGGACGTGCTGGCCG
GCCCCGGCGGCGGCGGCGGCCTTGGGCGGGTGGACGTACCCAGCGCTCGATTAAACAAAATATA
TTGTGTTACTATGTTTCACTAAATTTTTGAAGGCTGTGGGACTTTTTCGAATCATATGATCTCC
TAAAAGCTGTTTCACATTGTTTCAGTTCATTTTTATATTAAACTTGGGACTGCATTTTTTATGG
TTTTGTTTCAAAAGCCATTTTCTTCTGGGAAAACCTATTACCAAACACCAAGTGGATCAAAATAT
TTAAACATGCAGTTGCTGGGTGTATTATTTCACTCTTGTGGTTTTTTTGGCCTCACTCTTTGTG
GACCACTAAGGACTTTGCTGCTATTTGAGCACAGTGATATTGTTGTCAATTTCACTACTCAGTG
TTTTGTTTACCAGTTCTGGAGGAGGACCAGCAAAGACAAGGGGAGCTGCTTTTTTTCATTATTG
CTGTGATCTGTTTATTGCTTTTTGACAATGATGATCTCATGGCTAAAATGGCTGAACACCCTG
AAGGACATCATGACAGTGCTCTAACTCATATGCTTTACACAGCCATTGCCTTCTTAGGTGTGG
CAGATCACAAAGGTGGAGTATTATTGCTAGTACTGGCTTTGTGTTGTAAAGTTGGTTTTTCATA
CAGCTTCCAGAAAGCTCTCTGTGCGACGTTGGTGGAGCTAAACGTCTTCAAGCTTTATCTCATC
TTGTTTCTGTGCTTCTCTTGTGCCCATGGGTCATTGTTCTTTCTGTGACAACTGAGAGTAAAG
TGGAGTCTTGGTTTTTCTCTCATTATGCCTTTTGCAACGGTTATCTTTTTTGTGCATGATCCTGG
ATTTCTACGTGGATTCCATTTGTTTCAGTCAAATGGAAGTTTCCAAATGTGCTCGTTATGGAT
CCTTTCCCATTTTTATTAGTGCTCTCCTTTTTTGGAATTTTTTGACACATCCAATAACAGACC
AGCTTCGGGCTATGAACAAAGCAGCACACCAGGAGAGCACTGAACACGTCCTGTCTGGAGGAG
TGGTAGTGAGTGCTATATTCTTCATTTTGTCTGCCAATATCTTATCATCTCCCTCTAAGAGAG
GACAAAAGGTACCCTTATTGGATATTCTCCTGAAGGAACACCTCTTTATAACTTCATGGGTG
ATGCTTTTTCAGCATAGCTCTCAATCGATCCCTAGGTTTATTAAGGAATCACTAAAACAAATTC
TTGAGGAGAGTGACTCTAGGCAGATCTTTTACTTCTTGTGCTTGAATCTGCTTTTTTACCTTTG
TGGAATTATTCTATGGCGTGCTGACCAATAGTCTGGGCCTGATCTCGGATGGATTCCACATGC
TTTTTGACTGCTCTGCTTTAGTCATGGGACTTTTTGCTGCCCTGATGAGTAGGTGGAAAGCCA
CTCGGATTTTCTCCTATGGGTACGGCCGAATAGAAATTCTGTCTGGATTATTAATGGACTTT
TTCTAATAGTAATAGCGTTTTTGTGTTTATGGAGTCAGTGGCTAGATTGATTGATCCTCCAG
AATTAGACACTCACATGTTAACACCAGTCTCAGTTGGAGGGCTGATAGTAAACCTTATTGGTA
TCTGTGCCTTTAGCCATGCCCATAGCCATGCCCATGGAGCTTCTCAAGGAAGCTGTCACTCAT
CTGATCACAGCCATTACACCATATGCATGGACACAGTGACCATGGGCATGGTCACAGCCACG
GATCTGCGGGTGGAGGCATGAATGCTAACATGAGGGGTGTATTTCTACATGTTTTGGCAGATA
CACTTGGCAGCATTGGTGTGATCGTATCCACAGTTCTTATAGAGCAGTTGGATGGTTCATCG
CTGACCCACTCTGTTCTCTTTCTACTGCTATATTAATATTTCTCAGTGTGTTCCACTGATTA
AAGATGCCTGCCAGGTTCTACTCCTGAGATTGCCACCAGAATATGAAAAAGAACTACATATTG
CTTTAGAAAAGATACAGAAAATTGAAGGATTAATATCATACCGAGACCCTCATTTTTTGGCGTC
ATTCTGCTAGTATTGTGGCAGGAACAATTCATATACAGGTGACATCTGATGTGCTAGAACAAA
GAATAGTACAGCAGGTTACAGGAATACTTAAAGATGCTGGAGTAAACAATTTAACAATTCAG
TGGAAAAGGAGGCATACTTCAACATATGTCTGGCCTAAGTACTGGATTTCATGATGTTCTGG
CTATGACAAAACAAATGGAATCCATGAAATACTGCAAAGATGGTACTTACATCATG**TGAG**ATA
ACTCAAGAATTACCCCTGGAGAATAAACAATGAAGATTAAATGACTCAGTATTTGTAATATTG
CCAGAAGGATAAAAATTACACATTAAGTGTACAGAAACAGAGTTCCTACTACTGGATCAAGG
AATCTTTCTTGAAGGAAATTTAAATACAGAATGAAACATTAATGGTAAAAAAA

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FIGURE 28

MEEKYGGDVLAGPGGGGGLGPVDVPSARLTKYIVLLCFTKFLKAVGLFESYDLLKAVHIVQFI
FILKLGTAFFMVLFFQKPFSSGKTITKHQWIKIFKHAVAGCIISLLWFFGLTLCGPLRTLLLF
HSDIVVISLLSVLFTSSGGGPAKTRGAFFIIIAVICLLLFNDNDLMAKMAEHPEGHHDSALTH
MLYTAIAFLGVADHKGGVLLLVLAALCKVGFHTASRKLSVDVGGAKRLQALSHLVSVLLCPW
VIVLSVTTESKVESWFSLIMPFATVIFVVMILDFYVDSICSVKMEVSKCARYGSFPFIFISALL
FGNFWTHPITDQLRAMNKAHQESTEHVLSGGVVVSAIFFILSANILSSPSKRGQKGTIGYS
PEGTPLYNFMGDAFQHSQSIPRFIKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTN
SLGLISDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGFINGLFLIVIAFFVF
MESVARLIDPPELDTHMLTPVSVGGLIVNLIGICAFSHAHSHAHGASQGSCHSSDHS SHMH
GHS DHGHGSHSGSAGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIADPLCSLSTA
ILIFLSVVPLIKDACQVLLRLPPEYEKELHIALEKIQKIEGLISYRDPHFWRHSASIVAGTI
HIQVTSDVLEQRIVQQVTGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMESMK
YCKDGTIIM

Important features of the protein:**Signal peptide:**

amino acids 1-46

Transmembrane domains:amino acids 59-77, 101-119, 150-167, 205-223, 239-258, 267-284,
305-324, 343-360, 421-440, 452-469, 486-505, 522-539, 592-612,
621-641**N-glycosylation site.**

amino acids 721-725

Glycosaminoglycan attachment site.

amino acids 143-147

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 225-229

Tyrosine kinase phosphorylation sites.

amino acids 750-758, 756-764

N-myristoylation sites.amino acids 14-20, 46-52, 102-108, 112-118, 144-150, 317-323,
347-353, 369-375, 372-378, 437-443, 462-468, 529-535, 549-555,
553-559, 579-585, 582-588, 583-589, 584-590, 605-611, 737-743**Multicopper oxidases protein:**

amino acids 561-569

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FIGURE 29

GGCACGAGGGCAGGATATTAGAAATGGCTACTCCCCAGTCAATTTTCATCTTTGCAATCTGCA
TTTTAATGATAACAGAATTAATTCTGGCCTCAAAAAGCTACTATGATATCTTAGGTGTGCCAA
AATCGGCATCAGAGCGCCAAATCAAGAAGGCCTTTCACAAGTTGGCCATGAAGTACCACCCTG
ACAAAAATAAGAGCCCGGATGCTGAAGCAAATTCAGAGAGATTGCAGAAGCATATGAAACAC
TCTCAGATGCTAATAGACGAAAAGAGTATGATACACTTGGACACAGTGCTTTTACTAGTGGTA
AAGGACAAAGAGGTAGTGGAAGTTCTTTTGAGCAGTCATTTAACTTCAATTTTGATGACTTAT
TTAAAGACTTTGGCTTTTTTGGTCAAAACCAAAACACTGGATCCAAGAAGCGTTTTGAAAATC
ATTTCCAGACACGCCAGGATGGTGGTTCAGTAGACAAAGGCATCATTTCCAAGAATTTTCTT
TTGGAGGTGGATTATTTGATGACATGTTTGAAGATATGGAGAAAATGTTTTCTTTTAGTGGTT
TTGACTCTACCAATCAGCATAACAGTACAGACTGAAAATAGATTTTCATGGATCTAGCAAGCACT
GCAGGACTGTCACTCAACGAAGAGGAAATATGGTTACTACATACACTGACTGTTTCAGGACAGT
AGTTCTTATTCTATTCTCACTAAATCCAACCTGGTTGACTCTTCCTCATTATCTTTGATGCTAA
ACAATTTTCTGTGAACATTTTTGACAAGTGCATGATTTCACTTTAAACAATTTGATATAGCTA
TTAAATATATTTAAGGGTTTTTTTTTTTTTGACAAATTCAACATTCAACGAGTAGACAAAATGCT
AATTATTTCCCTGATTAGGAAAGTTTCTTTAAAAAACACGTAATTTTGCCTAGTGCTTTTTTCT
CTACCTGCCCTTGGGCTCACTAATATCACCAGTATTATTACCAAGAAAATATTGAGTTTACCT
GATTAACTTTTAAAGTTAATTGTAGATTTAAATTGTGTGAACCTAATGATTTTTGCAGTGAA
ACCTTTACTAATTCAAAGTTGCATGTTCTATGACATCTGTGACTTGCGTTGCAGAGTGACAT
GAACTGTATAATTGAGTCATTCAGTAAAGGAGAACAGTATCTTGGTTAATTGCTACTGAAAG
GTTGAGAAAGGAATGGTTTGATATTTACCACAGCGCTGTGCCTTTCTACAGTAGAACTGGGGT
AAAGGAAATGGTTTTATTGCCCATAGTCATTTAGGCTGGAAAAAAGTTGAAAACCTTAACGAAA
TATTGCCAAGAGATTGTTATGTGTTTGGTTCCAGCCTAAAAATGATTTTGAGTGTTGAAATC
ATAGCTACTTACATAGCTTTTTTCATATTTCTTTCTTAGTTGTTGGCACTCTTAGGTCTTAGTA
TGGATTTATGTGTTTGTGTGTGTGTAGTTTATCCTCTCTCTCATCTTTATCTAGAGATTGACT
GATACCTCATTCTGTTTGTAACACAGCCAGTAATTTCTGTGCAACCTTACTATGTGCAATAT
TTTTAAATCCTGAGAAATGTGTGCTTTTGTTCGGATAGACTTATTTCTTTAGTTCTGCACT
TTTCCACATTATACTCCATATGAGTATTAATCCTATGGATACATATTAAACAAGTGTCTCAT

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FIGURE 30

MATPQSIFIFAICILMITELILASKSYYDILGVPKSASERQIKKAFHKLAMKYHPDKNKSPDA
EAKFREIAEAYETLS DANRRKEYDTLGHSAFTSGKGQRGSGSSFEQSFNFNFDDLKDFGFFG
QNQNTGSKKRFENHFQTRQDGGSSRQRHHFQEFSFGGGLFDDMFEDMEKMFSFSGFDSTNQHT
VQTENRFHGSSKHCRTVTQRRGNMVTYTD CSGQ

Important features of the protein:

Signal peptide:

amino acids 1-23

Nt-dnaJ domain signature.

amino acids 27-59, 66-90

Glycosaminoglycan attachment site.

amino acids 96-100

N-myristoylation sites.

amino acids 32-38, 99-105, 102-108, 126-132, 211-217

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FIGURE 31

AAAGTTACATTTTCTCTGGAACCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTGG
GCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACAAT
TCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCTGAG
ATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCAAATG
CAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCTACGCA
TTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTCTCTGTA
CTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGAAACAGTG
TACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCTGGATCCCC
AGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATCACGGCCACT
GTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTGGAGCATCCTG
AAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGATCACCAAAGAT
GGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTCCTTGTGGCCTAC
TGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGGGGGTATTCCAGTG
CACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGACATTTCGTGAAGGCC
ATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAAGGAGAGGCCATTCCC
CTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGTGGTCGTGCCACTGTTC
GTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGGTGGTCCTCCCAGACACC
TTGAAAATAACCAATTACCCCAAGTAAATCAGCTGCAGAAGGGAGGAGGTGGATGCCTGT
GCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGATCTCATAGGTTTGCGGAAGG
GCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACCATGAGGGGACAAGTTGTGTT
TCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTCTAG
AAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACTGACTGAGGCTTAGGGGATGTG
ACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACCCTGGGAAAAGTGACTTCATCCCT
TCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACCTACACACCTGCTAAACACACACAC
ACAGAGTCTCTCTATATATACACACGTACACATAAATACACCCAGCACTTGCAAGGCTAGA
GGGAAACTGGTGACACTCTACAGTCTGACTGATTCAGTGTCTTCTGGAGAGCAGGACATAAATG
TATGATGAGAATGATCAAGGACTCTACACACTGGGTGGCTTGAGAGAGCCACTTTCCCAGAAT
AATCCTTGAGAGAAAAGGAATCATGGGAGCAATGGTGTGAGTTCACTTCAAGCCCAATGCCG
GTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGTAGGTGACCTGGAGGAAGGTCACAGCCACA
CTGAAAATGGGATGTGCATGAACACGGAGGATCCATGAACTACTGTAAAGTGTGACAGTGTG
TGCACACTGCAGACAGCAGGTGAAATGTATGTGTGCAATGCGACGAGAATGCAGAAGTCAGTA
ACATGTGCATGTTTGTGTGCTCCTTTTTTCTGTTGGTAAAGTACAGAATTCAGCAAATAAAA
AGGGCCACCCTGGCCAAAAGCGGTAAAAA

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FIGURE 32

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGET
VYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSI
LKHPFNRNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSGGIP
VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFVGFM LILVVVPL
FVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-44, 134-138

Tissue factor proteins.

amino acids 92-120

Integrins alpha chain proteins.

amino acids 232-263

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FIGURE 33

GAGACACGCGAGCGGGGAGACCTCCAAGGCAGCGAGGCATCGGACATGTGTGTCAGCACATCTGG
GGCGCACATCCGTCGAGCCCCGAGGGGAGATTTGCCGGAACAATTCAAACCTGCGATATTGATCT
TGGGGGTGACTGTCCCTGGCCGGCTGTCCGGTGGGAGTGCAGTGTGCACTCGCTCGGAAGTG
TGTGCGAGTGTGTATGTGTGTGTGCCGTGTCCGGCTCCCCCCTTCCCCCGTTTTCCCGTCGA
GTGATGCACTTGGAATGAGAATCAGAGGATGGAAATAGTCTGGGAGGTGCTTTTTCTTCTTCA
AGCCAATTTTCATCGTCTGCATATCAGCTCAACAGAATTCACCAAAAATCCATGAAGGCTGGTG
GGCATAACAAGGAGGTGGTCCAGGGAAGCTTTGTTCCAGTTCCTTCTTCTGGGGATTGGTGAA
CTCAGCTTGGAATCTTTGCTCTGTGGGGAAACGGCAGTCGCCAGTCAACATAGAGACCAGTCA
CATGATCTTCGACCCCTTTCTGACACCTCTTCGCATCAACACGGGGGGCAGGAAGGTCAGTGG
GACCATGTACAACACTGGAAGACACGTATCCCTTCGCCTGGACAAGGAGCACTTGGTCAACAT
ATCTGGAGGGCCCATGACATACAGCCACCGGCTGGAGGAGATCCGACTACACTTTGGGAGTGA
GGACAGCCAAGGGTCGGAGCACCTCCTCAATGGACAGGCCTTCTCTGGGGAGGTGCAGCTCAT
CCACTATAACCATGAGCTATATACGAATGTCACAGAAGCTGCAAAGAGTCCAAATGGATTGGT
GGTAGTTTTCTATATTTATAAAAGTTTCTGATTCATCAAACCCATTTCTTAATCGAATGCTCAA
CAGAGATACTATCACAAGAATAACATATAAAAAATGATGCATATTTACTACAGGGGCTTAATAT
AGAGGAACATATCCAGAGACCTCTAGTTTCATCACTTACGATGGGTGATGACTATCCCACC
CTGCTATGAGACAGCAAGTTGGATCATAATGAACAAACCTGTCTATATAACCAGGATGCAGAT
GCATTCTTTGCGCCTGCTCAGCCAGAACCAGCCATCTCAGATCTTTCTGAGCATGAGTGACAA
CTTCAGGCCTGTCCAGCCACTCAACAACCGCTGCATCCGCACCAATATCAACTTCAGTTTACA
GGGGAAGGACTGTCCAAACAACCGAGCCCAGAAGCTTCAGTATAGAGTAAATGAATGGCTCCT
CAAGTAGGGGAACAAAGCCAAGAAGATCCACCTCAGTGAAATGCTACAACCTGTGAATTGACG
TAACCTAGAATGTCCCCCTTCTTGCTTCTCTCTCCTTCTTTCCCCCAAGCCTCATTCTTCTT
GGGATTGGCCCTTTCTTCATGAAAAGTGTCTGCGAAACCATGGCAGAGGAATACATCTCTCAC
ACATACTCACAAACACACACACAAGCACTTGACATACATACAAACACATGCAAAACATACCTA
CACACACACACTCTCTTACAACCTCCATCATGGGAAGTCAAGTTTCAGAAACAAAAGTCTCAT
TCATAAGAGGTCTTAGAAGAAAATAACCAGTTAACCTGATTTCAATTTTGATACCGTTTTCT
GAACTAATAAATCTACCCAATGAGACTTTTCAGCCTTTGTACATACAAAATTCTTCCAAAAGA
GAGAGGAGAAAATACAGCTCTGATGGCATCAAACGGACTTTGCATCAAGTAATTTAGATAGT
GTCCTAGGATCCTTTGAGGGTGTGGTAGCAGGTGAGCAGGACAAAGTTGACCAAGGACACTT
ATTTCTAGATTATGATTCTTCTGTTTACTCAACAATTTACAAAGAAAAAAGGACAGACATTG
AAGAGCTACACATTGTATATATATCACCACAGACTATAAGGAAATGGAATTATTTCCCTCTTT
GTCACATATCTGTAGTAGGATTTGCCAAGATCAGAAATGATCCATTTGCTGTTTCTTGTTTTT
CAAAGGTCATACATTGTGTTTGGTTATTGTTACCAGCTCAATAAATGTGTTTAAACGAGTTAAT
TTCATTTTTCTGGCTTTGGTCTGTTCTCCTTCCCTACAGGCTAAGCCCTGGCTCCATGCAACT
GCATTCTTTGATTTCACTTGTTCCTTCATCTACATGTTTTGTTTCAATTTGCAGCCAGTTTTTAC
TGAGTTTGTGGCAATCAGGAATGCATTTGCTAAGCAAGTATGACTTTAATTCCACTCCATGGC
TCAATCATTACATGAGGTGAGCTTCAGCCTGAGATAGCAGGCGACAGACTTCTTGCGTTTTCA
AACTGCCATGCCCCCTGTGATGCTCCCGTGAAGGAATGCACTTTGCCTTGTAAGTTCCTGG
GAAAGGGGTATGTTTTCTCTCCAGGTGCAGCCAGATCTCACAAAGTACAAAACGAATGCCTTT
CTTTCTTGTTTATAATGGTCACTCACTGTGTTGGTTACTGTCAAGAAATCAATAAATGTGT
TTAACAAGTTA

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FIGURE 34

MEIVWEVLFLQLQANFIVCISAQQNSPKIHEGWWAYKEVVQGSFVPVPSFWGLVNSAWNLCSVG
KRQSPVNIETSHMIFDPFLTPLRINTGGRKVS GMTMYNTGRHVSLRLDKEHLVNI SGGPMTYSH
RLEEIRLHFGSEDSQGSEHLLNGQAFSGEVQLIHYNHELYTNVTEAAKSPNGLVVVSIFIKVS
DSSNPFLNRMLNRDTITRITYKNDAYLLQGLNIEELYPETSSFITYDGSMTIPPCYETASWII
MNKPVYITRMQMHSRLRLSQNQPSQIFLSMSDNFRPVQPLNNRCIRTNINFSLQKDCPNNRA
QKLQYRVNEWLLK

Important features:**Signal peptide:**

amino acids 1-20

Eukaryotic-type carbonic anhydrases proteins.

amino acids 126-162, 220-269, 43-91

N-glycosylation sites.

amino acids 116-119, 168-171, 302-305

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FIGURE 35

GTCGGAACCCCTCAGGCCACCCTCGGGAGTCTGGGGTCCAGAGGGGTGTCCCTGTACCCCTTGAC
ACAGGACCCTCACTCTGCAGGGATAAGCCAGCTGCGCCTGCAGCCTAGGGTGCCAAGGAGGCTGCTGA
TTGTGGCCACAGCCTCATCTGAACGCCAGGAGACCAGGATACCGAGGCACCGGATCCCTCTCTGTG
CCCTGGGGAGCCCCAGTGCTGCCAGTCACCCAGGGCTGAGGTCTGCGTCCCTAGTGGTGCAAGGCC
TGGTAGGACCACGGGGCAGGGAATGTGAGCGCCATCCGAGCTCACGGTGTCTTGAGTCGCGGCTTCGT
GACTTTGGCAGGGGCTCCGGACCAGTGACCCAGTCAAACCCAGAGGGTCTTGGGCGGCAGCGACGA
AGGAGGTATTAGGCTCCAGGCCAGGTGGGGCCGAGCGCCCCAGCCATCCACCATGGTGGTGGCACA
CCCCACCGCCACTGCCACCACCACGCCACTGCCACTGTACGGCCACCGTTGTGATGACCACGGCCA
CCATGGACCTGCGGGACTGGCTGTTCTCTGCTACGGGCTCATCGCCTTCCTGACGGAGGTTCATCGAC
AGCACCACTGCCCCCTCGGTGTGCCGTGCGACAACGGCTTCATCTACTGCAACGACCGGGGACTCAC
ATCCATCCCCGCAGATATCCCTGATGACGCCACCACCCTCTACCTGCAGAACAACCAGATCAACAACG
CCGGCATCCCCAGGACCTCAAGACCAAGGTCAACGTGCAGGTTCATCTACCTATACGAGAATGACCTG
GATGAGTTCCCATCAACCTGCCCCGCTCCCTCCGGGAGCTGCACCTGCAGGACAACAATGTGCGCAC
CATTGCCAGGGACTCGCTGGCCCGCATCCCGCTGCTGGAGAAGCTGCACCTGGATGACAACCTCCGTGT
CCACCGTCAGCATTGAGGAGGACGCTTCGCCGACAGCAAACAGCTCAAGCTGCTCTTCCTGAGCCGG
AACCACCTGAGCAGCATCCCTCGGGGCTGCCGCACACGCTGGAGGAGCTGCGGCTGGATGACAACCG
CATCTCCACCATCCCGCTGCATGCCTTCAAGGGCTCAACAGCCTGCGGCGCCTGGTGCTGGACGGTA
ACCTGCTGGCCAACCAGCGCATCGCCGACGACACCTTCAGCCGCTACAGAACCTCACAGAGCTCTCG
CTGGTGCGCAATTGCTGGCCGCGCCACCCCTCAACCTGCCAGCGCCACCTGCAGAGCTCTACCT
GCAGGACAATGCCATCAGCCACATCCCTACAACACGCTGGCCAAGATGCGTGAGCTGGAGCGGCTGG
ACCTGTCCAACAACAACCTGACCACGCTGCCCCGCGGCTGTTGACGACCTGGGGAACCTGGCCAG
CTGCTGCTCAGGAACAACCTTGGTTTTGTGGCTGCAACCTCATGTGGCTGCGGGACTGGGTGAAGGC
ACGGGCGGCGCTGGTCAACGTGCGGGGCTCATGTGCCAGGGCCCTGAGAAGGTCCGGGGCATGGCCA
TCAAGGACATTACCAGCGAGATGGACGAGTGTGTTTGGACGGGGCCGAGGGCGGCGTGGCCAATGCG
GCTGCCAAGACCACGGCCAGCAACCACGCCTCTGCCACCACGCCCCAGGGTTCCTGTTTACCCCTCAA
GGCCAAAAGGCCAGGGCTGCGCCTCCCCGACTCCAACATTGACTACCCCATGGCCACGGGTGATGGCG
CCAAGACCCTGGCCATCCACGTGAAGGCCCTGACGGCAGACTCCATCCGCATCACGTGGAAGGCCACG
CTCCCCGCCTCCTCTTTCCGGCTCAGTTGGCTGCGCCTGGGCCACAGCCCAGCCGTGGGCTCCATCAC
GGAGACCTTGGTGACGGGGGACAAGACAGAGTACCTGCTGACAGCCCTGGAGCCCAAGTCCACCTACA
TCATCTGCATGGTCACCATGGAGACCAGCAATGCCTATGTAGCTGATGAGACACCCGTGTGTGCCAAG
GCAGAGACACCGCAGCTATGGCCCTACCACCACACTCAACCAGGAGCAGAACGCTGGCCCCATGGC
GAGCTTGCCCCCTGGCGGGCATCATCGGCGGGCAGTGGCTCTGGTCTTCCTCTTCTGGTCTGGGG
CCATCTGCTGGTACGTGCACCAGGCTGGCGAGCTGCTGACCCGGGAGAGGGCCTACAACCGGGGCAGC
AGGAAAAAGGATGACTATATGGAGTCAGGGACCAAGAAGGATAACTCCATCCTGGAAATCCGCGGCC
TGGGCTGCAGATGCTGCCCATCAACCCGTACCGCGCCAAAGAGGAGTACGTGGTCCACACTATCTTCC
CCTCCAACGGCAGCAGCCTCTGCAAGGCCACACACACCATTTGGCTACGGCACCACGCGGGGCTACCGG
GACGGCGGCATCCCCGACATAGACTACTCCTACACATTCATGCCCCGCCACCCGGGCTGCCCCGCCTCA
GCCCCAGCTGCCCTGGCGTGCCATGTGGCTTTGCCAGCCTGCTGCAATCCAAGAGAGCAAGGAAGA
GAAATTCCATGGGTGACTTTCTCCGAGAAAGCAAAGTTTGGGGAGGGCTGACGATTTTGTAGAACA
CAACAGTGACAATTTTTTTTTTAAAGAATAGAAGGCAGGAGGGGAATTTCGACATTGTTGAAGACATAA
TTTATACCAAGTTATGCCAGTTGGGGAGGGAAGGACTAAAAATAATATTGCAGGCAGGGCTGGGTGG
GTTTTTTTTTTTTCCCCCTGAACTGGAAGGATACTACCTGTACAACATCTGTGGACACCTCATGCTCT
GTTCAAGGCCATCACAAGGAACCGCCAGGGAGAAGCAGCCGGCTCTCAAAGCTCCCACGAGCTCTC
CCGCACTGGCCACTCGCTGGCGACCCGATGGAAGTTTTCAGGCTCCTCACAAGGAGAGAGGGAAG
AAAAGATCTTTTGGCCTGGAGATATGGTCTGAAATCTCTCCCTGGCTTATTCCATACCATTTCCCT
TGCAGATTTGCAGAAACATGGCATCTTTCAGTGCATTCTTTGAACAATCATGTAGTCGATTAAAAAAA
AAAACAACTTTTTTTTTTCTAGGCTGAAGCCCTCTTCAGTTCCATGCACCACGCTCCGTAGAAGCCCC
GGCGGAAGCCGTAGCTTTCCCTGCCACCTGGAGGTGCATCTGTCTGCCTGTCTATCCCTGTGCGGGTG
TCTCTAAGTACAGATGGGTAGATAGAGCCACATGCACGGTCCTTACCGTTCTTCTTGGGTGAGTTCTT
ACCATTTCTGAACAATAGAATTGTGAAAGTGTTAAAAA

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FIGURE 36

MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRCNDG
FIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDEFPINLP
RSLRELHLQDNNVRTIARDSLARIPLEKLHLLDDNSVSTVSIIEEAFADSKQLKLLFLSRNHL
SSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIADDTFSRLQNLTE
LSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLDLSNNNLTTLP RGLFD
DLGNLAQLLLRNNPWFCGCNLMWLRDWVKARAAVVNV RGLMCQGPEKVRGMAIKDITSEMDEC
FETGPQGGVANAAAKTTASNHASATTPQGSFLT LKAKRPGLRLPDSNIDYPMATGDGAKTLAI
HVKALTADSIRITWKATLPASSFRLSWLR LGHSPAVGSITETLVQGDKTEYLLTALEPKSTYI
ICMVTMETS NAYVADETPVCAKAETADSYGPTTTLNQE QNAGPMASLPLAGIIGGAVALVFLF
LVLGAICWYVHQAGELLTRERAYNRGSRKKDDYME SGTKKDNSILEIRGPGLQMLPINPYRAK
EEYVVHTIFPSNGSSLCKATHTIGYGTTRGYRDGGIPDIDYSYT

Important features of the protein:

Transmembrane domain:

amino acids 552-573

N-glycosylation sites.

amino acids 249-252, 305-308, 642-645

Leucine zipper pattern.

amino acids 182-203, 299-320

Phospholipase A2 aspartic acid active site.

amino acids 57-67

FIGURE 37

[illegible]

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FIGURE 38

MAEPGSHHLSARVRRRTERRIPRLWRLLLWAGTAFQVTQGTGPELHACKESEYHYEYTACDS
TGSRRWRVAVPHTPGLCTSLSDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGTGIRFDE
WDELPHGFASLSANMELDDSAESTGNCTSSKWVPRGDYIASNTDECTATLMYAVNLKQSGTV
NFEYYPDSSIIFFEFFVQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNNVLYWRTTAFSVW
TKVPKPVLVRNIAITGVAYTSECFPCPKPGTYADKQSSSFCKLCPANSYSNKGETSCHQCDDPK
YSEKSSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKICSEDLEGAVKLPASGVKTH
CPPCNPGGFFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVGFEYKWWNTLPTNMETTTLVSGI
NFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLLVVPGFRPPQSVMAADTENKEVARITFVFETL
CSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYIIIEENTTTSTFWAFQRTTFHEASRKYTN
DVAKIYSINVTNVMNGVASYCRPCALEASDVGSSCTSCPAGYYIDRDSGTCHSCPPNTILKAH
QPYGVQACVPCGPGTKNNKIHSCLYNDCTFSRNTPTRTFNYNFSALANTVTLAGGPSFTSKGL
KYFHHFTLSLCGNQGRKMSVCTDNVTDLRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVS
SQPVSLADRLIGVTTDMTLDGITS PAELFHLES LGIPDVIFFYRSNDVTQSCSSGRSTTIRVR
CSPQKTVPGLSLLPGTCS DGTCDGCNFHFLWESAAACPLCSVADYHAIVSSCVAGIQXTTYVX
REPKLCSGGISLPEQRTICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLV
MNATLKDCLPAADSCAIMEGEDVEDDLIFTSKKS LFGKIKSFTSKRTPDGFDSPVPLKTSSGG
PDMDL

Important features of the protein:**N-glycosylation sites:**

amino acids 153-156, 390-393, 391-394, 404-407, 544-547, 576-579,
672-675, 717-720, 947-950

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

amino acids 15-18, 563-566, 709-712

Casein kinase II phosphorylation sites:

amino acids 42-45, 59-62, 81-84, 146-149, 168-171, 282-285, 331-
334, 340-343, 431-434, 449-452, 465-468, 523-526, 557-560, 761-
764, 780-783, 835-838, 860-863, 893-896, 949-952

Tyrosine kinase phosphorylation sites:

amino acids 50-56, 109-116

N-myristoylation sites:

amino acids 77-82, 88-93, 152-157, 268-273, 288-293, 320-325,
400-405, 405-410, 414-419, 463-468, 599-604, 616-621, 634-639,
644-649, 839-844, 874-879, 912-917, 916-921

Amidation site:

amino acids 707-710

Cell attachment sequence:

amino acids 162-164

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FIGURE 39

GGGAAGGGGTTCTGGGCTGCCGCAGGCACACAGGCCAGAGCTTCGTGGATACCTGCAGGGCCC
AAAGGTCCCTCCCTGTTTTGAAGAGTGAGTGATGGCTATGAGGTAGCGGCCAGGCTGATCACC
CCTGCGTTGGCTGGAGGCAGAATTCTGTAAATCCTCGCCAAGTCTTTCTCCAGGGCCACTGGTT
AGCTCATCTCAGCCTCCTCTGGGAGCATCAACACCAACATGGCACAGGGGACTGCAGTGGTGT
GCTTTGGACCTGTGTACCCACCCAAGGCTAAAGGCAGAGCCAGGTGACTTTGCGGGGGTCTCT
TCTCTAGGATTATCTGTACTTCCCCTCTGTCTCTTTTACTACGGGAGATCGAGCTAGCTATA
ACCCACCTTCTTTTCATGAGAACCACACTAAATTGCAAAAATTATCCCAGTGCTGGAGGAGGGC
AGCAGGTTGAGATTATGTTGGCAGGAAGAATGTTGGCATTGATTGGCACGCAGGGGACGAGAG
CTGCTTTGTGCTTTAAAGGAGCCAAGTTACACCCTGTTTAACCCTGCCTTCAAAGGGACGACT
CTGTAAGATTCTCTGCTACTTATTCAAGTTGACACGATGCCCTTCACACTCCACCTGAGGTCC
CGCCTTCCCTCTGCCATAAGGAGTTTGATTCTACAAAAGAAACCAACATCAGAAATACATCC
AGCATGGCTGGAGAGCTCCGACCAGCCAGCCTGGTGGTCTGCCCAGGTCCCTTGCTCCAGCT
TTTGAAAGATTCTGCCAGGTCAACACTGGTCTCTACCCCTGCTGGGCCAGAGTGAGCCAGAA
AAGTGGATGCTGCCCCCTCAAGGTGCTATCTCAGAGACCAGGATGGGCCATCCCCAGTTCTGG
AAATACGAGTTCGGTGCCTGCACCGGTAGCCTGGCTTCGCTGGAGCAGTACTCGGAGCAGCTG
AAGGACATGGTGGCCTTCTTCCCTGGGCTGCAGCTTCTCCCTGGAGGAGGCCTTGGAGAAAGCG
GGGCTCCCCAGAAGAGACCCAGCAGGTCACAGCCAGGCGGGTGCATACAAGACAACAGTGCCT
TGTGTTACCCATGCTGGCTTCTGCTGCCCTCTGGTGGTACGATGAGGCCCATTTCCAAGGAC
AAGCTGGAAGGGCTGGTGCGGGCCTGCTGCTCCCTCGGAGGTGAGCAGGGGGCAACCTGTTTAC
ATGGGCGACCCAGAAGTGTGGGAATCAAAGAGCTTTCCAAACCTGCCTACGGGGATGCCATG
GTGTGTCCCCCAGGGGAGGTTCCAGTGTCTGGCCTTCTCCGCTGACCAGTCTCGGAGCTGTC
AGCAGCTGTGAGACCCCACTGGCTTTTGCCAGCATCCCAGGCTGCACAGTTATGACTGACCTG
AAGGATGCAAAGGCTCCACCTGGTTGTCTACCCCAGAGAGAATTCCAGAGGTCCATCACATT
TCCAAGATCCTCTGCACTACAGCATCGCGTCAGTCTCTGCTTCTCAGAAGATCAGAGAACTA
GAGTCTATGATCGGCATAGACCCAGGGAACCGGGGGATTGGGCACCTGCTCTGTAAAGATGAG
CTGCTGAAGGCCCTCTCTCTCGCTGTCCCATGCCCGCTCAGTGCTCATCACCCTGGGTTCCTCC
ACACATTTCAATCATGAGCCTCCAGAAGAGACAGATGGCCACCAGGAGCTGTTGCTCTGGTT
GCCTTCCTGCAGGCCTTGGAGAAGGAGGTTCGCCATAATCGTTGACCAGAGAGCCTGGAACCTG
CACCAGAAGATTGTTGAAGATGCTGTTGAGCAAGGTGTTCTGAAGACGCAGATCCCGATATTA
ACTTACCAAGGTGGATCAGTGGAAGCTGCTCAGGCATTCTGTGCAAAAATGGGGACCCGCAG
ACACCTAGATTTGACCACCTGGTGGCCATAGAGCGTGCCGGAAGAGCTGCTGATGGCAATTAC
TACAATGCAAGGAAGATGAACATCAAGCACTTGGTTGACCCCATTTGACGATCTTTTTCTTGCT
GCGAAGAAGATTCCTGGAATCTCATCAACTGGAGTCGGTGATGGAGGCAACGAGCTTGGGATG
GGTAAAGTCAAGGAGGCTGTGAGGAGGCACATACGGCACGGGGATGTCATCGCCTGCGACGTG
GAGGCTGACTTTGCCGTCAATTGCTGGTGTCTTAAGTGGGGAGGCTATGCCCTGGCCTGCGCA
CTCTACATCCTGTACTCATGTGCTGTCCACAGTCAGTACCTGAGGAAAGCAGTCGGACCCCTCC
AGGGCACCTGGAGATCAGGCCTGGACTCAGGCCCTCCCGTCCGTCATTAAAGGAAGAAAAAATG
CTGGGCATCTTGGTGCAGCACAAAGTCCGGAGTGGCGTCTCGGGCATCGTGGGCATGGAGGTG
GATGGGCTGCCCTTCCACAACACCCACGCCGAGATGATCCAGAAGCTGGTGGACGTCACCACG
GCACAGGTGTAAACCGTCCATGTTCCGTGTGAGCAGAGTCCCTACCAACGGGCAGGTCTGCATC
CGGGGAGAATGCAGCTGCTTCTGGCGACAATCCTGCTAGTAAACACTGGTCTTCCGTGAGCAA
CGAACACTCGCCTGGCCTGGGAAACTGCATGCCCACTTTCTGGGAGGGGTTAGTGCAGGTGCC
GTGGACAAAGGACAACATTTCTCTGGGGCTTTTTAACTTTTATTCCTAAGACTCTAAAGGCGT
TGATTTCAACCCTCCTTCACTCTGGCTTCTTCAGGCAACCCACGTGGTCTCCTATGAGAATCT
TCTCGACAGTTACTTATGGGGACACTTGTGAACAATTAAGTCCAGGGCAGAGCATGAGAACA
AACATTTCCAGGCCATGTAGGATAGGATACTCCAGACTCCAGTCATCCTCCCCCATCCATGGT
TTCTGTTACTCATGGTTTCAGTTACTCATAGCCAACTGCAGACCGAAAAATACTAAATGAAAAA
TTTCAGAAATAAACAACTCTTAAGTTTAAAAA

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FIGURE 40

MPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAGELRPASLVVLPRSLAPAFERFCQVNTGPL
PLLGQSEPEKWMPLPPQGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFLGCSF
SLEEAL EKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCPLVVTMRPIPKDKLEGLVRACCSL
GGEQGQPVHMGDPELLGIKELSKPAYGDAMVCPGGEVPVFWPSPLTSLGAVSSCETPLAFASI
PGCTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQKIRELESMIGIDPGNRG
IGHLLCKDELKASLSLSHARSVLITTGFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAI
IVDQRAWNLHQKIVEDAVEQGVLTQIPILTYQGGSV EAAQAF LCKNGDPQTPRFDHLVAIER
AGRAADGNYYNARKMNIHLVDPIDDLFLAAKKIPGISSTGVGDGGNELGMGKVKEAVRRHIR
HGDVIACDVEADFAVIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQAWTQAL
PSVIKEEKMLGILVQHKVRSVSGIVGMEVDGLPFHNTHAEMIQLVDVTTAQV

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 358-378, 517-539

N-glycosylation site.

amino acids 28-32

Tyrosine kinase phosphorylation site.

amino acids 444-452

N-myristoylation site.

amino acids 98-104, 102-108, 123-129, 149-155, 181-187, 190-196,
238-244, 308-314, 399-405, 413-419, 448-454, 477-483, 482-488,
487-493

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 233-244, 531-542

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FIGURE 41

CTTTCCTGTTTTATCCGCAGCCCTTTTCTTCTTTGAGTTAGTAAAGATTTATTCTGTAACCTG
ACACTCATCTGGCCCTTTGCAGTTTGCCAGCCATATTCCCATGTGATTTCCCCTGGATCCAG
GCCCCATCCGGCTGGCAGGAGGGGGCTCTGACGTACAGGTTGGAAATCAGAAGTCTGTGAGA
GCGCGGGAGTGCATGGCAGCTCTGGGTCCCAGACCTGGCCCGACCCCTCTGCTTCACCTECAG
CTCTGCTGCTCCTCTACTCTTGGGTGAGATCCCTTTGGAGCCACAGCGAGGAACCCTGTGGT
CCTCAGGCAGGTGTACCTTGAGTCAGCCAGGAGCCCTCTTTTCCTGTGTCAAAGCCTGCCCTC
GGGCTCTGCTCACCTCTGGTGACCCCTCCAAGATGCCCCTGCCCTCAGTTTCCCCTCATGATCT
GGCCTCTGCCCCCTTCTCTAGCCACAGCCTCTAGTACACTTTAGCAATACCACCAGACTAGTT
AGAGTTCCCCACTCACCAAGCAAGACCATGCAGTTTCATGCCTCTGTGCCTTCGCTCATGCTGT
TTCTTCCGACTGGAATGCCTTCCCCTGCTCCTCCTGCCTTGTCTGCCTGGCAAGTTCATCTCT
CACGATCCCCCTCAAAGGCCCCCTCCTCCAGGAAGGCAACCCCTGTGCCCCCTCCCCTCCAGGCT
ACCTCTGCACTTTGTCAATGCTTCTCTTGTGGCACTTATCACACTGTATTTTACTTGTTTACA
TGTTTGTCTCCCCTTCTAGACTGTGAATCCTTAAGGGCATGGACTGTATCTTATGCATCTCTG
TATTTCTGCGCCTAGCACGGTGCCTAGCACACAGTAGGCGCTCAATAAATGTTGAATGAATGA
ATGATTT

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FIGURE 42

MQFHASVPSLMLFLPTGMPSAPPALSAWQVHLSRSPQRPPPPGRQPLCPSPPGYLCTLSMLL
LWHLSHCILLVYMFVSPSRL

Important features of the protein:

Signal peptide:

amino acids 1-22

Microbodies C-terminal targeting signal.

amino acids 81-83

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FIGURE 43

GTTTCCAACAAGGATGATATGAAGACTTCCCTGAAGAAAGTTGTGAAGGGACCTCCTACGAGA
TGATGATGCAGTGTGTGTCCCGCATGTTGGCCCACCCCCTGCATGTCATCTCAATGCGCTGCA
TGGTCCAGTTTGTGGGACGGGAGGCCAAGTACAGTGGTGTGCTGAGCTCCATTGGGAAGATTT
TCAAAGAGGAAGGGCTGCTGGGATTCTTCGTTGGATTAATCCCTCACCTCCTGGGCGATGTGG
TTTTCTTGTGGGGCTGTAACCTGCTGGCCCACTTCATCAATGCCTACCTGGTGGATGACAGCT
TCAGCCAGGCCCTGGCCATCCGGAGCTATACCAAGTTCGTGATGGGGATTGCAGTGAGCATGC
TGACCTACCCCTTCCTGCTAGTTGGCGACCTCATGGCTGTGAACAACCTGCGGGCTGCAAGCTG
GGCTCCCCCTTACTCCCCAGTGTTCAAATCCTGGATTCACTGCTGGAAGTACCTGAGTGTGC
AGGGCCAGCTCTTCCGAGGCTCCAGCCTGCTTTTCCGCCGGGTGTCATCAGGATCATGCTTTG
CCCTGGAG**TAA**CCTGAATCATCTAAAAAACACGGTCTCAACCTGGCCACTGTGGGTGAGGCCT
GACCACCTTGGGACACCTGCAAGACGACTCCAACCCAACAACAACCAGATGTGCTCCAGCCCA
GCCGGGCTTCAGTTCATATTTGCCATGTGTCTGTCCAGATGTGGGGTTGAGCGGGGGTGGGG
CTGCACCCAGTGGATTGGGTACCCGGCAGACCTAGGGAAGGTGAGGCGAGGTGGGGAGTTGG
CAGAATCCCCATACCTCGCAGATTTGCTGAGTCTGTCTTGTGCAGAGGGCCAGAGAATGGCTT
ATGGGGGCCCAGGTTGGATGGGGAAAGGCTAATGGGGTCAGACCCACCCCGTCTACCCCTCC
AGTCAGCCCAGCGCCCATCCTGCAGCTCAGCTGGGAGCATCATTCTCCTGCTTTGTACATAGG
GTGTGGTCCCCTGGCACGTGGCCACCATCATGTCTAGGCCTATGCTAGGAGGCAAATGGCCAG
GCTCTGCCTGTGTTTTTCTCAACACTACTTTTCTGATATGAGGGCAGCACCTGCCTCTGAATG
GGAAATCATGCAACTACTCAGAATGTGTCCTCCTCATCTAATGCTCATCTGTTTAATGGTGAT
GCCTCGCGTACAGGATCTGGTTACCTGTGCAGTTGTGAATACCCAGAGGTTGGGCAGATCAGT
GTCTCTAGTCCTACCCAGTTTTAAAGTTCATGGTAAGATTTGACCTCATCTCCCGCAAATAAA
TGTATTGGTGATTTGGAAAAAAAAAAAAAAAAAA

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FIGURE 44

MMMQCVSRMLAHPLHVISMRCMVQFVGREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLIGDV
VFLWGCNLLAHFINAYLVDDSFSQLAIRSYTKFVMGIAVSMLTYPFLLVGDLMAVNNCGLQA
GLPPYSPVFKSWIHCWKYLSVQGQLFRGSSLLFRRVSSGSCFALE

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 51-72, 97-114

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 160-163

N-myristoylation sites.

amino acids 34-39, 100-105, 123-128, 165-170

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FIGURE 45

GCTCACTCTTTGGGTCCACACTGCCTTTATGAGCTGTAACACTCACTGGGAATGTCTGCAGCT
TCACTCCTGAAGCCAGCGAGACCACGAACCCACCAGGAGGAACAACTCCAGACGCGCAG
CCTTAAGAGCTGTAACACTCACCGCAAGGTCTGCAGCTTCACTCCTGAGCCAGCCAGACCAC
GAACCCACCAGAAGGAAGAACTCCAAACACATCCGAACATCAGAAGGAGCAAACCTCGTGACA
CGCCACCTTTAAGAACCGTGACACTCAACGCTAGGGTCCGCGGCTTCATTCTTGAAGTCAGTG
AGACCAAGAACCCACCAATTCCGGACACGGCAAAGTAACATCCTAGACATGGCTTTAGAGATC
CACATGTCAGACCCCATGTGCCTCATCGAGAACTTTAATGAGCAGCTGAAGGTTAATCAGGAA
GCTTTGGAGATCCTGTCTGCCATTACGCAACCTGTAGTTGTGGTAGCGATTGTGGGCCTCTAT
CGCACTGGCAAATCCTACCTGATGAACAAGCTGGCTGGGAAGAACAAGGGCTTCTCTGTTGCA
TCTACGGTGCAGTCTCACACCAAGGGAATTTGGATATGGTGTGTGCCTCATCCCAACTGGCCA
AATCACACATTAGTTCTGCTTGACACCGAGGGCCTGGGAGATGTAGAGAAGGCTGACAACAAG
AATGATATCCAGATCTTTGCACTGGCACTCTTACTGAGCAGCACCTTTGTGTACAATACTGTG
AACAAAATTGATCAGGGTGCTATCGACCTACTGCACAATGTGACAGAACTGACAGATCTGCTC
AAGGCAAGAACTCACCTGACCTTGACAGGGTTGAAGATCCTGCTGACTCTGCGAGCTTCTTC
CCAGACTTAGTGTGGACTCTGAGAGATTTCTGCTTAGGCCTGGAAATAGATGGGCAACTTGTC
ACACCAGATGAATACCTGGAGAATTCCCTAAGGCCAAAGCAAGGTAGTGATCAAAGAGTTCAA
AATTTCAATTTGCCCGTCTGTGTATACAGAAGTTCTTTCCAAAAAGAAATGCTTTATCTTT
GACTTACCTGCTCACCAAAAAAGCTTGCCCAACTTGAAACACTGCCTGATGATGAGCTAGAG
CCTGAATTTGTGCAACAAGTGACAGAATTCTGTTCCCTACATCTTTAGCCATTCTATGACCAAG
ACTCTTCCAGGTGGCATCATGGTCAATGGATCTCGTCTAAAGAACCTGGTGCTGACCTATGTC
AATGCCATCAGCAGTGGGGATCTGCCTTGATAGAGAATGCAGTCCTGGCCTTGGCTCAGAGA
GAGAACTCAGCTGCAGTGCAAAAGGCCATTGCCCACTATGACCAGCAAATGGGCCAGAAAGTG
CAGCTGCCCATGGAAACCTCCAGGAGCTGCTGGACCTGCACAGGACCAGTGAGAGGGAGGCC
ATTGAAGTCTTCATGAAAACTCTTTCAAGGATGTAGACCAAAGTTTCCAGAAAGAATTGGAG
ACTCTACTAGATGCAAAACAGAATGACATTTGTAAACGGAACCTGGAAGCATCCTCGGATTAT
TGCTCGGCTTTACTTAAGGATATTTTTGGTCTCTAGAAGAAGCAGTGAAGCAGGGAATTTAT
TCTAAGCCAGGAGGCCATAATCTCTTCATTGAGAAAACAGAAAGAACTGAAGGCAAAGTACTAT
CGGGAGCCTCGGAAAGGAATACAGGCTGAAGAAGTTCTGCAGAAATATTTAAAGTCCAAGGAG
TCTGTGAGTCATGCAATATTACAGACTGACCAGGCTCTCACAGAGACGGAAAAAAGAAGAAA
GAGGCACAAGTGAAAGCAGAAGCTGAAAAGGCTGAAGCGCAAAGGTTGGCGGCGATTCAAAGG
CAGAACGAGCAAATGATGCAGGAGAGGGAGAGACTCCATCAGGAACAAGTGAGACAAATGGAG
ATAGCCAAACAAAATTGGCTGGCAGAGCAACAGAAAATGCAGGAACAACAGATGCAGGAACAG
GCTGCACAGCTCAGCACAAACATTCCAAGCTCAAAATAGAAGCCTTCTCAGTGAGCTCCAGCAC
GCCCAGAGGGCTGTTAATAACGATGATCCATGTGTTTTACTCTTAAAGTGCTAAATATGGGAGT
TTCCTTTTTTTACTCTTTGTCACTGATGACACAACAGAAAAGAACTGTAGACCTTGGGACAA
TCAACATTTAAATAAACTTTATAATTATTAAA

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FIGURE 46

MALEIHMSDPMCLIEFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAGKNK
GFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLLSSTF
VYNTVNKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFFPDLVWTLRDFCLGLEI
DGQLVTPDEYLENSLRPKQGSQQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLETLP
DDELEPEFVQQVTEFCSYIFSHSMKTLPGGIMVNGSRLKNLVLTYVNAISSGDLPCIENAVL
ALAQRENSAAVQKAI AHYDQMQQKVQLPMETLQELLDLHRTSERAIEVFMKNSFKDQVDSF
QKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAVKQGIYSKPGGHNLFIQKTEEL
KAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQALTETEKKKKEAQVKAEEKAEQRL
AAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEEQKMQEQMQEQAAQLSTTFQAQNRSL
SELQHAQRAVNNDPCVLL

Important features of the protein:**Transmembrane domains:**

amino acids 31-49, 114-131

N-glycosylation sites.

amino acids 90-94, 144-148, 287-291, 563-567

N-myristoylation sites.

amino acids 45-51, 283-289

Prenyl group binding site.

amino acids 583-588

ATP/GTP-binding site motif A (P-loop).

amino acids 45-53

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FIGURE 47

CACTCATTTCATTCCAAAGGGTCTCTCAAGGCAATGGTAATGTGCAAGGAGGTGATACCTAAAT
GAATGACCAAAAAGAACATGCTTCTGCTTTTGTGTGTCTCCTACATTTTAGACATTTGTTTGT
TCTCTTGGTAGCCTTTAAATTCCTTGAAGCCCAGGACCATGTCTCACTTACCTTTGTGTTTCC
ACTAAGTAGTCTACCTCCTGGAATTGGCAGATACTCAGTGAAAGCCTGTGAAATAAGTGATGT
CTATTTCTAGCATATTATTCTGAGATTTAATGATAGATTTAGTGATTGAATGAGATTTCCATT
TTCAAATACAGCAAAAGCATAACTATTTTCATTTCATTTCATATTCATTCAACTTCATTCTCAA
ATTAGGTCTGAGTTAACTAATAATTACCTTTGAAATGTGTGGGTATTGAGGCAATCAGGT
GGTGACATTGAGCTCTCAGCCAGAGTTTGTCTTCTGGAATTGATTTCAGTTCCATTGCATTGATT
TTTGTCTCTCAGAAGCCAAGGTTTCCCATGAAAAATCATTCCCACCTGAATTGGGCTGTGATTC
TTGCTGCGTTTAAGTAAAGGAAGCCTCTTGGTTCTAGTTCTGCAAACTTACACACTGAACTGG
GACAAGTTTTTGTGTTAGAGTAATGGCTGGGAAAAGAGGAACCTTTCATTTTATTGAGAAGTCA
AAAACAAAGGCCTCCAGCCACCTGGAGATGTTTTGTGTCAGACACCAGCCTGGCTCTGTCTT
TATGCCTAACAAATTGAGCATCCAGTCTTCTTTGTGCTGGGACCATTGCTCAGCTCTGCAAGGG
GAAAAGAGGGAGAAAGCCAGAGCTGCCAGGCTTCTTGCACTGGGGCCGGGGGAGGGTTCCTGG
GAAGCAGGTGCTCTCTGGCTTCTTGGTACGTGAGGCTCTCGGAGCTGCCTCTCCTCTGACCCT
CAGGTCTCACCAGTTTGCTCCAGGAGTATATTGAAAACATACCCAGTGCTCTCTCAAGCAC
CCACTGCTTAGAGGGCCCAGATTTCTTTTCCTTCTTTCCCTTGCAAGAGCTGGAGACTGCATCG
GGCATCTGGTGTGTTAACTAAACAGGAAAAGTACTAAAGGTCCACAGTGCTCATTGTGTAGA
CTAGCTGCCCTCCGATGGGTGCTCTGATTATCAGTGGTTCCAGTGCAGGGCCTGTCACTAAAC
AGGCCTCACTTCCTCCTTGGGGGCTTTCCCATGGGAGGTGTGGCTTTTTACTCTACATGGAAA
TGACTCTCTGCAGCCACAGAACACAGTCATTTTCTGAATTATCCCAGTCTCTCATGCGCCCTG
GATTCCTCCAGATGCCTTATATCTCTTGTCAGAAAGTTGTCTAAAATTTGGTTCCAGCTTCCA
AGCCTTGCCCTTTTGGCCTTCCTGGAAGTATTTTTGTGATGAGTCGTCTGTCATTATTCTCTA
AAATGATTTGCTTTTTGTTTCTTTTCATTTCCTATTTCCACCCACATATACACACATGCTTCTT
AACTTAGGGGATTACATGCCAATAAATCTATTGTTGAAAATGCACTAATACTATCGCAAAGAC
GAAAATTACAGGCTGAACCGTTGTAAGTCCATATGCTCCTCACTTACATGTGTGATGGAGT
TATGCCCAAATAAGTCCATCGTCAAGTTGAAAAATCAAATCAAGCCATCTTAGGTTGAGGAC
CATTTGTTTGTACCTCCAAAGATGTCATATCTTTAAACATACTCCCTAGCTTTTCTTTTACT
TTTTATTTTGAAGTAATTATAGAATCACAGAAAGTTGCAAAAAA

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FIGURE 48

MGALIISGSSAGPVTQASLPPWGLSHGRCGFLLYMENTLCSHRTQSFSELSQSLMRPGFLQM
PYISCAKLSKIWFPAKPCLLAFLEVFLMSRLSLFSKMICFLFLSFLFPPHIYTHAS

Important features of the protein:

Signal peptide:

amino acids 1-41

Transmembrane domain:

amino acids 88-107

Casein kinase II phosphorylation site.

amino acids 47-50

N-myristoylation site.

amino acids 24-29

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FIGURE 49

GGCTTCTACAGTCCACAACACCCACCAGCCCCAGGCCAGCAGAATGAGCCAGTGAGTGCCGGGGCTCCAGTT
TGGCTGTTGCTATGACAACGTGGCCACTGCAGCCGGTCTCTTGGGGAAGGCTGTGTGGGCCAGCCAGCCATGC
CTACCCCGTGCGGTGCTGCTGCCAGTGCCCATGGCTCTTGTGCAGACTGGGCTGCCCGCTGGTACTTCTGTTGC
CTCTGTGGGCCAATGTAACCGCTTCTGGTATGGCGGTGCCATGGCAATGCCAATAACTTTGCTCGGAGCAAGA
GTGCATGAGCAGCTGCCAGGGATCTCTCCATGGCCCCGTGCTCCCCAGCCTGGGGCTTCTGGAAGGAGCACCCA
CACGGATGGTGGCGGCAGCAGTCTGCAGGCGAGCAGGAACCCAGCCAGCACAGGACAGGGGCCGCGGTGCAGAG
AAAGCCCTGGCCTTCTGGTGGTCTCTGGCGGCAAGACCAACAGCCTGGGCCAGGGGAGGCCCCCACACCCAGGC
CTTTGGAGAATGGCCATGGGGGAGGAGCTTGGGTCCAGGGCCCCCTGGACTGGGTGGAGATGCCGGATCACCAGC
GCCACCTTCCACAGTCTCTCTACAGATCTCACTTCCACCTCTCCAGGATTAGCTTGGCAGGTGTGGAGCCCT
CGTTGGTGCAGGCAGCCCTGGGGCAGTTGGTGGGCTCTCTGCTCAGACGACACTGCCCCGGAATCCAGGCTG
CCTGGCAGAAAGATGGCCAGCCCATCTCTCTGACAGGCACAGGCTGCAGTTCGACGGATCCCTGATCATCCACC
CCCTGCAGGCAGAGGACGCGGGCACCTACAGCTGTGGCAGCACCCGGCCAGGCCGCGACTCCCAGAAGATCCAAC
TCCGCATTATAGGGGGTGACATGGCCGTGCTGTCTGAGGCTGAGCTGAGCCGCTTCCCTCAGCCCAGGGACCCAG
CTCAGGACTTTGGCCAAGCGGGGGCTGCTGGGCCCTGGGGGCCATCCCTCTTACACCCACAGCCTGCAACA
GGCTGCGTTTGGACCAGAACCAGCCCCGGGTGGTGGATGCCAGTCCAGGCCAGCGGATCCGGATGACCTGCCGTG
CCGAAGGCTTCCCGCCCCAGCCATCGAGTGGCAGAGAGATGGGCAGCCTGTCTCTTCTCCAGACACCAGCTGC
AGCCTGATGGCTCCCTGGTCATTAGCCGAGTGGCTGTAGAAGATGGCGGCTTCTACACCTGTGTGCTTTCAATG
GGCAGGACCGAGACCAGCGATGGGTCCAGCTCAGAGTTCTGGGGGAGCTGACAATCTCAGGACTGCCCCCTACTG
TGACAGTGCCAGAGGGTGATACGGCCAGGCTATTGTGTGTGGTAGCAGGAGAAAGTGTGAACATCAGGTGGTCCA
GGAACGGGCTACCTGTGACGGCTGATGGCCACCGTGTCCACCAGTCCCAGATGGCAGCTGCTCATTACAACT
TGCGGGCCAGGGATGAGGGCTCTACATGTGCAGTGCCTACCAGGGGAGCCAGGCAGTCAGCCGAGCACCAGG
TGAAGGTGGTCTCACCAGCACCCACCGCCCAGCCAGGGACCCTGGCAGGGACTGCGTCGACCAGCCAGAGCTGG
CCAAGTGTGATTTGATCTCTGCAGGCCCAGCTTTGTGGCAATGAGTATTACTCCAGCTTCTGCTGTGCCAGCTGTT
CACGTTTCCAGCCTCAGCTCAGCCCATCTGGCAGTAGGGATGAAGGCTAGTTCAGCCCCAGTCCAAAATAGTT
CATAGGGCTAGGGAGAAAGGAAGATGGACTCTTGGCTTCTCTCTGGCTGGCAAAGGGAGTTATCTTCTGGAA
TACATTAGCTCTTTCAAAAACCCACCCAGTGTTAGCCTCAACGGCAGCCAGTTACCAGCTTCTCTCTGTAGCCT
TCAGCAGTGTGTGTCATCTCTGACATAACCACAGGCTGCTGTTTTCAAGAAGAGCAATCTGTTTGGATAAGAAAA
CCTTTACTTTACAGCTTCCCTTTATAATTTGTTACACAGGAATAGTTAAATGCATTTGTTTGTGTTTTTTGAG
ACGGAGTTTTCACTCTGTGTCAGGCTGGAGGGCAATGGCGCGATCTCAGCTCACTGCAACCTCCGCTCTCCTGG
GTTCTTGATTCTCCTGTGTCAGCCTTCTGAGTAGCTGGGATTACAGATGCCTATCACCATGCCTGGGTAATTTTT
GTATTTTTAGTTGAGATGGGGTTTTCGCCATGTTGGCCAGGCTGGTCTCGAAGTTCTGACCTCAGATGATCTGCCC
GCCTCAGCTCCCAAAGTGGGATTACAGGCATGAGCCACCGCCAGCCATCAATGCATTTTTTTTTTATTTTT
TTTTTTGAGACAGAGTTTCGCACTTCTTGCCCAGGCTGGAGTACAATGGTGGGATCTTGGCTCACTGCAACCTCC
ACCTCCTGGGTTCAAGCGCTTCTCCAGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTATGTGCCACCATGCCT
GGCTAATTTTTGTATTTTTGGTGGAGACGGGGTTTTCCATGTTGGTCAAGTGGTCTTGAAGTCCCAGCCTCAGG
TAATCCGCCCCGCTCCGCTCCCAAATGCTGGGATTAGAGGTGTGAGCCACTGTGCCCAGCCCATCAATGTGTT
TTAAAGCTAGCTGTGAGGTTCCACTTAATTTAAAGCTGGGCAGGGAGATGTGTAATGATTTCAAAGTTAACACC
TGTTTTGTTTTCTAAAGGGCATGCCAAGTCTGCTGTATCAGGGAAGTATTCTGTGCTAAAATCAGCGATGGTTCA
TTGCTCTAGTCTCTCTCACCCCTTCTAGGCAGTGCATCAGTCAGCTCTAAATCTGGTGCAGAGGGTTAACAGCATA
ACCCTTGTGGCAAATGGAATAGATGTTAAGACCTCAAATAGGGATTGGGATGAAACAGCTGCAGTTAGCACT
GTTATCTGAGCATGAAAGAACTGGAACGCTCCTTACGTCGAGATGTTGGACCTGGAAGCCCTCCTGAGGCCAAC
ATGCAAATCTGGCTGTGACGGTTCTCTGACACCTGTGTAAAGCTGACCAGCCTGCTCTGTACAGTGACAATGAG
GAGCCCCCTCTTCCCTTAAGTAGGAATCTGTGAAGCAAATGTTTGTGCTGCCAAAGACAAATCAGACTGTCACTCA
TTAAAAACAGCATTAGCAGGATGAGGATAGCAATGGGGAAGGGTTGTGGGCAATGCAGTAACAGGGAAATGGCTT
CAGAAATGGTTTGAGTTGGAAGACAACATTCTTCATCTCTCAGGACTTCTAATTCCTTGATGCTAAAAGAAGAGG
CATGGATTCTATGAGCTTCAAGTCCCTTTCCACTTAACCTTCTACAAATCTTTCAGAGGACTGCCTAGTAGCA
AAGGTTATTCTGGACACAGGAAGACGGGCATTACAGGGACCAAAGCTCTGAAAGGTGACTTTTATTACCAACA
CACTGGCTGGAAAAGGGACAAACACATCACGGGTGAGTGATACTTCTCAGTCTTCTACTCATTCAACAAAGG
AAATGTGGGCTGGGGCAGAGGTCTTTTTTCAATTAATACTGGAAAAATATTGAAGAGCATCCATGTTCACTTATG
GCTGGTTTTGCTATAGAAATTGGAAATAAAGGCCACTTTTTTG

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FIGURE 50

MGPVVPSLGLLEGAPTRMVAAAVLQASRNPASTGQGPRCRES PGLLVVSGGKTNSLGQGRPPT
PRPLENGHGG RSLGPGPLDWVEMPDHQRHPSTAPPTDLTSHLSRISLAGVEPSLVQAALGQLV
RLSCSDDTAPESQAAWQKDGQPISSDRHRLQFDGSLIIHPLQAEDAGTYSCGSTRPGRDSQKI
QLRIIGGDMAVLSEAELSRFPQPRDPAQDFGQAGAAGPLGAIPSSHPPQANRLRLDQNQPRVV
DASPGQRIRMT CRAEGFPPPAIEWQRDQGPVSSPRHQLQPDGSLVISRVAVEDGGFYTCVAFN
GQDRDQRWVQLRVLGELTISGLPPTVTVPEDGTARLLCVVAGESVNIRWSRNGLPVQADGHRV
HQSPDGTLLIYNLRARDEGSYMCSAYQGSQAVSRSTEVKVVSPAPTAQPRDPGRDCVDQPELA
NCDLILQAQLCGNEYYSFCCASC SRFQPHAQPIWQ

Important features of the protein:

Signal peptide:

amino acids 1-16

Tyrosine kinase phosphorylation site.

amino acids 392-400

N-myristoylation sites.

amino acids 9-15, 50-56, 112-118, 146-152, 173-179, 195-201,
220-226, 229-235, 280-286, 306-312, 336-342, 397-403.

Myelin P0 protein.

amino acids 153-182

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FIGURE 51

CAGGCAGAAGCGAACAAAGACCCAGCAAGAGAAGGCAGAGGCTAAGACCCATCCCGTATCTGC
TCTCCTGAAATAATTCTGGAGTCATGCCTGAAATGCCAGAGGACATGGAGCAGGAGGAAGTTA
ACATCCCTAATAGGAGGGTTCTGGTTACTGGTGCCACTGGGCTTCTTGGCAGAGCTGTACACA
AAGAATTTTCAGCAGAATAATTGGCATGCAGTTGGCTGTGGTTTCAGAAGAGCAAGACCAAAAT
TTGAACAGGTTAATCTGTGGATTCTAATGCAGTTCATCACATCATTCATGATTTTCAGCCCC
ATGTTATAGTACATTGTGCAGCAGAGAGAAGACCAGATGTTGTAGAAAATCAGCCAGATGCTG
CCTCTCAACTTAATGTGGATGCTTCTGGGAATTTAGCAAAGGAAGCAGCTGCTGTTGGAGCAT
TTCTCATCTACATTAGCTCAGATTATGTATTTGATGGAACAAATCCACCTTACAGAGAGGAAG
ACATAACAGCTCCCCATAATTTGTATGGCAAACAAAATTAGATGGAGAAAAGGCTGTCCTGG
AGAACAATCTAGGAGCTGCTGTTTTGAGGATTCCTATTCTGTATGGGGAAGTTGAAAAGCTCG
AAGAAAGTGCTGTGACTGTTATGTTTGATAAAGTGCAAGTTCAGCAACAAGTCAGCAAACATGG
ATCACTGGCAGCAGAGGTTCCCCACACATGTCAAAGATGTGGCCACTGTGTGCCGGCAGCTAG
CAGAGAAGAGAATGCTGGATCCATCAATTAAGGGAACCTTTCAGTGGTCTGGCAATGAACAGA
TGACTAAGTATGAAATGGCATGTGCAATTGCAGATGCCTTCAACCTCCCCAGCAGTCACTTAA
GACCTATTACTGACAGCCCTGTCTAGGAGCACAACGTCCGAGAAATGCTCAGCTTGACTGCT
CCAAATTGGAGACCTTGGGCATTGGCCAACGAACACCATTTCGAATTGGAATCAAAGAATCAC
TTTGGCCTTTCCTCATTGACAAGAGATGGAGACAAACGGTCTTTCATTAGTTTATTTGTGTTG
GGTTCCTTTTTTTTTTTTAAATGAAAAGTATAGTATGTGGCACTTTTTTAAAGAACAAAGGAAATA
GTTTTGTATGAGTACTTTAATTGTGACTCTTAGGATCTTTCAGGTAAATGATGCTCTTGCACT
AGTGAAATTGTCTAAAGAACTAAAGGGCAGTCATGCCCTGTTTGCAAGTAAATTTCTTTTTTA
TCATTTTGTGTGCTGGCTAAACTTGGAGTTTGAGTATAGTAAATTATGATCCTTAAATATT
TGAGAGTCAGGATGAAGCAGATCTGCTGTAGACTTTTCAGATGAAATTGTTTCATTCTCGTAAC
CTCCATATTTTCAGGATTTTTGAAGCTGTTGACCTTTTCATGTTGATTATTTTAAATTGTGTG
AAATAGTATAAAAATCATTGGTGTTCAATTATTTGCTTTGCCTGAGCTCAGATCAAAATGTTTG
AAGAAAGGAACCTTTATTTTTTGCAAGTTACGTACAGTTTTTATGCTTGAGATATTTCAACATGT
TATGTATATTGGAACCTTCTACAGCTTGATGCCTCCTGCTTTTATAGCAGTTTATGGGGAGCAC
TTGAAAGAGCGTGTGTACATGTATTTTTTTCTAGGCAAACATTGAATGCAAACGTGTATTTT
TTTAATATAAATATATACTGTCTTTTCATCCCATGTTGCCGCTAAGTGATATTTTCATATGT
GTGGTTATACTCATAATAATGGGCCTTGTAAGTCTTTTCACCATTTCATGAATAATAATAAATA
TGTAAGTGTGGCATGTAATGCTTAGTTTTCTTGATTTTACTTCTTTTTTTAAATGTAAGGACC
AACTTCTAACTAATTGTTCTTTTGTTGCTTTAATTTTTTAAAATTACATTCTTCTGATGTA
ACATGTGATACATACAAAAGAATATAGTTTAATATGTATTGAAATAAAACACAATAAAATT

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FIGURE 52

MPEMPEDMEQEEVNI PNRRVLVTGATGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLD
SNAVHHIIHDFQPHVIVHCAAERRPDVVENQPDAAASQLNVDASGNLAKEAAVGAFLIYISSD
YVFDGTNPPYREEDI PAPLNLYGKTKLDGEKAVLENNLGAAVLRIPILYGEVEKLEESAVTVM
FDKVQFSNKSANMDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQMTKYEMAC
AIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKLETLGIGQRTPPFRIGIKESLWPFLIDK
RWRQTVFH

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 105-127

N-glycosylation site.

amino acids 197-201

N-myristoylation site.

amino acids 303-309

Short-chain dehydrogenases/reductases family proteins.

amino acids 18-30

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FIGURE 53

TGGGCTCCCTCCAGCACTGCTGTTGCCTGCTGCCTAAGATGGGTGACACTTGGGCCCAGCTTCCCTGGCCCTGGGG
CACCCACCCAGCAATGCTGCTGATCTCCCTCCTCTTGGCAGCCGGGTTGATGCACTCGGATGCCGGCACCAGCT
GCCCCGTCCCTTTGCACATGCCGTAACCAGGTGGTGGATTGTAGCAGCCAGCGGCTATTCTCCGTGCCCCCAGACC
TGCCAATGGACACCCGAAACCTCAGCCTGGCCCAACCCGCATCACAGCAGTGCCGCTGGCTACCTCACATGCT
ACATGGAGCTCCAGGTGCTGGATTTGCACAACAACTCCTTAATGGAGCTGCCCCGGGGCCTCTTCTCCATGCCA
AGCGCTTGGCACACTTGGACCTGAGCTACAACAATTTAGCCATGTGCCAGCCGACATGTTCCAGGAGGCCCATG
GGCTAGTCCACATCGACCTGAGCCACAACCCCTGGCTGCGGAGGGTGCATCCCCAGGCCTTTTCAGGGCCTCATGC
AGCTCCGAGACCTGGACCTCAGTTATGGGGGCTGGCCTTCTCAGCCTGGAGGCTCTTGAGGGCCTACCGGGGC
TGGTGACCCCTGCAGATCGGTGGCAATCCCTGGGTGTGTGGCTGCACCATGGAACCCCTGCTGAAGTGGCTGCCGAA
ACCGGATCCAGCGCTGTACAGCAGATTCTCAGTGGCTGAGTGCCGGGGCCCTCCTGAAGTCGAGGGCGCCCCGC
TCTTCTCACTCACTGAGGAGAGCTTCAAGGCCTGCCACCTGACCCTGACCCTGGATGATTACCTATTTCATTGCGT
TCGTGGGCTTTCGTGGTCTCCATTGCTTCTGTGGCCACCAACTTCTCCTGGGCATCACTGCCAACTGCTGCCACC
GCTGGAGCAAGGCCAGTGAAGAGGAAGAGATCTGACATGCCTGCCTCTCATCCCTCCATGCTGCTGACCGCCACA
GCTGCTGGCCACCAGACGCCCTCCCTGATTGCTCACTCTGGTTCATGGTGACCTGGCTGCCTCAGTCATGGTTC
AAGCAAGGTGGGACACTCATTTTGTATGAGCATCTGCTTTGGGCCAGGCGGCACGCTAGGAATTGGGAACATCA
AGTGAATGACTCACTCCCTGCCCTCAAGGCCTTCCCTCTGGTCAAGGAGAGAGATCCAAAACTATTCCCTTT
AAGACTATATGTCAGGACTCTGAGCACGTCAATTATGGAGGCCAGAGGAGGAGCCATCATCTGTATCTAGCAATG
TCCATGAGAATTATAAGATTAGAGTGATTTGTGAAGTGGGTGCATCAGGAAATATCTACTTTGTGAGGTAGGCAAA
GAAGGGTGTCTGCACATGGCAGAGGCCAGAAATGCATAGTGTGCTGTGTTGAGAAGAGTGAACAGTTCCTGGTC
ACTTACTTGTATAGAGGGGGTGTGGCACAGAACTCAAACCTACCCCTCACCTCCTGACACCAAACTGTCAGCTC
TCAGCAATGCCAGCCTGCCTACAGGGAGTAAAGAACACCTCTATGACAGCCCTGGCCTCCTTCCAGCAGC
TACCAGGTGAGACCACCTCCAGTGACTGCCCCATATGACCAATGTCACCAGTTGGTGAGGTCCCAGGCAGCA
GGCTGAGGATGGACACTTTCAATGCCCTTGTCTCTGCTCTCACTCAAGTTTGTCTCAGAAGAGAGAGGCAGGA
GGCCCAGCAACTGGGGCAGCAAGAGTCCCTGGCAGCTTGGGATCCTAATCATGTGACTGTTCTTGCCACAGTGCTC
ATGCCACAGGGTCTCACCAGGAAAGTGCCTGTGGGCCACAGACCCACAGCCTGGCAGCACCCAGAGCTAAAAGG
GGACAAAGGCAGCACAGTTATGACCATATGAGGCTTTGCATTTTCTTCTAAGCAACTTACCCACGTTAAGCATGA
GGGTGAGAGAGCTATTAAATACTAAGCCCTTGCCAGTGTCAGGTACTTTGAAAAGCTCTCTGCACAAACCATTC
CTTTGACACACACACACAAATCTTTGAGGTGAACGCTGTTGTTCCCATTTTACGGATGAGGCAACTAAGGCT
CAGAGAGGTTAAAGTCACATGCCACTATGAGCAAGATAAAGTCTGTGCTTTTCTACTGCCCCATCCAAGTTGGG
GAACATCACCATTCCCTCTAGAGTTATATAAATTCAAATTCAACTAGAGCTGACAAAGTTCCTCATAAGGTCCAG
GCACTCCTCTGGGCACTTTTATATCTATTGACTCACTTCTTTCAATTCTCACAGCAAACTGCCTGGTGGTTTTT
ATTATCCCCATTGACAGATGAATTAATCGTAGAGAGTTGAGTGACTTACCAAGGTTGTCTGGATAAGCTAG
AAGGAAGGCGGTAGGCAGCTCCATTACGGGAACTGCATCTAATCAGTCAGTCAAAAACTAAGTAACCTTTACGAG
CAAAGCACAAATTATCATCATCGTGGTCTTCTTCATCAGTTTCGTGAGCAGCATCATTATCTTCCCTCTATTTGTT
CAGCACCGGATAGTTTCATGAGTATTTTTGCATCATTCTCCTTGACTTTTACATCCCTGTGAGGAGGTAAATCA
AACATCAGTAATCTGTGTTTACAGATGGGGAAGGCTCTCAAGGTTGGATATGACTTGCTATGTGGCAAGGTTG
GGGCTCAACCCCTAACACAGTTCTCTTCCAGTGCTTCTCAAGTGCTTGGGGAAGAGAATGCCTCAGAAGGCTGG
GTAGTGGGCGCTGGAATTGAGCATCCATGAATGCTGTAGTGAAGATAAGCTAAATAGAAGGCAGCCAAACCTCT
GCTGTACAGATTGAATCTGCTACGGTAGGGCAAATTGCAGGCTCTGAAACAGAGACTACACAGGTAACACCTG
AATAGGAGACTCCTGCTTTACAATGTGTAGATAAAACATCAGCAATGGTGGCCATGGTGGCAGTCATGTGAAAAG
TAAGATCTTTGGGAATCAAGAAAGGAAGCTGTGTTAACCCTCCTGCTCAAGCCCTGCTGCGTGTGTTGCAAGAG
ATACTAAGAGAGCAAGAAAGCTATAGGTGAGAACCTCTGCAGTTTAGGAGAAGAACATCAAGGCACAGTCCACA
TGCTGATAAGTCTGGCCAGGAGGAGAATTAACAGGGGCTTTCCACACCTCCCTTGCCCCAAGCTCCAGCGGTA
TTCTATCAGCCCATCCTCCTGGAAAGCCTGAAAGGAATGAAGGAGGCTAATAAGTCATCTTCCAGGAAGGCATCC
CTCACTCGTGCTTCCCTGAGCTAGTCAACCAAAAGAGTCTTCAGAACTTTGCTAGACCTGAAGTACTTGAACCT
GTGTCCCCTGAATCTTTCTTACAACATCTGGGACAAATCCCTGGTCTGTGACATCCGAAGCAGAACTGTGCCCT
GCTCTCTCCTTCTGTGATGACCAAGGATGGTGAACCTCAAGTTGTTCTCTACAAGCCAGGCCAGCAACCTAAATAC
TTGGAGAGGAACTTTTAGAACTATAATCCTGACAAAATAGAAAAGTTTCCCATAGGGGCATACCATAATACTAT
AATAACCTCCAGGAACTATTGTTTGCCAAAATGTAGTTAATATATTTAAGATATATGCTTTTTTGCATAGGAC
TAGAACCAGAAAAGACACAAATGCCCCCTGACATCAATGTCTCTTCTAGTGGGACAATTTGGTCTCCATTAAT
GCCAAACCTTTCTGAACAGGATACATGGCTTTTAAAGGACAGATGTTTCTCCTGCTGCTAGAAGTTCCTCAGTTT
ACTAGAGCACAATGAGGAAAGTATTCAACCTCCCTACTGCCAAGGAATCCCTGCTTCTCCCCACCGCCATCAT
CTTGTCCAAGCTATCAGAAGCAACCTTCTAGAGATAATCTAACAATCCTGATTAGAATTGCTCCCATATCCCTGG
TGACCACAGGCTTCATTCAAATGTCCAACTGGTTAACATGTATGTGATGGGGTATCTCTGCATCTGTATGTCT
GTCTGCGAGGTTCTTGTATATTGGCTGTCCGCTGACTTGGGACAGATCTCTCTAGAAGTTGGGTTAGTTCTCT
GACATAGTCCCTCAGCTCAGCTGAGTGGCTAAATATGCATAAATAAGCATGCCTAAATAGGCATATATAGGT
TGGTGCAAAAGTAATTGCGGTTTTTGGCATTAAAAATGATGGCAAAAATCCCAATTACTTTTGGCTCAATCTAAT
ATTACATTGCTTGATAGATTAAGATGGAATCCACCAGGTTTAGGGTAGGACTGGATGCTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 54

MLLISLLLAAGLMHSDAGTSCPVLCTCRNQVVDCCSSQRLFSVPPDLPMDTRNLSLAHNRTAV
PPGYLTCYMELOVLDLHNNSLMELPRGLFLHAKRLAHLDSLNNFVSHVPADMFQEAHGLVHID
LSHNPWLRRVHPQAFQGLMQLRDLDSLGGGLAFLSLEALEGLPGLVTLQIGGNPWVCGCTMEP
LLKWLRNRIQRCTADSQLAECRGPPEVEGAPLFSLTEESFKACHLTTLDDYLFIAFVGFFVS
IASVATNFFLLGITANCCHRWSKASEEEEEI

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 241-260

N-glycosylation sites.

amino acids 52-55, 81-84, 107-110

Tyrosine kinase phosphorylation site.

amino acids 148-154

N-myristoylation sites.

amino acids 11-15, 263-268

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 175-185

Leucine zipper pattern.

amino acids 77-98

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FIGURE 55

GGCTGCGCCCAGGCCGGCGGGCCCCAGCAGCTGCGAACCGCCGGCGCACCCACCTGTTTCCGCGC
CCGGGGACTTCCCCGGCGGGGCTCAGAAAGTGTGGGGTGGTTCGCTTGGCTTCCCCTGGCGTCA
GCGACCCAGGGTAACCTCCTCCACTGCTGCGTGCCGTGCAGGCCTGCCTGTGTGAGAGCCACG
TGTGCCGCGCTCTGGGCACAGCCTTGGAAGTGCAGGACCGCGACGGCAGCAGAGCAGAAACCT
TACAGAAACATGAAGCCCTCAACCATCTGCTACTCAGTTATTCGGGGCTGACGGCGGCTTCTA
GAACATCCAGGTGTTCTGCAGATGCGGAGAACTCATCCTGTAGTCACCAGATGGAGTCCCAAAC
AGCCAAGCAGATGTAAGGCCTGTGCTGTGGCTCTGAGGCCCTGAATACAGAAGGGTCACTTTC
TTAGTGGCCAAAGAGCAGTTGTTGACATTGATGTCTAATTATTGAACACGACCAGTCATTTTA
CTGAGCTGCAGTGAGGAAACACTGACCATAGAAGATCAAGCCAAATGAGGGATTGCAAATTTT
CTGATTCTTTTGAATTAGGATTCCAGATGGGGGCTCATTTCTACAGCCCCCAACATTTCTAT
AGCCGTTATCACTGCCATCACCCTGCCACCAGCATCTTCTTGCAGATTCCACCCCTGCTCCC
CAGAGACTTCCTGCTTTGAAAGTGAGCAGAAAGGAAGCTCTCAGAAAAATCTCTAGTGGTGGC
TGCCGTGCTCCAGACAATCGGAATCCTGCCTTCACCACCAATGGGCTGGCTTTTTCTAAAGGT
TTTGTGGCGGGAGTGAGTTTCTCAGGATTTCTTTATCCTCTTGTGGATTTTTCATCAGTGG
GAAACAAGAGGACAGAAAGCCAAACTTTGTGATTATTTTGGCCGATGACATGGGGTGGGGTGA
CCTGGGAGCAAACCTGGGCAGAAACAAAGGACACTGCCAACCTTGATAAGATGGCTTCGGAGGG
AATGAGGTTTGTGGATTTCCATGCAGCTGCCTCCACCTGCTCACCCTCCCGGGCTTCCTTGCT
CACCGGCCGGCTTGGCCTTCGCAATGGAGTCACACGCAACTTTGCAGTCACTTCTGTGGGAGG
CCTTCCGCTCAACGAGACCACCTTGGCAGAGGTGCTGCAGCAGGCGGGTTACGTCACTGGGAT
AATAGGCAAATGGCATCTTGGACACCACGGCTCTTATCACCCTCACTTCCGTGGTTTTGATTA
CTACTTTGGAATCCCATATAGCCATGATATGGGCTGTACTGATACTCCAGGCTACAACCACCC
TCCTTGTCACGCGTGTCCACAGGGTGATGGACCATCAAGGAACCTTCAAAGAGACTGTTACAC
TGACGTGGCCCTCCCTCTTTATGAAAACCTCAACATTGTGGAGCAGCCGGTGAACCTGAGCAG
CCTTGCCCAGAAAGTATGCTGAGAAAGCAACCCAGTTTCATCCAGCGTGCAAGCACCAGCGGGAG
GCCCTTCCTGCTCTATGTGGCTCTGGCCACATGCACGTGCCCTTACCTGTGACTCAGCTACC
AGCAGCGCCACGGGGCAGAAAGCCTGTATGGTGCAGGGCTCTGGGAGATGGACAGTCTGGTGGG
CCAGATCAAGGACAAAGTTGACCACACAGTGAAGGAAAACACATTCCTCTGGTTTACAGGAGA
CAATGGCCCGTGGGCTCAGAAAGTGTGAGCTAGCGGGCAGTGTGGGTCCCTTCACTGGATTTTG
GCAAACCTCGTCAAGGGGGAAAGTCCAGCCAAGCAGACGACCTGGGAAGGAGGGCACCGGGTCCC
AGCACTGGCTTACTGGCCTGGCAGAGTTCCAGTTAATGTACACGCACTGCCTTGTTAAGCGT
GCTGGACATTTTCCAACCTGTGGTAGCCCTGGCCCAGGCCAGCTTACCTCAAGGACGGCGCTT
TGATGGTGTGGACGTCTCCGAGGTGCTCTTTGGCCGGTCACAGCCTGGGCACAGGGTGCTGTT
CCACCCCAACAGCGGGGCAGCTGGAGAGTTTGGAGCCCTGCAGACTGTCCGCCTGGAGCGTTA
CAAGGCCTTCTACATTACCGGTGGAGCCAGGGCGTGTGATGGGAGCATGGTGCCTGAGCTGCA
GCATAAGTTTCTCTGATTTTCAACCTGGAAGACGATACCGCAGAAGCTGTGCCCTAGAAAG
AGGTGGTGCAGGAGTACCAGGCTGTGCTGCCCCAGGTCAGAAAGGTTCTTGCAGACGTCCTCCA
AGACATTGCCAACGACAACATCTCCAGCGCAGATTACACTCAGGACCCTTCAGTAACTCCCTG
CTGTAATCCCTACCAAATTGCCTGCCGCTGTCAAGCCGCATTAACAGACCAATTTTTATTCCAQ
GAGGAGGAGTACCTGGAAATTAGGCAAGTTTGGCTTCCAAATTTTCAATTTTACCCTCTTTACAA
ACACACGCTTTAGTTTAGTCTTGGAGTTTAGTTTGGAGTTAGCCTTGCAATATCCCTTCTGTA
TCCTGTCCCCCTCCACGCCGACCCGAGAGCAGCTGAGCTGCGCTGGCTCTGGGCAGGGAGTG
TGCTTAAATGGGAAGCACACGGGCTTTGGAGTCAGGCACAGGTGCCAGCTCCAGCTTTTGAAC
TTGGGCAATTGTTTAACTAACCTGCAAGTTGATTTTGAGGGTTAAATAAAGGCATACATGAA
AATGCCTGGCAACTTTAAAAA

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FIGURE 56

MGWFLKVLLAGVSFSGFLYPLVDFCISGKTRGQKPNFVII LADDMGWGDLGANWAETKDTAN
LDKMASEGMRFVDFHAAASTCSPSRASLLTGRLGLRNGVTRNFAVTSVGGLPLNETTLAEVLQ
QAGYVTGIIGKWHLGHHGSYHPNFRGFDYYFGIPYSHDMGCTDTPGYNHPPCPACPQGDGPSR
NLQRDCYTDVALPLYENLNIVEQPVNLSSLAQKYAEKATQFIQRASTSGRPFLLYVALAHMHV
PLPVTQLPAAPRGRSLYGAGLWEMDSL VGQIKDKVDHTVKENTFLWFTGDNGPWAQKCELAGS
VGPFTGFWQTRQGGSPAKQTTWEGGHRVPALAYWPGRVPVNVSTALLSVLDIFPTVVALAQA
SLPQGRRFDGVDVSEVLFGRSQPGHRVLFHPNSGAAGEFGALQTVRLERYKAFYITGGARACD
GSMVPELQHKFPLIFNLEDDTAEAVPLERGGAEYQAVLPEVRKVLADVLQDIANDNISSADYT
QDPSVTPCCNPYQIACRCQAA

Important features of the protein:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 353-373

N-glycosylation sites.

amino acids 117-120, 215-218, 356-359, 397-500

N-myristoylation sites.

amino acids 12-17, 33-38, 52-57, 97-102, 101-106, 113-118, 158-163, 328-333, 388-393, 418-423, 435-440, 436-441

Amidation site.

amino acids 382-385

Sulfatases signature 2.

amino acids 129-138

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FIGURE 57

TGGACAAGACACCTCCAGGAGCCCAGCTCACAGCCACCGGTACCTTCTTCCAGGACAAGCTGG
GGGCCTCCATGGGCGCCTGAGGGCCAGGCGCCAGGGCCGTGGGCACGAGT**ATGGT**GAGACACC
AGCCCCTGCAGTACTACGAGCCACAGCTGTGCCTCTCCTGCCTCACGGGCATCTACGGCTGCC
GTTGGAAGCGCTACCAGCGCTCCCATGATGATACCACACCGGGCACAGCGCCATTCCCTGCATG
TGGGGGCTGTGGCAGCAGTCACCATGCTCTCCTGGATCGTGGCAGGACAGTTTCGCCCCGTGCAG
AGCGGACCTCCTCCCAGGTGACCATTCTCTGTACCTTCTTCACCGTGGTGTTTGGCCCTCTACC
TGGCCCCCTCTCACCATCTCCTCTCCCTGCATCATGGAGAAGAAAGACCTCGGCCCCAAGCCTG
CTCTCATTGGCCACCGCGGGGGCCCCATGCTGGCTCCAGAGCACACGCTCATGTCTTCCGGA
AGGCCCTCGAGCAGAAGCTGTACGGGCTCCAGGCTGACATTACCATCAGCCTGGACGGCGTGC
CCTTCCCTCATGCATGACACCACCTGCGGGCGCACCACCAACGTGGAGGAGGAGTTCCCGGAGC
TGGCCCCGAGGCCTGCCTCCATGCTTAAGTGGACCACCTGCAGAGACTCAACGCTGGCCAGT
GGTTCCTGAAGACTGACCCCTTCTGGACAGCCAGCTCCCTGTCACCTCCGACCACAGAGAGG
CCCAGAACCAGTCCATCTGCAGCCTGGCAGAGCTCCTGGAGCTGGCCAAGGGCAATGCCACAC
TGCTGCTCAACCTGCGTGACCCGCCCCGGGAGCACCCCTACCGCAGCAGTTTTATCAACGTGA
CTCTGGAGGCCGTGCTGCACTCCGGCTTCCCCCAGCACCAAGGTCATGTGGCTGCCTAGCAGGC
AGAGGCCCTGGTGCGGAAGGTGGCTCCCGGCTTCCAACAGACATCAGGCTCCAAGGAGGCAG
TCGCCAGCCTGCGGAGAGGCCACATCCAGCGGTGAACCTGCGCTACACTCAGGTGTCCCGCC
AGGAGCTCAGGGACTACGCGTCTTGAACCTGAGTGTGAACCTCTACACAGTCAACGCACCGT
GGCTCTTCTCCCTGCTGTGGTGTGCGGGGGTCCCATCCGTACCTCTGACAACTCCACACCC
TGTCCCAGGTGCCTTCCCCCTCTGGATCATGCCCCGGACGAGTACTGTCTCATGTGGGTCA
CTGCCGACCTGGTCTCCTTACCCCTCATCGTGGGCATCTTCGTGCTCCAGAAGTGGCGCCTGG
GTGGCATAACGGAGCTACAACCCTGAGCAGATCATGCTGAGTGCTGCGGTGCGCCGGACAGCC
GGGACGTCAGCATCATGAAGGAGAAGCTTATTTTCTCAGAGATCAGCGATGGTGTAGAGGTCT
CCGATGTGCTCTCCGTATGTTTACAGACAACAGTTATGACACATATGCCAACAGCACCGCCACCC
CTGTGGGGCCCCGAGGGGGTGGCAGCCACACCAAGACCCTCATAGAGCGGAGTGGGCGT**TAGC**
TGAAGACATGTCTGTCCACCTGTACCTGACACAGAAGCTGGGGAGCCTAGGAGAGCTGGTGG
AAGTGTGTCTGAACTCGGAGTGCTCTGGGAGCGGGCTCCACAGCCTCCTTGTGGGCTCCAGCC
CCTTGTACGCCGACGCTCTCTTGAAGGGGACTCCCTGTCTCCTGAGGCCAGCTGGGCCAGG
ACTCCATCCTTTCAGATGCCCTGACGGCCTGGGGCTCCTTCTGGGAAGTATGGGGCTAGGG
CTTGGTCCCCCTCTTCTGAGGCCCTCTCCTGTATCCCGACCTGGAAGCTTTGATGGGTCTAGG
GCCATGCCATAACCCCTGTGGCAATGGAGTGTGTGGATGCTCACCTGTGCCATCTGTCTCCT
GTCTGTGCCAGGAGGCACCTGAGTTCTCTGCTGTTATCCTGCCCCAAGGGCCTGGGCCGAGCC
TCTACCTGAAGCAACTCTGCTCTTCTGTCTCAGTCTCAAAGCACAAGGAGGTTTACGCCAGGAG
GAAGCCAGCTGCAATGTGGAGACACGTCCTCCTCCCAACCCACCTCATGCCACCGCCAACCC
CCTGCCCCAGGAGCGGGCCTGAGCCACGTCCCTAGGAGCAGCTGGAGATGGCCAAAAGAGTG
AGCTCAGGACTACTGGATCCCATGCCCAGGTGTCCAGCAGACCTCAAGGCAGAAGGGTCACCT
AACCCAGGAGTCCACAGACTGATGTGACCTCAGGTTCACCATCAGTGGCCACAGGGCAGGGC
CCACCTGGTAGAAGTGTTCTGGATATGGCCAGGGTGGGTGTGTGGCTAAGTGGGCCTGAACAG
AGGGAACCTAGGGCCCTTGGCCAATGTGATTAAAGCTGCCATCTTGAAA

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FIGURE 58

MVRHQPLQYYEPQLCLSLTGIYGCWKRYQRSHDDTTPGTAPFLHVGAVAAVTMLSWIVAGQ
FARAERTSSQVTILCTFFTTFVFALYLAPLTISSPCIMEKKDLGPKPALIGHRGAPMLAPEHTL
MSFRKALEQKLYGLQADITISLDGVPFLMHD TTLRRTTNVEEEFPELARRPASMLNWTTLQRL
NAGQWFLKTDPFWTASSLSPSDHREAQNQSICSLAELLELAKGNATLLLNLRDPPREHPYRSS
FINVTLEAVLHSGFPQHQMVLPSRQRPLVRKVAPGFQQTSGSKEAVASLRRGHIQRLNLRYT
QVSRQELRDYASWNLSVNLYTVNAPWLFSLWCAGVPSVTSDNSHTLSQVPSPLWIMPPDEYC
LMWVTADLVSF TLI VGI FVLQKWRLLGGIRSYNPEQIMLSAAVRRTSRDVSIMKEKLIFSEISD
GVEVSDVLSVCSDNSYDTYANSTATPVGPRGGGSHTKTLIERSGR

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 47-61, 77-93, 335-350, 380-399

N-glycosylation sites.

amino acids 182-186, 217-221, 233-237, 255-259, 329-333, 462-466

Tyrosine kinase phosphorylation site.

amino acids 130-139

N-myristoylation sites.

amino acids 21-27, 48-54, 294-300, 404-410, 442-448, 473-479

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FIGURE 59

CCTGAGCAAACACAGCAGCCCGAGTGTTCCCAAGGCCAAAATGCTGAGAACGTCCACTCCTAA
TCTGTGTGGTGGTCTGCATTGCCGGGGCCCCCTGGCTCTCTTCTGGCATTCTCTGCCTCTGCCT
CATATTCTTGTTAGGCCAGGTGGGCTTGCTGCAGGGACACCCCCAGTGCCTGGATTACGGGGC
CCCTTTCCAGCCCCCTCTGCACCTTGAGTTTTGCTCTGACTATGAGTCCTTCGGCTGCTGTGA
TCAGCACAAGGACCGCCGCATCGCTGCCCGGTACTGGGACATCATGGAATATTTTGATCTGAA
GAGACATGAGCTGTGTGGAGATTACATTAAAGACATCCTTTGCCAGGAGTGCTCGCCCTACGC
AGCCACCTCTACGACGCCGAAAACACCCAGACGCCTCTCCGGAATCTCCCGGGCCTCTGCTC
TGATTACTGCTCTGCCTTCCATTCTAACTGTCACTCAGCCATTTCCCTGCTGACCAATGACCG
CGGCCTCCAGGAGTCTCATGGAAGGGACGGTACCCGCTTCTGCCACCTCCTGGACCTTCCTGA
CAAGGACTATTGCTTCCCTAATGTCTTGAGGAACGACTATCTCAACCGCCACCTGGGCATGGT
GGCCCAAGATCCTCAGGGCTGCCTGCAGCTCTGCCTGAGCGAGGTGGCCAACGGGCTGAGGAA
CCCCGTCTCCATGGTCCATGCTGGGGACGGCACCCATCGCTTCTTTGTTGCCGAGCAGGTAGG
AGTGGTGTGGGTCTACCTCCCTGATGGGAGTCGCCTGGAGCAACCTTCCTGGACCTCAAGAA
CATCGTGTGACCACCCCATGGATCGGGGATGAGAGAGGCTTCTTGGGGTTGGCTTTTACCC
CAAATTCGCCACAATCGCAAGTCTATATTTATTATTCTGCTGCCTGGACAAGAAGAAGGTAGA
AAAGATCCGAATTAGTGAGATGAAGTTTTCTCGGGCTGATCCTAACAAAGCTGACCTGAAATC
AGAGAGGGTCATCTTGAGATTGAAGAACCAGCCTCAAACCATAATGGCGGACAACCTTCTTTT
TGGCCTGGATGGCTATATGTACATATTCAGTGGGGACGGGGGACAGGCTGGAGATCCCTTTGG
CCTGTTTGGAATGCTCAGAACAAAAGTTCCCTGCTGGGAAAAGTTTTAAGGATCGATGTGAA
CAGGGCAGGCTCACATGGCAAGCGGTACCGAGTCCCCTCGGACAATCCATTTGTTTCTGAGCC
AGGGGCCCCACCCCGCCATCTATGCCTATGGGATCAGGAACATGTGGCGTTGTGCTGTGGACCG
AGGGGACCCCATCACGCGCCAGGGCCGAGGCCGGATATTCTGTGGGGACGTGGGGCCAGAACAG
GTTTGAAGAGGTTGACCTCATTTTGAAGGTGGAACTATGGCTGGAGAGCAAAGGAAGGGTT
TGCATGTTATGACAAAAAATTTGTCAATGCCTCTTTGGATGATGTTCTGCCAATCTATGC
TTATGGCCATGCAGTGGGGAAGTCAGTCACTGGAGGTTATGTCTATCGTGGTTGTGAATCCCC
AAATCTCAATGGCCTGTATATCTTTGGAGACTTCATGAGTGGTCGACTTATGGCTTTGCAGGA
AGATAGAAAAACAAGAAATGGAAGAAGCAGGATCTTTGCCTGGGCAGCACCCAGTCCTGTGC
CTTCCCAGGGCTGATCAGCACCCATAGCAAGTTCATCATCTCCTTTGCTGAAGATGAAGCAGG
GGAGCTGTATTTCTGGCGACCTCTTACCCAAGTGCCTATGCACCACGTGGATCTATTTACAA
GTTTGTGACCCCTCAAGGCGAGCACCCCCAGGCAAGTGCAAATACAAGCCAGTGCCCGTGAG
AACCAAGAGTAAGCGGATCCCGTTCAGACCACTCGCCAAGACAGTCTTGGAAGTGTAAAGGA
ACAATCAGAGAAAGCTGCTAGAAAATCTTCCAGTGCAACCTTAGCTTCTGGCCCAGCCCAGGG
TTTGTCTGAGAAAGGCTCCTCCAAGAAGCTGGCTTCTCCTACAAGCAGCAAGAATACATTGCG
AGGGCCTGGTACAAAGAAGAAAGCCAGAGTGGGGCCCCACGTCCGCCAGGGCAAGAGGAGGAA
GAGCCTGAAAAGCCACAGTGGCAGGATGAGGCCATCAGCAGAGCAGAAGCGAGCTGGCAGAAG
TCTCCCTTGACCTATTGGTCAAGGTGGCCGACAGGGTGACGTGAGAGAGGAGAGCCACCTCAT
CAAATGAAAGTCACTGCTGAATAAAGACCTTAGAAGTCTGGGAAGCCAGGGTAGAGGTGGGGC
AGGGCGGTTTTCTCTCCCTGGGAAATCTTGCTGTCTACTGAATAAATAAATGCACCTTCTCT
GTATGCAGTGCTTCTGTGGGAGACCATATCCAGATTGCTGGTGCACCTGGGTTATGGTAAGC
ACTAGTCCATGAGCCTGCTTGAATCACACTGGATGTCTCCGTTTTGTCTTGTAATGCCTAC
AACCTGAGGTAATAAATCAACATTTGCTCA

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FIGURE 60

MLRTSTPNLCGGLHCRAPWLSSGILCLCLIFLLGQVGLLQGHQPCLDYGPPFQPPLHLEFCSD
YESFGCCDQHKDRRIAARYWDIMEYFDLKRHELCDYIKDILCQECSPYAAHLYDAENTQTPL
RNLPGLCSDYCSAFHSNCHSAISLLTNDRLQESHGRDGTFRFCHLLDLPDKDYCFPNVLRNDY
LNRHLGMVAQDPQGCLQLCLSEVANGLRNPVSMVHAGDGTFRFFVAEQVGVVWVYLPDGSRL
QPFLDLKNIVLTTPWIGDERGFLGLAFHPKFRHNRKFYIYYSCLDKKKVEKIRISEMKVSRAD
PNKADLKSERVILEIEEPASNHNNGGQLLFGLDGYMYIFTGDGGQAGDPFGLFGNAQNKSSLLG
KVLRIDVNRAGSHGKRYRVPSDNPVFSEPGAHPAIYAYGIRNMWRCVDRGDPITRQGRGRIF
CGDVGQNRFEEDLILKGGNYGWRAKEGFACYDKKLCHNASLDDVLPYAYGHAVGKSVTGGY
VYRGCEPNLNGLYIFGDFMSGRLMALQEDRKNKKWKKQDLCLGSTTSCAFPGLISTHSHKFII
SFAEDEAGELYFLATSYPSAYAPRGSYKFVDPSTRAPPKCKYKVPVVRTKSKRIPFRPLAK
TVLDLLKEQSEKAARKSSSATLASGPAQGLSEKGSSKKLASPTSSKNTLRGPGTKKKARVGPH
VRQGKRRKSLKSHSGMRPSAEQKRAGRSLP

Important features of the protein:**Signal peptide:**

amino acids 1-41

Transmembrane domain:

amino acids 17-36

N-glycosylation sites.

amino acids 372-376, 480-484

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 645-649, 699-703

Tyrosine kinase phosphorylation site.

amino acids 81-89

N-myristoylation sites.amino acids 11-17, 37-43, 156-162, 165-171, 357-363, 365-371,
368-374, 408-414, 459-465, 548-554, 557-563**Amidation sites.**

amino acids 391-395, 696-700

Cell attachment sequence.

amino acids 428-431

Leucine zipper pattern.

amino acids 25-47

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FIGURE 61

CTCCATTAAACCACCACCAGCTCCCCAAGCCACCCCTTCAGCCATGAAAGTTCCTGCTCCTGGT
CTTGGCAGCCCTCGGATTCCTGACCCAGGTGATCCCAGCCAGTGCAGGTGGGTCAAAATGTGT
GAGTAACACCCCAGGATACTGCAGGACATGTTGCCACTGGGGGGAGACAGCATTGTTTCATGTG
CAACGCTTCCAGAAAATGCTGCATCAGCTACTCCTTCCTGCCGAAGCCTGACCTACCACAGCT
CATCGGTAACCACTGGCAATCAAGGAGAAGAAACACACAAAGGAAAGACAAGAAGCAACAAAC
GACCGTAACATCATAATAACCACTGCTATCGCCTCCACCAACTCAGAGAAATATCATTTCCAC
AGTTCCAATTCCTCCTACATTGCTGAGTACTAGCCAAGGCTCCTCTTTATGGGGCAGATATCT
ATAGCCAACCCCAAACTTCTGTCTTCTATCATTCTGTTCATCTAGTAACATAATTTGGAG
TTTGTATCTATCTTACGAGAACAATCATCATGCAGATTTCGTCCACAGGGGATCTGTTCAGTTTG
GGTCTCCAAATGAAAAATGTCAAGACAGAATTGGACATGCAAAAGATTGACTGGGAGAACAC
ACCTCTGATGGACAAAGGTGAGACAGAGCAGCCACAGGCAGGGAGAGCCTTCAGACTGCAACG
CTGGCCTGATACGTGTCAAAGGAGAGAGGGATAGAGGAGGATTGAATAGAAGGAGACTAAGAC
TGCAGCTCTAAGAAAGTCTCAGCCAAACAGATGGGGAGGCCCAAAGCAAGGCTTGCCCCTCAG
AGGAGCTCACGCAGGGCAGGAATAGCCAGGTTCTCATATCCCAGGGGTTTCAGACTTGGCTGAG
AACAGCCCCTGGAGAACATGGGGTGACTGCTACCATAGGTCTGGAAGTATGAGGCTGTCCACC
AACTATCCCCTTGAAGCAAGTTCTCTTGAAAGGAAATCTAAACAGTGCACCCCATGGCTGCC
ACGGAGTATAAGGAGGGAGAGAAAGGAGCTGAAAGTCTAGGTTTGGCCAGCTAGGTAGACTGA
CTTGTGAGGTATTTATTTATTCATTTGAGTAACAAAGCAGACAGAATACATAGCCACCATTGG
TAGTACACCCCAAAAGCAAGGATGGCATGATGCTGGTGACTCAAACGTGCCTACTCATGGTGT
CAAATTGGCATAATCCTCTTGGAAGCTGTGTGGAAATAAGCACAGAGAAGCAGAACTCTAAT
TGCTTAATCCACTAAACATTACTTCTGGGAATTGGCTCATCATAAATTATCCAAGAGAAAGCA
CAAAGTTATGGGCACAAAGGTTTTCCATATAATATTATTTAAAATGCTGAGAAAATGAAAAA
TCTAAATGGTGAAATATATACTAATGCCATCTATAAATACAAACAAATAGAATGTTTATAGAA
TAATGGAACATAATAACATTATTCAAATTTGCATTTATGCTATAGTTGTCAAATTTGTCTCCT
TATATGATACAAAACCTCATGAAATTATGACTTTTTTGTGGTTGGAAAGCAGAATTATGCA
TAAATTTCTCTTACAGTTCGATGCCCATTAGTTTTATATAACATTTATTTGACACGTACTGA
CTTCTATCTGAGAAGAACAACCAAAACACTCAGGCCTAAATAATTAAAAACGGTCCTA^{*}AAAA
CTAGCAAACCAGATAAGAAAAGATGT^{*}TAATGCCCATTCCTTAACCTTATGTCTTAGACCAAAAT
TAATTCTAGATGGTTTTAAATGACAGTGTAAGTAAAGTATTTAAAGATTGTGTGGTCAAA
TATTCAATTTAAGAGCAAGGAAATTCCTATAAATATAACAATAGAGGCAGAACTCATGTAAGA
ATAAATTGATTAGGTGGTATTAAATATTAAGTTCTTATGTATGTCAAAGATATCATTTTGAA
ATTCATCCATCTTATTGGGTATTGCAGGAGTTCATTCCTTTTTGTTTATAAATACTCTCCGT
CATATGAATAGTATTCAATTTGTATACTGGTTTGTGATGGACATTTGGGTGTTCCAGTTTA
TGGCTATTACAAATAAAGCTTCTATGAACATTTATGTACA

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FIGURE 62

MKFLLLVLAALGFLTQVIPASAGGSKCVSNTPGYCRTCCHWGETALFMCNASRKCCISYSFLP
KPDLPQLIGNHWQSRRRNTQRKDKKQQTTVTS

Important features of the protein:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 1-22

N-glycosylation site.

amino acids 50-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 79-82

N-myristoylation site.

amino acids 23-28

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FIGURE 63

GCGGAGCGCCTGGGAGAGGAGAAGGAGCCGACCTGCCGAGATGGAGGCGACCGGCACCTGGGC
GCTGCTGCTGGCGCTGGCGCTGCTCCTGCTGCTGACGCTGGCGCTGTCCGGGACCAGGGCCCG
AGGCCACCTGCCCCCGGGCCACGCCGCTACCCTGCTGGGAAACCTCCTGCAGCTACGGCC
CGGGGCGCTGTATTACAGGGCTCATGCGGCTGAGTAAGAAGTACGGACCGGTGTTACCATCTA
CCTGGGACCTGGCGGCCTGTGGTGGTCTGTTGGGACAGGAGGCTGTGCGGGAGGCCCTGGG
AGGTCAGGCTGAGGAGTTCAGCGGCCGGGGAACCGTAGCGATGCTGGAAGGGACTTTTGATGG
CCATGGGGTTTTCTTCTCCAACGGGGAGCGGTGGAGGCAGCTGAGGAAGTTTACCATGCTTGC
TCTGCGGGACCTGGGCATGGGGAAGCGAGAAGGCGAGGAGCTGATCCAGGCGGAGGCCCGGTG
TCTGGTGGAGACATTCCAGGGGACAGAAGGACGCCCATTCGATCCCTCCCTGCTGCTGGCCCA
GGCCACCTCCAACGTAGTCTGCTCCCTCCTCTTTGGCCTCCGCTTCTCCTATGAGGATAAGGA
GTTCCAGGCCGTGGTCCGGGCAGCTGGTGGTACCCTGCTGGGAGTCAGCTCCCAGGGGGGTCA
GACCTACGAGATGTTCTCCTGGTTCCTGCGGCCCTGCCAGGCCCCCAAGCAGCTCCTCCA
CCACGTACGACCTTGGCTGCCTTCACAGTCCGGCAGGTGCAGCAGCACCAGGGGAACCTGGA
TGCTTCGGGCCCCGCACGTGACCTTGTCGATGCCTTCCTGCTGAAGATGGCACAGGAGGAACA
AAACCCAGGCACAGAATTACCAACAAGAACATGCTGATGACAGTCATTTATTTGCTGTTTGC
TGGGACGATGACGGTCAGCACCACGGTCGGCTATACCCTCCTGCTCCTGATGAAATACCCTCA
TGTCCAAAAGTGGGTACGTGAGGAGCTGAATCGGGAGCTGGGGGCTGGCCAGGCACCAAGCCT
AGGGGACCGTACCCGCCTCCCTTACACCGACGCGGTTCTGCATGAGGCGCAGCGGTGCTGGC
GCTGGTGGCCATGGGAATACCCCGCACCCCTCATGCGGACCACCCGCTTCCGAGGGTACACCCT
GCCCCAGGGCACGGAGGTCTTCCCCCTCCTTGGCTCCATCCTGCATGACCCCAACATCTTCAA
GCACCCAGAAGAGTTCAACCCAGACCGTTTCCCTGGATGCAGATGGACGGTTCAGGAAGCATGA
GGCGTTCCCTGCCCTTCTCCTTAGGGAAGCGTGTCTGCCTTGGAGAGGGCCTGGCAAAAGCGGA
GCTCTTCTCTTCTTACCACCATCCTACAAGCCTTCTCCCTGGAGAGCCCGTGCCCGCCGGA
CACCTTGAGCCTCAAGCCCACCGTCAGTGGCCTTTTCAACATTCCCCCAGCCTTCCAGCTGCA
AGTCCGTCCCCTGACCTTCACTCCACCACGCAGACCAGATGAAGGAAGGCAACTTGGAAGTG
GTGGGTGCCCAGGACGGTGCCTCCAGCCTCAACAGTGGGCATGGACAGGGTTAATGTCTCCAG
AGTGTAACACTGCAGGCAGCCACATTTACACGCTGCAGTTGTTTTCCGGAGTCTGTCCCACGG
CCCACACGCTCACTTGACTCATGCTGCTAAGATGCACAACCGCACACCCATAACAACATAAA
GGGCCACAAAGCAACTGCTGGGTAGCTTTCCACAGACATAAATATAGTCCATCTGCAATCAC
AAGCACATAGCCAGGTAACCCACCAACTCCCCTGGATCTGCAGCCACACGTGGGAGTCTGGC
TGTCACCTTCACAAGCCACAGAAACGGCCACACATGTTTACAGCTCACACGCCCTCTCCATTC
ATCGAACTTCTCAGTGTCCCTGTCCCTGGTGCCTGGCACAGGGAACAGCATGCCCCCTCCGGG
GTCATGCCACCCAGAGACTGTGCTGTCTATGGCCCCAACTCATGCTCCCTCTCTTGGCTACA
CCACTCTCCCAGCCTGTGACCACCGATGTCCACACACCCCCAACCACTTGTCACACAGCTAC
CCACGTACAACATCGTCCTGGCTCCCCAGAGTATCTTCCCACTGAGACACGCCGCCCCCACAG
AGGCACAGTCCCCAGCCACCTCTGCAACTGCAGCCCTCAGTCACCCCTTTTAAAGCACCTGA
TTCTACCAAATGCAAACACATCTGGGTCTGCGATTATGCACAGAGACTTTGGACATACGAGGA
CCCTCAGACCGGAGGAACACCTGCCCAACCCCAACACGTGCTTATGTAACCACGTGGAAAGCG
GCCCCTGCTGCCCTCCACACACATACACACTCACTGATCTACAGCCCCTGTTCCGGCGTCA
GAGTCCCCACTAGACCCAGTGGAAGGGGTTAGAGACCAAGTAGGGGCCAGTTTCCAATTCACC
CTGTCAGGGAGTGAGCCGGATCTGACGTTCTTGTGACTTAAGGGTCCGGCTTGGGAATTA
GTTTGTCTTCTGGCCTTTAGCCTAAAAA

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FIGURE 64

MEATGTWALLLALALLLLTLALSGTRARGHLPPGPTPLPLLGNLLQLRPGALYSGLMRLSKK
YGPVFTIYLGWPWPVVVLVGQEAVERALGGQAEFEFSGRGTVMLEGTFDGHGVFFSNGERWRQ
LRKFTMLALRDLGMGKREGEELIQAEARCLVETFQGTEGRPFDPSSLQAQATSNVCSLLFGL
RFSYEDKEFQAVVRAAGGTLLGVSSQGGQTYEMFSWFLRPLPGPHKQLLHHVSTLAAFTVRQV
QQHQGNLDASGPARDLVDALLKMAQEEQNPGTEFTNKNMLMTVIYLLFAGTMTVSTTVGYTL
LLMKYPHVQKWVREELNRELGAGQAPSLGDRTRLPYTDAVLHEAQRLALVPMGIPRTLMRT
TRFRGYTLPQGTEVFPLLGSILHDPNIFKHPEEFNPDRFLDADGRFRKHEAFLPFSLGKRVCL
GEGLAELFLFFTTILQAFSLESPPDPTLSLKPTVSGLEFNIPPAFQLQVRPTDLHSTTQTR

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 294-313

Glycosaminoglycan attachment site.

amino acids 99-103

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 128-132

N-myristoylation sites.amino acids 51-57, 109-115, 115-121, 188-194, 207-213, 257-263,
284-290, 339-345, 370-376, 444-450**Amidation sites.**

amino acids 140-144, 435-439

Leucine zipper pattern.

amino acids 32-54, 39-61

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 433-443

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FIGURE 65

CGGACGCGTGGGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC
ATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC
TATCCCCTGAGCCCGATGGGGGCCTGATGGTGTCTCCCTAAGGACAGCATTTCAGTTTTCTTCTG
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC
CTTTGGGAAGACCATATCCTCCATACTCCTTGGCCGATTTCTCTTGGAACAACATCACTGATT
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT
CTCCCCGGGGAAACCGTTCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT
GCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCCTGGGCA
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGC
TGACCACAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGGCCCGCTCTCTGGAGGGAAGG
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTTGGAGCATCAAGTTCCAGCC
GGCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG
GGCTATTGATAAGGTCCCCTTGGTGTTCCTTCTTGATCTCCACACATTTCCCTTGGATGGG
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA
TTTATTTTTTTTTCACAGGGAAAAAAAAAAAA

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FIGURE 66

MRGSVECTWGWGHCAPSPLLLWTLTLLFAAPFGLLGKTRQVSLEVIPNWLGPLQNLLHIRAVG
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR
LLEFDSTNVSDTAAPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGS
LAFRVQAFSRSSRPAQPPRLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCPSMQE
QHSIDDEYAPAVFQLDQLLWGSLSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPFVDGLSPLVLGIMAVAL
GAPGLMLLGGLVLLLHHKKYSEYQSIN

N-glycosylation sites:

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234,
333-337

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 397-401

Casein kinase II phosphorylation sites:

amino acids 151-155, 249-253, 255-259

N-myristoylation sites:

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

Leucine zipper pattern.

amino acids 371-393

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FIGURE 67

CGGGACAGGCGCGTGAGGCCACAACACATGCGTGTATCTTGCTTGGGCTATCTTCCCTGCTCTGCCACGCCGGGT
CTGGAGAAGGGGTTTCAGCCCCAGGACATTTACTGAGAGTGGCGGAATATTGGGAGCCGCGATGTTCCCCCTTCG
GGCCCTGTGGTTGGTCTGGGCGCTTCTAGGAGTGGCCGGATCATGCCCGAGCCGTGCGCCTGCGTGGACAAGTA
CGCTCACCAGTTCGCGGACTGCGCTTACAAAGAGTTGCGTGAGGTGCCGGAAGGACTGCGTGCCAACGTGACGAC
GCTTAGTCTGTCCGCGAACAAGATCACTGTGCTGCGGCGCGGGGCTTCGCCGACGTACACAGGTACGTCGCT
GTGGCTGGCGCACAATGAGGTGCGCACCGTGGAGCGAGGCGCACTGGCCGTGCTGAGTCAGCTCAAGAACCTCGA
TCTGAGCCACAACCTTCATATCCAGCTTTCGGTGGAGCGACCTGCGCAACCTGAGCGCGCTGCAGCTGCTCAAAAT
GAACCACAACCGCTGGGCTCTCTGCCCCGGGACGCACTCGGTGCGCTACCCGACCTGCGTTCCTTGGCATCAA
CAACAACCGGTGCGTACGCTGGCGCTGGCCTTCGACGCGCTTAGCGCGCTGTACACTTGCAACTCTATCA
CAATCCCTTCCACTGCGGCTGCGGCTTGTGTGGCTGCAGGCTGGGCGCGGAGCACCCGGGTGTCTTACCCGA
GCCCCACTCCATTGCTTGTGCTCGCTCCCGCGCTGCAGGGGGTGGCGGTGTACCGCTGCCCCGCTGCCCCG
TGCACCGCCAGCGTCATCTGAGTGCCGAGCCACCGCTTGAAGCACCCGGCACCCACTGCGCGCAGGACTGGC
GTTCTGTGTACTGTCATCGCCGACGGCCACCTACGCTCGCTGCAATGGCAACTTCAGATCCCCGGTGGCAC
CGTAGTCTTAGAGCCACCGGTTCTGAGCGGGGAGGACGACGGGGTGGGGCGGAGGAAGGAGAGGGAGAAGGAGA
TGGGATTTGCTGACGAGACCCAAGCCAAACGCGGACTTCAGCACCCGCTTGCCCGGCGCCCCAGCCACACC
GCGCTTCTTGGCCCTCGCAAATGGCTCCCTGTTGGTGCCCTCCTGAGTGCCAAGGAGGCGGGCGTCTACACTTG
CCGTGCACACAATGAGCTGGGCGCAACTCTACGTCAATACGCGTGGCGGTGGCAGCAACCGGGCCCCAAAACA
CGCGCCTGGCGCGGGGGGAGAACCCGACGGACAGCCCCGACCTCTGAGCGCAAGTCCACAGCCAAGGGCCGGGG
CAACAGCGTCTGCTTCCAAACCCGAGGGCAAAATCAAAGGCCAAGGCTGGCCAAGGTGAGCATTTCTCGGGGA
GACCGAGAGCGAGCCGAGGAGGACACAAGTGAGGGAGAGGAGGCCGAAGACCAGATCCTCGCGGACCCGGCGGA
GGAGCAGCGCTGTGGCAACGGGGACCCCTCTCGGTACGTTTCTAACACCGCTTCAACCAGAGCGCAGAGCTCAA
GCCGCACGTCTTCGAGCTGGGCGTCATCGCGCTGGATGTGGCGGAGCGCGAGGCGGGGTGCAGCTGACTCCGCT
GGCTGCGCGCTGGGCGCTGGGCGCGGGGCTGGCGGAGCCCCGCGACCCGGGCGGCGACCCCTGCGCCTACT
CTATCTGTGTCCAGCGGGGGCGGGCGCGCAGTGCAGTGGTCCCGCTAGAGGAAGGCGTCAACGCCTACTGGTT
CCGCGGCTGCGGCGGGGTACCAACTACTCCGTGTGCTGGCGCTGGCGGGCGAAGCCTGCCACGTGCAAGTGGT
GTTTTCCACCAAGAAGGAGCTCCCATCGTGTGCTCATAGTGGCAGTGAGCGTATTCTCCTGGTGCTGGCCAC
AGTGCCCTTCTGGGCGCGCGCTGCTGCCATCTGGCTGGCTTAAACACCCGGGCAAGCCCTACCGTCTGATCCTGCG
GCCTCAGGCCCCCTGACCTATGGAGAAGCGCATCGCCGAGACTTCGACCCGCGTGTCTGCTACCTCGAGTCCGA
GAAAGCTACCCGGCAGCGCGGCGAGGCGGGCGGCGAGGAGCCAGAGGACGTGCAGGGGGAGGGCCTTGATGAAGA
CGCGGAGCAGGGAGACCAAGTGGGGACCTGCAGAGAGAGGAGAGCCTGGCGGCTGCTCACTGGTGGAGTCCCA
GTCCAAGGCCAACCAAGAGGAGTTCGAGGCGGGCTCTGAGTACAGCGATCGGCTGCCCCCTGGGCGCCGAGGCGGT
CAACATCGCCAGGAGATTAATGGCAACTACAGGACAGCGGAGGCTGAACCTCCGCGCGTCCGCGCCGCCATT
CCCGACCTCCACCTAGGCTGCTGGGAGCAGAGCTTAGGGCTGGCAGGACTTATGTCCCCCGTCCCCAACCTTC
ACCTACTCCTCCCCCTTACTACTCCCCAACCTTGACTACCAGGGACTTCTATTAGGGAGTGGGCGGATTTACCA
GTCCCTGCTACCCACGCTGCCATTCTCCCTGCGGGCTGAATCCCCTTCCCGCCAAGCACAGTGTATCTTAC
CCCATGCAAGACTCCACCCGAGACGGTGGGCGATATCTATGTCCCTCCATTCCCGTGCAGATTATCTGCGAAAT
CCACCCCGCAGCCCGCCCCACCGTGGGCTCTGGAGCCAGGGAACGAGCGAAGACTTTGGAAACCTCGCGGTAA
CGCGGTGGTTTCGGGGCGGAGCCAAGGCCAGTGAGTGTGGGGTCCACCTCGACCCCTCCTCCTCCCTTTC
TTTCTTTCTTTTATTTTATTTTATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
CAGGCTGGAGTGCAGTGGCGGATCTCGGCTCACTGCATCTTCCGCTCCCGGGTCAAGCGATTCTCCTGCCTC
AGCCTGCCTAGTAGCTGGGACTACAGGCGCGCGCCACCACGACCAGCTAATTTCTTCTATTTTATTTAGTAGACGG
GGTTTCACCATGTTGGCCAGGATGGTCTGGATCTCTTGACCTCAGGTGATCCATCTGCCTCGGCCTCTCAAAGTG
CTGGGATTACAGGCGTGAGGCACCGCGCCCGGCCCTCCTCCCTTCAATCCCTACTCCCAGAAGCCGGGATTCTG
TGGCAACCCCTAGTTTTAGTTCCAAAGCCTCCTGCCGCGAGGGAACCAATCCTTCTGCTCCTCCACCCGCCAC
GCACTTCTGGCCAGTTGGAGTCCAGCCCGGTGCCTGGGGCGCTTTCAGCTCCGCGCTCAGATTTTCTGTTTTC
GTTGTTTTCAAAGACAGCGACATTTCCGGTCTGGTGCTAACACCCCTTCCAGCCTCTGGGAAAATGAGTGTG
TGTGTGCGGGGGTAGGGAGGGAATGCGTTTTCTGTGCTCTCTCTCTAATTAAGCGCCGAGGACCGCGCGCC
CCTTGGCGGCTGAGCCTGTGGACTTGGTCCGGGCAATTTCTGTTGTCCGTGTGTTGGGCTTTCGGAGGTCTGT
GCGCCCAACAGCGCGCTCCCGCGGCTCCACCCGAGCCAGCCCTAGCTGGAAAGCGCGGAGGCGGAGGAAGCT
CACTGTGGCTCCCGGGCGGCTCTCTGGAGGCTCGCGCCCTAGTTTCGCACAAAGCCTGCTGACTGTGC
GACTGTGCGACGGGATCCGGATGGAGCCGAGCCCTCCGTCTCGGCTCTCGGTCTCGGCTCGCCCCGCCCCAC
CCGCCCCGTCTCGCGGGAATCGTGTGTCGCGCGGTGAGTCCCTGACAAGCGTGCCCTGTAGGAGAAAAGTC
TGTGTCTCTGTGAAGTGTGACCGTGTAGTGTAGGGGGCGGGCGGGGGGGCGGATGGGCGGGGAGGGAGGGAGGG
GAGGGGCGCGCGCGGCGGACTCGGGGCGGGTCTTTTTTCCATTTTGAAGAAAGCGTGGGGTGGGGTGGGG
GGAGTTTCAGTCTCGGGATCAGCCCTCTCCGGAAGCGCAGCACAAAGCGGGCCTGGGACGGAGTAGCCCCC
GGAGCCCGTGCCCTTTCTAAACGCGCTGTATGCAGTCAATAAAACAATCGATTGAAA

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FIGURE 68

MFPLRALWLWVWALLGVAGSCPEPCACVDKYAHQFADCAKELREVPEGLPANVTTLSSLANKI
TVLRRGAFADVTQVTSWLAHNEVRTVEPGALAVLSQLKNLDLSHNFISFPWSDLRNLSALQ
LLKMHNHRLGSLPRDALGALPDLRSLRINNRLRTLAPGTFDALSALSHLQLYHNPFHCGCGL
VWLQAWAASTRVSLPEPDSIACASPPALQGVVYRLPALPCAPPSVHLSAEPPEAPGTPLRA
GLAFVLHCIADGHPTPRLQWQLQIPGGTVVLEPPVLSGEDDGVGAEEGEGEGDGDLLTQTQAA
TPTPAPAWPAPPATPRFLALANGSLLVPLLSAKEAGVYTCRAHNELGANSTSIRVAVAATGPP
KHAPGAGGEPDQGAPTSEKSTAKGRGNSVLPSKPEGKIKGQGLAKVSILGETETETEPEEDTSE
GEEAEDQILADPAEEQRCGNGDPSRYVSNHAFNQSAELKPHVFELGVIALDVAEREARVQLTP
LAARWGPGPGGAGGAPRPGRRPLRLLLYLCPAGGGAQVQWSRVEEGVNAYWFRGLRPGTNYSVC
LALAGEACHVQVVFSTKKELPSLLVIVAVSVFLLVLATVPLLGAACCHLLAKHPGKPYRLILR
PQAPDPMEKRIAADFDPRASYLESEKSYPAGEAGGEEPEDVQGEGLDEDAEQGDPSGDLQRE
ESLAACSLVESQSKANQEEFEAGSEYSDRLPLGAEAVNIAQEINGNYRQTAG

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 587-610

N-glycosylation sites.

amino acids 52-55, 121-124, 337-340, 364-367, 474-477, 563-566

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 397-400

Casein kinase II phosphorylation sites.amino acids 19-23, 202-205, 289-292, 246-249, 411-414, 431-434,
433-436, 440-443, 544-547, 583-586, 650-653, 700-703**N-myristoylation sites.**amino acids 15-20, 48-53, 165-170, 296-301, 351-356, 362-367,
390-395, 419-424, 514-519, 536-541, 557-562, 561-566, 610-615,
661-666, 716-721**Amidation site.**

amino acids 522-525

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 10-20, 603-613

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FIGURE 69

GGCGGCGGGAGCAGCGAAGGGGGCGGCAGGGATCCTCCAGGCTGCCGGCTGGGAAGGCGTGGG
CGACCCGGTGTGTGGCGCGCCCAGAGCCCCGCGTTTCAGCCCTAGGGAAGGAAGCCAGTTGAG
GGAAGTTCTCCATGAATGTACGTCACAATGATGATGACCGACCAAATCCCTCTGGAACCTGCCA
CCATTGCTGAACGGAGAGGTAGCCATGATGCCCCACTTGGTGAATGGAGATGCAGCTCAGCAT
GTTATTCTCGTTCAAGTTAATCCAGGTGAGACTTTCACAATAAGAGCAGAGGATGGAACACTT
CAGTGCATTCAAGGACCTGCTGAAGTTCCTATGATGTCACCCAATGGATCCATTCTCTCCCAT
CATGTGCCTCCAGGTTATATCTCACAGGTGATTGAAGATAGTACTGGAGTCCGCCGGGTGGTG
GTCACACCCCAGTCTCCTGAGTGTTATCCCCAAGCTACCCCTCAGCCATGTCTCCAACCCAT
CATCTCCCTCCCTATCTGACTCACCATCCACATTTTATTTCATAACTCACACACGGCTTACTAC
CCACCTGTTACCGGACCTGGAGATATGCCGCTCAGTTTTTCCCCAGCATCATCTTCCCCAC
ACAATATATGGTGAGCAAGAAATTATACCATTTTATGGAATGTCAAGCTACATCACCCGAGAA
GACCAGTACAGCAAGCCTCCGCACAAAAAAGTGAAGACCGCCAGATCGATCGCCAGAACC
CTCAACAGCCCTCCTTCTTCTATCTACAAAAGCAGCTGCACAACAGTATACAATGGCTATGGG
AAGGGCCATAGTGGTGGAAGTGGCGGAGGCGGCAGCGGTAGTGGTCCCGGAATTAAGAAAAA
GAGCGACGAGCAAGAAGCAGCCCAAAGTGAATGATTGAGACTTGCAAGAATATGAGTTGGAA
GTAAAGAGGGTGCAAGACATTCTTTCGGGAATAGAGAAACCACAGGTTTCTAATATTCAGGCA
AGAGCAGTTGTGTTGTCTGGGCTCCCCCTGTTGGACTTTCCTGTGGACCCACAGTGGTCTT
TCCTTCCCTTACAGTTACGAGGTGGCCTTATCAGACAAAGGACGAGATGGAAAAATACAAGATA
ATTTACAGTGGAGAAGAATTAGAATGTAACCTGAAAGATCTTAGACCAGCAACAGATTATCAT
GTGAGGGTGTATGCCATGTACAATTCGTAAGGGATCCTGCTCCGAGCCTGTTAGCTTCACC
ACCCACAGCTGTGCACCCGAGTGTCTTTCCCCCTAAGCTGGCACATAGGAGCAAAAGTTCA
CTAACCTGTCAGTGGAAAGGCACCAATTGACAACGGTTCAAAAATCACCAACTACCTTTTAGAG
TGGGATGAGGGAAAAAGAAATAGTGGTTTCAGACAGTGCTTCTTCGGGAGCCAGAAGCACTGC
AAGTTGACAAAGCTTTGTCCGGCAATGGGGTACACATTCAGGCTGGCCGCTCGAAACGACATT
GGCACCAGTGGTTATAGCCAAGAGGTGGTGTGCTACACATTAGGAAATATCCCTCAGATGCCT
TCTGCACCAAGGCTGGTTCGAGCTGGCATCACATGGGTACGTTGCAGTGGAGTAAGCCAGAA
GGCTGTTACCCGAGGAAGTGATCACCTACACCTTGGAATTCAGGAGGATGAAATGATAAC
CTTTTCCACCCAAAATACACTGGAGAGGATTTAACCTGTACTGTGAAAAATCTCAAAAGAAGC
ACACAGTATAAATTCAGGCTGACTGCTTCTAATACGGAAGGAAAAAGCTGTCCAAGCGAAGTT
CTTGTGTTGTACGACGAGTCTGACAGGCCTGGACCTCCTACCAGACCGCTTGTCAAAGGCCCA
GTTACATCTCATGGCTTTAGTGTCAAATGGGATCCCCCTAAGGACAATGGTGGTTCAGAAATC
CTCAAGTACTTGCTAGAGATTACTGATGGAAATCTGAAGGTGAAGTTTTTGGCAATTGTTTT
ATTCAAATCCAATAGCAAGCTCTGTTTTCTAATATAGTAAATGTCTTTATAGTAATAGTGAGT
AATCATTAATTCTAAAGATAGAATTATTATTACAATAAACAACTTTAGTCACATATTGGCAG
TTTTTCTATTTCAAACACAGCACCAGAGATCAGAGTCTACTTGAACTTACATTTGTGTTATT
TAACAATTTTTCTGTATCTTTTTCATTTGGTGTGTTTTGTTTTGTTTATCTTTTGTGTTTTCT
TTGGTTTGGTTTGTGTTTTGTTTTGTTTTGAGATACGATCTCTGTACACAGGCTGGAGGGC
AGTGGCACAGACATGGCCCATGTCAGTCTCAGACTCCTGGGCTTAAGTGACTCTTCTGCCACA
GAAGATGAGGAAGAATACATTTTTCATAGTGATGGGGTCTCACTATGTTATCTAGGCTGGTCT
CAAACCTCTGGCCTCAAGCAACCCTCCACCTTGGCCTCCCAAAGTGCTGGGACTATAGACATG
AATCACCACACTCAGCTTCCATGTCTTTTTATGAACTAGGGTTCCTAATTAATCAGATAAATT
TGGTATTTTCATCTCCTAACTTGCCATATGTTTTCTGGAAATCTTATAAGCAGCCGAGAGTG
GTGGCTCACGCTGTAGTCCCAGCACTTTGGGAGGCTGAGGTGGGTGGTCAGGAGATCAAGACC
ATCCTGGCCAACATGGTGAAACCCGCTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTG
GCAGGCACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGAAGAATTGCTTGAACCCAGCAG
GCGGAGGTTGCAGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGTGACAGAGTGAGACTC
TGCTCTCAAAAAAAAAAAAA

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FIGURE 70

MMMTDQIPLLELPPLLNGEVAMMPHLVNGDAAQHVLVQVNPGETFTIRAEDGTLQCIQGPAEV
PMMSPNGSIPPIHVPPGYISQVIEDSTGVRVVPVTPQSPECYPPSYPSAMSPTHHLPPYLTHH
PHFIHNSHTAYYPPVTGPGDMPPQFFPQHHLPHTIYGEQEIIIPFYGMSSYITREDQYSKPPHK
KLKDRQIDRQNRNLNSPPSSIIYKSSCTTVYNGYKGKHSGGSGGGSGSGPGIKKTERRARSSPK
SNDSDLQEYELEVKRVQDILSGIEKPQVSNIQARAVVLSWAPPVGLSCGPHSGLSFPYSYEVA
LSDKGRDGKYKIIYSGEELECNLKDLPATDYHVRVYAMNSVKGSCSEPVSFTHSCAPECP
FPPKLAHRSSSLTLQWKAPIDNGSKITNYLLEWDEGKRNSGFRQCFFGSQKHCKLTKLCPAM
GYTFRLAARNDIGTSGYSQEVVCYTLGNIPQMPSAPRLVRAGITWVTLQWSKPEGCSPEEVIT
YTLEIQEDENDNLFHPKYTGEDLTCTVKNLKRSTQYKFRLTASNTEGKSCPSEVLVCTTSPDR
PGPPTRPLVKGPVTSHGFSVKWDPPKDNGGSEILKYLLEITDGNSEGEVFGNCFIQIQ

Important features of the protein:**N-glycosylation sites.**

amino acids 69-73, 254-258, 401-405

Glycosaminoglycan attachment sites.

amino acids 229-233, 234-238, 236-240

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 416-420, 535-539

Tyrosine kinase phosphorylation site.

amino acids 319-326

N-myristoylation sites.amino acids 52-58, 227-233, 228-234, 230-236, 231-237, 232-238,
235-241, 239-245, 402-408, 610-616**Amidation site.**

amino acids 414-418

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 290-301

ATP/GTP-binding site motif A (P-loop).

amino acids 546-554

CUB domain proteins profile.

amino acids 294-301

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FIGURE 71

AAGTCATTCAAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTT
GCTGTAACCTGCTGCTCAGTCCACCATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAAACCAGGAAGCCGAA
GACCTGTTCTATCAAAGTTCACCTTGCTTCTTGGAAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATG
AATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAATGTATCCACTACAAGAA
ATTGAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGTCTCAGAAGACAAG
AGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAAACCCAGATAAT
CCACAAGAATGCTTATTACTTGAACCAGGTTTGAATGAAATAATGGCAACAGTTTAGACTACAATGAGAGGCTC
TGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTGAAA
AATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGACTATGAAGTAAATGGGGTA
GATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATAT
GAACATCTTCATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTTCTATATCAGTCCAATTGGATGCCTC
CCTGCTCATTGCTTGGTGATATGTGGGGTAGATTTTGGACAATCTGTACTCTTTCAGAGTTCCCTTTGGACAG
AAACCAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAG
AAGTTCCTTGTATCTGTTGGTCTTCTTAATATGACTCAAGGATTCTGGGAAAATTCATGCTAACGGACCCAGGA
AATGTTTCAGAAAGCAGTCTGCCATCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACA
AAGGTGACAATGGACGACTTCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGCTGCA
CAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGAAAATCATGTCACTTTCTGCA
GCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCAACCCGATTTTCAAGAAGACAATGAAACAGAAATAAAC
TTCCTGCTCAAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATG
GTCTTTAAAGGGGAAATTTCCCAAAGACCAGTGGATGAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGGGGTG
GTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGTTTCTGATGATTACTCATTC
ATTCGATATTACACAAGGACCCTTTACCAATCCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGC
CCTCTGCACAAATGTGACATCTCAAACCTCTACAGAAGCTGGACAGAACTGTTGTAAAGAAATACCTCAAATGTT
GAACCTCTCCTAGTATTAGTATTACTCATTTCATGCCTAGGTTTGTATTTGATTTCTTTGTTCTAAAAAGAAA
ATTTTATGGCCTCAAATGTCTCTATTACAAACCAAAACATTTAATTTGTGGTCAGACAGGAACCTAGACCATAC
AACAATTGGGTGGGCCACCTCTTTCTCCCTATCATACTACAGCCCTCTCTTCTGTTAATTGGAAGGAAAGAG
CGGTTTAGGGTGGAAATATATCTGTTAATATGCATTCTTTCTTATCTGCCAGAAGCAAATTTAGCCAAGTCAAAG
AGAAGAAACCATAGATCATAGATGTAATATATGTACATCTGGAACCCCTCAAAGGCCCTGAACCCCTTTTTTT
TGTGTAGCAATATGCTGAGGCTTGGAAAATCAGAACCCCTGGACCCTAGCATTGGAATGTTGTAGGAGCAAGAA
CATGAATGTAAGCCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAGAATTCCTT
TGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCCAAAGCATCAAAGTGAGGATAAGCCTAAATCAGCTC
TTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATGAGGC
AGTACTTTTTTAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAA
GAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGG
CCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATAC
AGCCAACACTTGACCTCCTAACAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGA
TAGTGGTTGGCATTGTCACTCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAG
AAAATCCTTATGCTCCATCGATATTAGCAAAGGAGAAAAATAATCCAGGATTCCAAAACACTGATGATGTTTCAGA
CCTCCTTTTAGAAAAATCTATGTTTTCTCTTGGAGTGATTTTGTGTATGTAAATGTTAATTTATGGTATAG
AAAATATAAGATGATAAAGATATCATTAATGTCAAACCTATGACTCTGTTTCAGAAAAAAATTTGTCCAAAGACA
ACATGGCCAAAGGAGAGAGCATCTTCATTGACATTGCTTTTCAGTATTTATTTCTGTCTCTGGATTTGACTTCTGTT
CTGTTTCTTAATAAGGATTTTGTATTAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTTCAGGGA
TAATCTAAATGTAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTGGATCT
TGTATGGAATATGGATGGATCACTTGTAAAGACAGTGCCTGGGAACCTGGTGTAGCTGCAAGGATTGAGAATGGCA
TGCATTAGCTCACTTTCAATTAATCCATTGTCAAGGATGACATGCTTTCTTCACAGTAACTCAGTTCAAGTACTA
TGGTGATTTGCCACAGTGATGTTTGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATC
CAGGGAACAGGTAGAGGACATTGCTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAAAACCTA
GAGCCAGGGGCTCCGTGAACCTCCCAGAGCATGCCTGATAGAACTCATTTCTACTGTTCTCTAACTGTGGAGT
GAATGGAAATTTCAACTGTATGTTCAACCTCTGAAGTGGGTACCCAGTCTCTTAAATCTTTTGTATTTGCTCACA
GTGTTTGAGCAGTGTGAGCACAAAGCAGACACTCAATAAATGCTAGATTTACAAAA

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FIGURE 72

MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMN
NAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTI
YSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNE
MARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY
PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFQKPNIDVTDAMVDQAWDAQRI FKEAEKFF
VSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGGH
IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLK
QALTIVGTLFPFTYMLEKWRWMVFKGEIPKDQWMKKWEMKREIVGVVEPVPHDETYCDPASLF
HVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLL

Important features of the protein:**Signal peptide:**

amino acids 1-17

N-glycosylation sites.

amino acids 53-57, 90-94, 103-107, 322-326, 432-438, 546-550

N-myristoylation sites.

amino acids 260-266, 286-292, 395-401

Cell attachment sequence.

amino acids 204-207

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 371-381

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FIGURE 73

CCCACGCGTCCGAGCGGGGTGGACAAAGTGGCGTGTGTGCTGCGACCCCGAGGGAAGATGAACG
GGACGCGGAAGTGGTGTACCCTGGTGGACGTGCACCCAGAGGACCAGGCGGCGGGCAGGA
AGACCTATGCCATGGTGTCCAGCCACTCAGCTGGTCATTCTCTGGCTTCAGAACTGGTGGAGT
CCCATGATGGACATGAGGAGATCATTAAGGTGTACTTGAAGGGGAGGTCTGGAGACAAGATGA
TTCACGAGAAGAATATTAACCAGCTGAAGAGTGAGGTCCAGTACATCCAGGAGGCCAGGAACT
GCCTACAGAAGCTCCGGGAGGATATAAGTAGCAAGCTTGACAGGAACCTAGGAGATTCTCTCC
ATCGACAGGAGATACAGGTGGTGTAGAAAAGCCAAATGGCTTTAGTCAGAGTCCCACAGCCC
TGTACAGCAGCCCACCTGAGGTGGACACCTGTATAAATGAGGATGTTGAGAGCTTGAGGAAGA
CGGTGCAGGACTTGCTGGCCAAGCTTCAGGAGGCCAAGCGGCAACACCAGTCAGACTGTGTGG
CTTTTGAGGTCACACTCAGCCGGTACCAGAGGGAAGCAGAACAAAGTAATGTGGCCCTTCAGA
GAGAGGAGGACAGATGTCCAGAGTGATTGGAGAATGTCCTGGGGGAATGAAGTTCCTTCCACA
AACACAGCTCAGTTCTTAGCAACAACTGTTTGTCTTTCTACTTGCTCCATCTGCAGCCTACG
CTGCCCTGGCCTCCTGCAGACAGATAGTGGGGTTACCTGGCAAGGCCTGGTGAGAGCCAGTGA
ACCTAAGCTTTGACTGGGTGGCCTTGTCTTTCTGGGGAGGAGGGAATGTACATTCAGGGAGTA
GCCTTTTGCGGAAAAATTCTCTAGGGCTACAGACAGTCATGTGTGACTTCTCTCTGCTGTGAA
AACTCCCAGAGTCTCTTTAGGGATTTTCCCTAAGGTGTACCACCAGGCACACCTCAGTCTTCT
TGACCCAGAGCCTGAAAACCTGTTTTCACTGGGTTCACCAGTCCCAGCAAATCCTCTTTGTA
TTTATTTTGCTAAGTTATTGGTGGTTTTGCTTACATCTCATGATTGATATAATACCAAAGTTC
TATAGCCTTCTCTTGCAATTTGGATTGTCTGAAACCGGGAAACTGTTCCCATTAGGCTT
GTTAATGTCAGAGTGACACTATTATGAATCTTTCTCTCCCTTTCCTCTGCCTGTTTCTTCTCT
CTTTCTCCTTCAAACCTTGCTCTGCAGCTAAGGAAGGTGAGTCTACTTTCCTGAGGCTTTGGG
GTCAGAGTATATGTTGTTTGGAGAAAGAGGGCAATCAGGACTCTTCTGGGACCCAGATGAGTT
CTTCACTAGCCCTTCTGAACCCCTTGCTCCATAATTGGTCTTTTATCCTGGCTCTGAATGACC
CTGCAGGTCATCATGGTTTTCTTTTTTTATTGTTTTTTTTTTTTCTGAGACAGAGTCTCACT
CTGTACCCAGGCTGGAGTGCAGTGGCGCGATCTCAGCTCACTGCAACCTCTGCCTCCCGGAT
TTAAGCGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTGTGCCACCACGCCTG
GCTGATTTTTGTATTTTGTAGAGATGGGGTTTACCATACTGGCTAGGCTGGTCTCGAATT
CCTGACCTCAGGTGATCCACCCACCTCGGCTTCCCAAAGTGCTAGGATTATAGGCTTGAGCTA
CTGCGCCCCGGCCCATGGTGTTTTCTTTAGGGCTCTTCTACAGCCTTGAGAAGTAGATAGGC
ATCAGAGTATGGTACTATAGGAATCAGAAAAATTCAAACAAATGTGGATTAAAGTGTTTAGGC
TCTATGTGGCTCACGCAGCCAGAATCCTTAAGTCTGTGTGTTTCTGTGTCTCAAGACTGGGCT
CACATTCTGGCTTTGTCCATAACAATGCTCTGGGATTTACGGGAGTTCCTCATTTGTAAAAT
GAGGGGGTCAGAGCAGGTGATATCCATGTTTCTCCCTTCTGATATTGTTGTCTGTGGCATA
TTCTTTGTATGGCGAATTTAATAAATTATATTAATGTGTCA

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FIGURE 74

MNGTRNWCTLVDVHPEDQAAAGRKTYAMVSSHSAGHSLASELVESHGHEEIIKVYLKGRSGD
KMIHEKNINQLKSEVQYIQEARNCLQKLREDISSKLDRLGDSLHRQEIQVVLEKPNGFSQSP
TALYSSPPEVDTCINEDVESLRKTVQDLLAKLQEAKRQHQSDCVAFEVTLSTRYQREAEQSNVA
LQREEDRCPE

Important features of the protein:

Signal peptide:

amino acids 1-39

N-glycosylation site.

amino acids 2-6

Amidation site.

amino acids 21-25

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FIGURE 75

GCTTGCACACATGGCTCCGGAGGCTCCGGTTGCCCATCCGAGCCCCTGCCAGGCTCTAACGTTCCCAACTGACAA
CACCAGTAACATAAATATAGGAGCAGATGGTGGGGACGGGCTGTGCGAGCGGCTCCTTTGCAGAGGTCTCCGGACT
GCAGATAAGGCTCAGGCCCTTTTGTGAGAAGCAGACCAGCCTGGGGGCTGGCGGCAGGACACCTGTGTCTGCATG
CTGAAGAAGATGGGTGAGGCCGTGGCCAGAGTAGCAAGGAAGGTCAACGAGACGGTGGAGAGCGGCTCTGACACT
CTGGACCTGGCCGAGTGCAAGCTGGTCTCCTTTCCATTGGCATCTACAAGTCTGCGGAATGTCTCTGGCCAG
ATCCACCTCATCACCTGGCTAACAACGAGCTTAAAGTCCCTCACCAGCAAGTTCATGACCACATTCACTCAGCTC
CGAGAGCTCCACCTGGAGGGGAACCTTCTACACCGCTCCCCAGCGAGGTCACTGCCCTGCAGCACCTCAAGGCC
ATTGACCTGTCCCGAACCAGTTCAGGACTTCCCTGAGCAGCTTACCGCCTGCCGGCGCTGGAGACCATCAAC
CTGGAGGAGAACGAGATCGTAGATGTGCCCGTGGAGAAGCTGGCCGCCATGCCAGCCTTGCGCAGCATCAACCTC
CGCTTCAACCCACTCAACGCCGAGGTGCGCGTGATCGCCCCGCGCTCATCAAGTTGACATGCTCATGTCTCCG
GAAGGCGCAAGAGCCCCCTACCTTAGGCCACCCTCCTCATGCCACCCAGCAAGGGACAGAGGCCACAGGCCTG
GAACCCTGGAAGGAGGGAGGCCCATGGGAGGCCAAGCCTGGGGGCTGGGGGCGGCTGGGCGGAGCAGCAGCTGG
TGGGTGGGGTGCGAGCTGGTCTGGATAGATAGCTTACAGCAGTAGTGGGCTCTGGAATGCCAAGGGAAGAGGCAA
GGTGGGGCCTGCAGCCTGGACTCGGCACTCACAGCTGCTGTGCAAACTCAGGCAGATCTCCTGCCCTCTCTGAGC
CTTGTCACCTTGAAAAAACAGGACCCTTTCCCTCCTTTGGGCTCCCTGGAGGTTTTAAAGCAGTACGTGCCCTCCA
AGTTACCTCCAGATCAGCAGGCACAGGTGGGCATTGCCAGGTATTTTCTGAGCCCCCTGCGGGTTTGAGGCCTTGT
TTTTAGTGCTGAGAGCCAGTTGCTGCCCTGAGAAGAGAAGACAACCTCCATCTATTTATTGCTTCTGAGAACTG
ACCTGGATGCGGCCCTCTGCAGGGCCAGTCTTCACTCCTGTGGTCCCTGGACTGGTGGGAACCTGAACCTAGGAG
TCCTGGGAGAGCTGTGGTGGGAATATGGGCTGGCACTGCTGCAGGGCAAGAACATTCATGTAGGAGCCCCGAGGAC
CANCANGCTGGGAATGGGAGCAAGTCAGTCAGCTCTGTCACTCCACAGTTAACAATTTGGCGGGGTGGGAA
GTCCTGAGTGCTCCGTCCCTCTAGCATCACTCTGAGCTGCGGGAGAGGTGGCCAGAGAACAGCAGAGTCAGTT
ACACCTGCAGCTCTTGTCTAAAGTGATTAGATGGCCACCCTCACCAGTGTCCAGTCCAGCAGCAGCCTGGCTGCC
TTGTCTATGGCCTCCTGGGGGAGAAGGCGATGTGGACCACGGGATTTGTAGCCAGCCAGCTCCCAGGCCAACGCC
CAAAGCCCTGATGACCTGGTTCTTCTGAGGCCCTCAACCTGGCATCTTAGGGTATGGTTCAGGCAACAGGGTGACC
AGCTGTCTGGTTTCCAGGACATGGAACCTTCAATGCTAAACTGGGACATTACCCAGCAAGTGGGGATGGTTG
GTCCCCTACCAGGAGAGGGCCTGGGGCTCTTGCTTCCCGAGAAGCCTGTGGCTTGAAGAACCTTGACTGCTTGG
TCCTCAGGTATCTACCTCCCACCTTCTCCTCATCTGTGGAGCAAGCCAACCTCAGTGCCCCAGACCCACCTGATC
TGCATCTTTGTTTGTCTCCAGAGACACCTGAGGCCCCAGAGCTTGAGGCAAGCCAGGCCGTCCAAATCCTGTGTG
CCGTGGACGAGTGGCCACTTTACTACTCCTAAGGCTAAGATGTTGAGAGCTCAGACCACTGCTCAGAGCAGTAAT
CCCTGCTCAGAAATGCTCCCAGTTCCCTCGTCCCTGCCAGGTCTCTTGTCTCTTGGGAAGGAACCTGATAGGTCGG
GCCATTGTTGGGCCATCACTGAGCGCTCAGTATCTCAAGAGACTCTGTTCACTCTGCTCGTATCCCAAGGCCTGG
TTGGTCAAACCTCTGGGCAAAGGGTTTTTCAGGATGAGGAGGTCAAGACAGGATGTCCAGAGCTACCGAGTTCATCT
GTGGGTGTTGGGGCAAGTGGGGGCTGAAGTCTGTGAGGCTGCGCTGGCCCCACCTGCCTTGTGCCCTGGAGT
GGGGTTTTCTCCTTGTGAAGAAGAGGCATCCTTCTCTGATGTGCACAAACACAATGTATGACCAGAGCCTTGCAA
CTCAAAGTGTGGTCTGTGGACCAGCAGCGGCAGTGACACCTGGGAGCTTGTAGGAATGCAGAGTCTAGGCCTCA
CCCTATACCTCCCGACTCAGACCCTGCATTTTAGCAAGACCCCCAGCTGATTCTATAAGCACTTTAGAGTTTGA
GAAGCAAGGACCTAGGCTGGGGATGTCTCCGAGCAGAGGGTGAAGTTTCTCAGTCTCTCCCTGCCACTTCC
AGGGATCTGAGCCTGTGTTGAGCCTCCTCCCTAAGGCTAAGATGTTGAGAGCTCAGACCACTGCTCAGAGCAGTAAT
TCTGATGGCACTCCTGAAGAAGGGAGTGTGACCTGCAGTACCAGGAGATGAGGGTAGGTGTGCCAGCCCTC
CAGACCCGGCCTTCTGTTAAGCCCTGCATGCCAAGCTGCCTGCTGCCAGGCTCCTCACCTCAGGCCTTTGAA
GGGGCAGCTTCTGGAAGTTGTTTTCTCCTCTGCTTGGAGAGTTTGGCCTTGTCTGTCTTGAAAGTGTGGGCAGC
CACAGATGCCCCCAATCAGAGCTCACAGTGAGTGAGCCCCTAAGCTTCAGTCTGCAATAAAGAATGCATTGGTT
TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 76

MLKKMGEAVARVARKVNETVESGSDTLDLAECKLVSFPIGIYKVLARNVSGQIHLITLANNELK
SLTSKFMTTFSQLRELHLEGNFLHRLPSEVSALQHLKAIDLSRNQFQDFPEQLTALPALETIN
LEENEIVDVPVEKLAAMPALRSINLRFNPLNAEVRVIAPPLIKFDMLMSPEGARAPLP

Important features of the protein:

N-glycosylation sites.

amino acids 17-21, 47-51

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FIGURE 77

CACCAACAAGCAATCGTTCATGAGAAAGCCGTGCACCCGCTGCAGTTGGGCCATGTGGTCCGCATCGTATTCCAC
TAGGTCCCCATTGTACACCAAGTACTGTCCCGCGCTCTCCAGCAGATGCCTGCAGCCTTCCACCTTCTCAAGCAG
GGTGGTGTGAGTGCCTGCTTTCTTCTCGCTGGACCGGAGCCGTGCGGGGAGGCACCCCGGGGGTGGAGAA
AAAGCCGGCCTGGCCTCGGAGGTGGTCTCGGCCCCCGCCCCACCGACTCCCTCCTCCCTCCAGAGGCGGCGGC
GGCTCCGGCGGCAGCAGCGGCAGGCAGCAACGTAAGCGGGATGCTCTCCAGGCTGCTTTTCTGCTCGGTACAGAA
ATGGCTGAGCTGGTACATCTCGCTCTCCAGGTAGGAGATCTCGCGGGCCGTCTCTATGAACTGCCGGTAGTTCTG
GTAGACGTTGCGCTTCAGGTTCTGCGCCGTCTCCTCCGCCAGCGCCTGGATGCGCTGCCGGTGTCTGGAGGTC
CCGGTCCCCATCCGACTGCTGCGAGAGCTGCTTACGTAACGCCGCGCCTCAAACCCCCCTGACTCCAGCTGCCG
ACGAGGCGGGCTCGCCCCACTGTCCGACATCGCCATCGCCATTTCTCTCCGGGTCTCACGCACTCACTGTCACTA
TCGGCGCCGAGCCGCGCGGCTGTCTAGACCCACCAAGGCCAACCGAGCTCCTGGGCTGAGGAAGCAGGAATG
GGAACGAGACGAGTACGCCTGCGCCGGGTCTGAGCGTCAGACACTGCGCCTGCGCAAGTGGGCGGAGCGCAGACA
TTGCGCCTGCGCAGCAATGCCATCGGTTAAAGCGCATGCGCAAGATGAGCTATTGCGGAAGTGAGGGGAGGGAGA
GGCCGAGAGAAATTTCCGTACTGCGCATGAACCGAGCGTGACGTTGAGGTTTGAATAACCGGCAAAGAGTAAAG
CTGAAACTAGCTTCTGAAAGCTTCTGAGGCCCGAGCCCTGTGAGCCAGGTTCTGCGCCCACTAGGAGGTGT
CATGCTGACTGCTTTTTTAAAGCCCTAGAATCTTGGCTTCGGCGTTTGGGGTAAGCTCCGTTCTCGTTCTCAA
GCGCGTTTCCGCGAATCTCGCGGGATTGACGGGCGCTCTCGAGAGCCGGCATCTCCTAGGAGCTAGTCTGGTC
CTCGGCTAGGCGGCTTGGGGTTCGCGGCGTAACCTGGGGAGCCAGCCTGACGCCGCGGACCCCGCCTGTGATCCTG
GCAACGATGGATGATGACTTGATGTTGGCACTGCGGCTTCAGGAGGAGTGGAACTTGCAAGGAGGCGGAGCGCGAT
CATGCCCAGGAGTCCCTGTGCTAGTGGACGCGTCTGGGAGTTGGTGGACCCACACCGGACTTGCAGGCACTG
TTTGTTCACTTTAACGACCAATTTCTTCTGGGGCCAGCTGGAGGCCGTCGAGGTGAAGTGGAGCGTGCGAATGACC
CTGTGTGCTGGGATATGACAGCTATGAAGGGAAGGGTGAATGTGTTCCATCCGTCTCAGCGAACCCTTTTGAAG
TTGAGGCCAAGAAAGGATCTTGTAGAGACCTCCTGCATGAAATGATACATGCCTATTTATTTGTCACTAATAAC
GACAAAGACCGAGAAGGGCATGGTCCAGAAATTTGTAAACATATGCATCGCATCAACAGCCTGACTGGAGCCAAAT
ATAACGGTATACCACTATTTTACGATGAGGTGGATGAGTATCGGCGACACTGGTGGCGCTGCAATGGGCGCTGC
CAGCACAGGCCACCGTATTACGGCTATGTCAAACGAGCTACTAACAGGGAACCTCTGCTCATGACTATTGGTGG
GCTGAGCACCAGAAAACCTGTGGAGGCCTTACATAAAAAATCAAGGAACAGAGAATTACTCAAAAAAGGCAAA
GGAAAGGCAAACTAGGAAAGGAACAGTATTGGCCGAGAGAATAAAGGTACCTTCGTGTATATTTCTTCTGATT
TTTATGTGACCATAGCTATGATGTAAAGACAATACTGTCTTCAGAGAACTGGTATTAAGATAAACTTAAGGATC
GTTTCTGGTGTAGAAGCTTCAAGTGTAGCTTAAGGAAAAATCCCCTGTCCATGAAATGATGGTAGGAAAC
AGACTTTGCTCTGTACAGAAGTAAGTAAAGTAGGAATAGTTTCCATGGATATTTTTATTTTTATTAACTTTTT
CAGTTTCTTTTTATTTCAAAGAAACAAAATTAATCTCTGATAATATTTGAGGTAAAGTTCCTTTCCCTATCTTGA
CTCACTGAGTTATTAGGAAACAGAAGGCAAAAGATTGTCAAATAAAAAACAATAATTCAAGTAACAATGCCCGG
AATATACGTCCTAACTACACCCCTTCTATCAGCTGGATTCTATCCAAGTGAATCTATTGATGTATGTATGTTCA
TTCAAAGAAATGGGAAAAGGATATGACATATATTTGCCAGTACTTCATCTTCAAGATTTACCCTTTTCTGTGAAG
TTCAGAGTTACTGAAGATGCTTCTTCCCTTGGGAAGTTGTTGACCCAAGAACATAGGTTATATTTCCCAAATCTT
TAATTATTGAGTGAAAAGAGCTATAGATGAATTGATATGGAAAGACCGTATCTTCATTTTCTGTAGTAGAAGAAA
GATAAGAAATGAGGCAGCAGATTTTCCCTCCTGGAATTACACATAAAGGACACTAAGCAATTTTCAAGGTAAATGT
TGCCTTGTGTTGGTCTTTGGCATGATAAGATTCTTTATTTAAATATGAGAGAATTTTTTTTTATCCTTTATATT
CTCTCAATATCAGAATCCTGAATCTGAAGATTGCCCTCCTCCCATTAATAGGATTGTATGGATGTAAGATGGA
ATAAAATACTAGTCTTCAATTTGAGAAAAGTACATTAGTTTAAATGTTTGTACTGTATTTCTTTTGTAGTTGA
GGCACTTACATAACAATCTTCTTTGCTTTTTTGGCAGATAAACCCAAACAGAGGTGAGGCCCAGCTAGTAATCCCT
TTTAGTGGGAAAGGATATGTTCTAGGAGAAAACAGCAATTTACCTTCACCTGGGAACTGATCACTTCACATGCC
ATTAATAAAACCAAGATCTTTTAAATCAAACCATTCAGCAAATGCTGTAAGACCTAATTTCTAAAATCAAGGTG
AAATTTGAACAGAATGGTTCAAGTAAAAATTTCTCATCTGGTCTCCCTGCTGTAGTAACAGTCACCAAAATGTT
CTAAGCAACTACTTTCTAGAGTATCATTTGCCAACCAAAAGGCTTTTCAGAGGTGTGAATGGATCTCCAAGGATA
AGTGTAAACAGTTGGCAACATCCCTAAAACCTCAGTCTCTTCTAGTTCTCAGAGAAGGGTTTCATCTTCTAAGATA
TCCCTAAGAAATTTCTTCAAAGTAACGGATCAGCATCTGTGATGCCATCCCAGGATGTGAGTGGGTCTGAAGAT
ACATTTCCCAAATAAACGACCTAGGCTAGAAGATAAAAAAAA

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FIGURE 78

MDDDLMLALRLQEEWNLQEAERDHAQESLSLVDASWELVDPTPDLQALFVQFNDQFFWGQLEA
VEVKWSVRMTLCAGICSYEGKGGMCSIRLSEPLLKLRPRKDLVETLLHEMIHAYLFVTNNDKD
REGHGPEFCKHMRINSLTGANITVYHTFHDEVDEYRRHWWRCNGPCQHRPPYYGYVKRATNR
EPSAHDYWWAEHQKTCGGTYIKIKEPENYSKKGKGKAKLGKEPVLAAENKGTfVYILLIFM

Important features of the protein:**Signal peptide:**

amino acids 1-41

N-glycosylation sites.

amino acids 148-151, 217-220

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 184-187

Casein kinase II phosphorylation sites.

amino acids 30-33, 121-124, 154-157, 187-190, 192-195

Tyrosine kinase phosphorylation site.

amino acids 211-218

N-myristoylation sites.

amino acids 59-64, 85-90, 146-151

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 108-117

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FIGURE 79

CGGACGCGTGGGTGGCAACCAGGAGAAGCCAAACTTGGTCCCCCGGCTCGCGGAGTGCCTGCG
AGCGGTGCTC**ATG**GCGCTCTATGAGGTCTTCTCTCACCCGGTCGAGCGCAGTTACCGCGCGGG
GCTCTGCTCCAAAGCCGCGCTGTTCTGCTGCTGGCCGCTGCGCTCACGTACATCCCGCCGCT
GCTGGTGGCCTTCCGGAGCCACGGGTTTTGGCTGAAGCGGAGCAGCTACGAGGAGCAGCCGAC
CGTGGCTTCCAACACCAGGTGCTGCTCGTGGCCCTGCTCGGACCCGAAAGCGACGGGTTTCT
CGCCTGGAGCACGTTCCCCGCTTCAACCGGCTGCAAGGGGATCGCCTGCGCGTCCCGCTCGT
TTCGACTAGAGAAGAAGACAGGAACCAGGATGGGAAGACGGACATGTTACATTTTAAGCTGGA
GCTTCCCCCTGCAGTCCACGGAGCACGTTCTCGGTGTGCAGCTCATCCTGACTTTCTCCTATCG
ATTACACAGGATGGCGACCCTCGTGATGCAGAGCATGGCGTTTTCTCCAGTCCTCCTTTCTGT
CCCCGGATCCCAGTTATACGTGAACGGAGACCTGAGGCTGCAGCAGAAGCAGCCGCTGAGCTG
TGGTGGCCTAGATGCCCCGATACAACATATCCGTGATCAACGGGACCAGCCCCCTTGCCTATGA
CTACGACCTCACCCATATTGTTGCTGCCTACCAGGAGAGGAACGTTACCACCGTCCTGAATGA
TCCCAACCCCATCTGGCTGGTGGGCAGGGCCGAGATGCTCCATTTGTGATTAATGCTATCAT
CCGATACCCTGTGGAAGTCATTTCTTATCAGCCAGGATTCTGGGAGATGGTAAAGTTCGCCCTG
GGTACAGTATGTCAGCATCCTGCTTATCTTCTCTGGGTGTTTGAAAGAATCAAGATCTTCGT
GTTTCAGAATCAGGTGGTGACCACCATTCCTGTGACAGTGACGCCCCGGGAGACTTGTGTAA
GGAGCACTTATCC**TAG**AAAGGCCATTTCTGAAGACTCAGCAGGACCGTGGCTGCCTCATTGTC
ATCTTCTGGGAACATCTTAGGACCTTTTGAAAGAGCCCAGCGGACACCTGCGGGCTTGTGTGC
TTTTCCCTCAGAGACAACGGTTCTTTCCGTTTTTGCTCTACACAGTTCCGTATCTTCAGAGCT
CCTGCAGAATTGTCAGGGACTAGTTTGTGGAAGGTCTGAGAGTTCTGGAGGCTATAATTAG
CTTTTTGGGTTTTCTTCTTTGCCTTAGCGTTGAATTTAGGAGAAAATTGCAGTCAGTTCAG
ACATCTTGGAAGAGTCCCATCTCTGGTCAAGCAGAGACTTTTCTCTGTTGAACTGAGGAAC
ACACTGTGCATTTCTTCTTCTGTTGTGAGCCACTCTTACTCTTTTCAGGGCTCTCTTGTGAC
AAACATGCCAATCACTAGCACTTGCACCCCTGGGCTTCTCCATTTCCCATTCACAGCTTTGA
TTTCCAGAGCTGAGGCCTTTAACTGGAGACCTGGAGGGGCAGGGCCCCAAGGGCAAGGGCCGCA
TTAGCACAGGCAATCAGGGAGGGCCGCTGAAGGACACTTGGACCGTCCACCTGCCCCAGCCCA
ACAGTCAGTCATCTGTCATCAGCTCAGCTGAGCAGCCCTGGATCTTTGCCGTACTGTGACTGG
GCTCTTTGCCCTATTTTTCCCTCTGTCTGTGCCCTGGATGGCAGGCTGAAGTCAGAGGGGCT
GTTTCATTCTCAGCCCCCTCAGCAGCACTGGGGGAAGAAAGCATTGTCACAACAGGTTCTTTC
TGGCCCTCACCCAACAGCCTGGGCACCTGGCCCTCCTCCTCTTGACAGCCCTCCCCCTTCT
GCAAAGGACAGGGGCGACAGGGGTGGTGTGGGATTGGCTCCCGCTGCCTGACAACCACAAG
TTTATTTGGAAGGCTAGCGGGAAGCCCAGCGGCTGGCGTTTCCCTGACTAAGGAACAGGGTG
CCCATCAGAGTGGGGCGGGCAGCTTTGGGAAGGACACAAGAAGCAGTAAGAGTGTAAGAGGA
TGCTGGCCTGGGCAGGCCAGTCCAGCCTGGCCACTAGCAGAATACCAAGCAGTCCAGTGGATT
ACCCTCGTGGCTAAGCAAGTGTCTGCAGGAGCAGAGATGGCTGGAAGGGGCTCTGCACACGG
AAGATGGCTTGTTACAGCCATTACCTCCTGAGGATGTGGGCAGTCTCCTCCAAGAACACATG
GAGCTGCTTCTGATCCCAAGCAGGTCAATTGCCACTGGAAGGACATGGCCCCGGTGATCCATG
CTTCATGCCCACCCAGAAACACACCCCTCAGTGTGTGCCTCAGTTTACTTTGGAGATCAGTTG
TCGTTTTTAGTGCTCCTTTAGGCTTACTAAAACAGTTTTGGAAACAAAGCTATTTTGAAGTAT
TCAAGCAGAGGAATTCCCTAACTGACCCCTTGTCTTTTTTTAATATTACAGGCTGTTTTAT
ATGCCTAAATTTTTTTCTTAAGATCTAAACGAAAAATAGTTTCTTGTTTAAATTCACATAAGG
CAATGAGATATGGAAGATGACAAGATACGTATAAACATTGGTTTGCATCTTATTAAATTATT
CTAATGCAAATCTTGATAAAGAACCATGATGTTTTGTAACCTTTCTAATTAAAATGTTCAAA
ATGAG

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FIGURE 80

MALYEVFSHPVERSYRAGLCSKAALFLLLAALTYIPPLLVAFRSHGFWLKRSSYEEQPTVRF
QHQVLLVALLGPESDGFRAWSTFPAFNRLQGDRLRVPLVSTREEDRNQDGKTDMLHFKLELPL
QSTEHLVGVQLILTFSYRLHRMATLVMQSM AFLQSSFPVPGSQLYVNGDLRLQQKQPLSCGGL
DARYNISVINGTSPFAYDYDLTHIVAAYQERNVTTVLNDPNPIWLVGRAADAPFVINAIIRYP
VEVISYQPGFWEMVKFAWVQYVSILLIFLWVFERIKIFVFQNVVTTIPVTVTPRGDLCKEHL

Important features of the protein:**Signal peptide:**

amino acids 1-34

Transmembrane domain:

amino acids 268-284

N-glycosylation sites.

amino acids 194-198, 199-203, 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 51-55

Tyrosine kinase phosphorylation site.

amino acids 250-259

N-myristoylation site.

amino acids 187-193

Cell attachment sequence.

amino acids 307-310

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FIGURE 81

GCCGGGAGCTTCCCTG**ATG**GTGCCGCCGCTCCGAGCCGGGGAGGAGCTGCCAGGGGCCAGCTGGGCAGGAGCCT
GGGTCCGCTGCTGCTCCTGGCGTTGGGACACACGTGGACCTACAGAGAGGAGCCGGAGGACGGCGACAGAGA
AATCTGCTCAGAGAGCAAAATCGCGACGACTAAATACCCGTGTCTGAAGTCTTCAGGCGAGCTCACCACATGCTA
CAGGAAAAAGTGCTGCAAAGGATATAAATTTGTTCTTGACAATGCATCCCAGAAGATTACGACGTTTGTGCCGA
GGCTCCCTGTGAACAGCAGTGCACGGACAACTTGGCCGAGTGTGTGTACTTGTATCCGGGATACCGATATGA
CCGGGAGAGACACCGGAAGCGGGAGAAGCCATACTGTCTGGATATTGATGAGTGTGCCAGCAGCAATGGGACGCT
GTGTGCCACATCTGCATCAATACCTTGGGCAGCTACCGCTGCGAGTGCCGGGAAGGCTACATCCGGGAAGATGA
TGGGAAGACATGTACCAGGGGAGACAAATATCCCAATGACACTGGCCATGAGAAGTCTGAGAACATGGTGAAAGC
CGAACTTGCTGTGCCACATGCAAGGAGTTCTACCAGATGAAGCAGACCGTGCTGCAGCTGAAGCAAAAGATTGC
TCTGCTCCCCAACATGCAGCTGACCTGGGCAAGTATATCACTGGTGACAAGGTGCTGGCCTCAAACACCTACCT
TCCAGGACCTCCTGGCCTGCCTGGGGGCCAGGGCCCTCCCGGCTCACCAGGACCAAAGGGAAGCCCAGGCTTCCC
CGGTATGCCAGGCCCTCCTGGGCAGCCCGGGCCACGGGGCTCAATGGGACCCATGGGACCATCTCCTGATCTGTC
CCACATTAAGCAAGGCCGGAGGGGGCCCTGTGGGTCCACCAGGGGCACCAGGAAGAGATGGTCTAAGGGGGAGAG
AGGAGCGCCTGGGGCCAGAGGGTCTCCAGGACCCCTGGTCTTTGACTTCCTGCTACTTATGCTGGCTGACAT
CCGCAATGACATCACTGAGCTGCAGGAAAAGGTGTTCGGGCACCGGACTCACTCTTCAGCAGAGGAGTTCCCTTT
ACCTCAGGAATTTCCAGCTACCCAGAAGCCATGGACCTGGGCTCTGGAGATGACCATCCAAGAAGAAGTGAAC
AAGAGACTTGAGAGCCCCAGAGACTTCTACCC**ATAG**CACATCCCAACACCGTCACGCCAAAGGAAGAGAAAGAT
CAACTCACCTGCAGTTAAACCATCTAAAGAGAAGAAAGACCACTGGAGACCTAGAAAACATACATTTTTCTCTTC
TCTTCTCCTGACGTCTCTCCACTCCTCTCTTCCAAATACGATGCTATTTTCAGAGTCCCCTCCTAGGCCTGCAG
ACATGAGGGAGTGAATGATTGATTTACCTGCTTCTACTAAGAGTCCATTGGGGTGGTTTGCATTGTAACCTTTTC
TTTTACATCCTATTTTCCAGGAACCTTTGGATTAAAGTACTCTCACAGTGTCTTAAATCATAAATCTTGAAGTT
AAATTTGGCAGAGTATCAAAAGGGGAAAATGACAAAGTGAGCTCTAAGAAAATGTGAGGCTACTTCTAAGATGT
GTGTTACAATAGACCATAACTCCTCTAGTATCAAAATTTGGGGCTCTTCAGTTAAAAGGGGTGGGGAGGACAAA
CGTGTGATGTGCTTTGGTGGAGAATTTTTCTGTGCTTCTAGTAGACTTTAAATATTGTATCCCTTTGTCAA
ACCTTGTTTTCCCAATTAATTAAGAGAGGAGAGAATTAATGGCGTTTAGAGAAGATAGAAAAGAATCACAGT
CATATATTTACTGTTATATAGATTGCCACATTCTAAAATTCAAATACGGTGCTTAAGGTTTCATGCCATGCTTAT
CTGTAAGTATCCTATTTAGGGAAGAAGATTAACTCTCTTTTCAAAAAACAAAGTGAATGCCTGGATTACAT
TAAACAATGGGCTCTCGTTTGCTATAATATTTTAAAGCTGTTTAAATCAACAGTGGAGTCTGCTCTATAAATATA
GATTATTTGTTCAATAAAGTGGCTGAGCTTAGAGAGAGGTGCAGAATTCCTGGTTCTGAGCAGGTGCCAGAGG
TACCATTAGGTGCCATGATCCAGGCTGAACCAATATACAGTGGGGCTGAAGTCTGCAAGGAGGTTGCTGGCTTGG
GCTGACCTCACTAATGCCATCAGCAGCGGTAGGTAAATTTTTCTCCTTGGGTATTACAAGTTTTTGTCTGGAGC
CAACCAAGCTTGCCACCAACATATTGAGAGTAATACACTATTGAAAGTTATCTTGGATGGGGAGAAAAAAAATA
GTGGTTTTCTTGTGTTGCAAAAACCTTCTTCTATTCTCATTTTTTTCTTAATTTCTTAAATTTAGTCCAAGTTC
CAGTTCTTTTAGGCCTTCTCTTTGATTTATTTTCCCTGCATGTGAGAAGCAGTTCAGAAAAAGGTCTATATCTC
CACCTCCTAGTGAGTTAGAGTGTCTTCTCAGAGACCTCTGGGTGGCAAAGGGAAGCATGTTCTGCCAAGGTTT
GCTGTGGATTGAGAAGCACCAGGAGCAAGAGACCAGAAGGATGATCTGCTCCTTTGTAACGTTGTTGAGGGCCCT
CTTGTTTCCAATGAGCAGCTTATAGGTTACTCACAGTCCACTTTCTCACTGGACACACAAAGTGGCTCTTTATCT
ACCTTTGCGGGAGATTTTCACTCTCCTGCAATGATCGTTCTCACACTCATATTAGCTCATGTTGGAATTTCCCA
TCCTGCCATGTCCTTTCCCATTTCTTTTGGCTTTTTTGCTCCACCTTTTAGCCACATCATTTAACTCCACTA
CTGTGAAAGCTTGCTTAAAGAAAATCCCTCTTGGCCGGGTGTGGTAGCCACGCCTCTAATCCCAGCACTTTGGG
AGGCTGAGGCGGGGAGATCACAAGGTGAGGAGATCGAGACCAGCCTGACCAACATGGTGAAACCCTGTCTCTACT
AAAAATACAAAATTAGCTGGGCGTGTGGCACACACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAA
TTACTTTAACCTGCGGGGGGAGCCTAGATTGCGCTACTGCACTCCAGCCTAGGCAACAGAGGGAGACTCTGTCTC
ATTAAAAA

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FIGURE 82

MVPPPPSRGGAARGQLGRSLGPLLALLLALGHTWTYREEPEDGDREICSESKIATTKYPCLKSS
GELTTCYRKKCKCKGYKFVLGQCIPEDYDVCAEAPCEQQCTDNFGRVLCTCYPGYRYDRERHRK
REKPYCLDIDECASSNGTLCAHICINTLGSYRCECREGYIREDGKTCTRGDKYPNDTGHEKS
ENMVKAGTCCATCKEFYQMKQTVLQLKQKIALLPNNAADLGKYITGDKVLASNTYLPGPPGLP
GGQGPPGSPGPKGSPGFPGMPGPPGQPGPRGSMGPMGSPDLSHIKQGRRGPVGPFGAPGRDG
SKGERGAPGPRGSPGPPGSFDFLLMLADIRNDITELQEKVFGHRTSSAEFPLPQEFPSYP
EAMDLGSGDDHPRRTETRDRLRAPRDFYP

Important features of the protein:**Signal peptide:**

amino acids 1-34

N-glycosylation sites.

amino acids 142-148, 182-188

Tyrosine kinase phosphorylation site.

amino acids 125-132

N-myristoylation sites.

amino acids 10-16, 143-149, 155-161, 196-202, 250-256

Amidation site.

amino acids 299-303

Aspartic acid and asparagine hydroxylation site.

amino acids 150-162

Cell attachment sequence.

amino acids 176-179

Clq domain proteins.

amino acids 247-280

Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 144-165

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FIGURE 83

ATCTGAGTGAGCTAACTGACACAATGAACTGTCAGGCATGTTTCTGCTCCTCTCTCTGGCTC
TTTTCTGCTTTTAAACAGGTGTCTTCAGTCAGGGAGGACAGGTTGACTGTGGTGAGTTCCAGG
ACCCAAGGTCTACTGCACTCGGGAATCTAACCACACTGTGGCTCTGATGGCCAGACATATG
GCAATAAATGTGCCTTCTGTAAGGCCATAGTGAAAAGTGGTGGAAAGATTAGCCTAAAGCATC
CTGGAAAATGCTTGAGTAAAGCCAATGTTTCTTGGTGACTTGCCAGCTTTTGCAGCCTTCTTT
TCTCACTTCTGCTTATACTTTTGCTGGTGGATTCCTTTAATTCATAAAGACATACCTACTCTG
CCTGGGTCTTGAGGAGTTCAATGTATGTCTATTTCTCTTGATTCACCTGTCAATAAAGTACATTC
TGCAAAAGCAAAAA

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FIGURE 84

MKLSGMFLLLSLALFCFLTGVFSQGGQVDCGEFQDPKVYCTRESNPHCGSDGQTYGNKCAFCK
AIVKSGGKISLKHPGKC

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 26-32, 52-58, 56-62, 69-75

Kazal serine protease inhibitors family signature.

amino acids 40-63

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FIGURE 85

GGAGCAGACACACAGACCCGGGCGGAGGCCCTCTTCTAGCCCTGCGGGAACCGGACAGTTC
CCCAACTGGGGACTCTGGAACCACAGCTCCTAAATCATCAAATTCTCAAGCTTTTTTTTTTCCC
TCTCTTCGTCCCAGCCATCCCAGTCTTCTTCTTCTTTTTTTTTTTTTTAACCTATTGTTTTTT
TCGCTCCTGTCAATTATGAAAGTGGTCACGCCATTCAATATTAAGACTTGGAGGGAATTGGGGA
AAGAAAAGAAAGAATCTAAAAGAAGAGAAGCGACCGGTGCTTTTAAGGGTGTCTAATTTTCAA
AAGAGACGTCTGGGAGTATTTTGCTCTGGGCGTTTGGAGCAACTTCGCGGACAGCGGAGCTCG
CCCAGCATGGATGTTCCAGGTTACAGGCGCCTTCTTCTGAGAACGACCCTGGCCTTGAACG
TCAGAGCCGGGGACGAAGGCCCGGAGGCTGCTGCGAGCTCCGCGCGTTCCCTTCGCGCCCTT
CCGCGCCGCTCGCGCCGGCGCCGGCCTCCACCCCGCGCGCCGCTCCACACAGTCCCGATGC
AGGCGCCCGGCGGGGGCCACTCGGGCTGCGGCTGATGATGCCCGGGCGCCGGGGGGCGCTGC
GCGAGCCTGGCGGCTGCGGATCCTGCCTGGGGGTGGCGCTGGCCCTGCTGTTGCTGCTACTGC
CCGCCTGCTGCCCCGTGCGGGCGCAGAACGACACGGAGCCCATCGTGCTGGAGGGCAAGTGCC
TGGTGGTGTGCGACTCCAGCCCGTCGGCGGACGGCGCCGTCACCTCCTCCCTAGGCATCTCCG
TGCGCTCCGGCAGCGCCAAGGTGGCCTTCTCCGCCACGCGGAGCACCAACCACGAGCCGTCCG
AGATGAGCAACCGCACCATGACCATCTATTTGACCAGGTATTAGTAAATATTGGCAACCACT
TTGATCTTGCTTCCAGTATATTTGTAGCACCGAGAAAAGGGATTTATAGCTTCAGCTTCCACG
TGGTCAAAGTGTATAACAGACAAACCATCCAGGTCAGTTTAATGCAGAATGGCTACCCAGTGA
TCTCGGCCTTTGCAAGGAGACCAGGATGTCACCAGAGAAGCTGCTAGCAATGGCGTGCTGCTGC
TCATGGAAAGGGAAGACAAAGTGCATCTCAAACCTTGAGAGAGGCAACCTCATGGGGGGCTGGA
AATACTCCACATTCTCGGGCTTCTTGGTGTTCCTCTATAACACAGAGCCCCCTAGATGGTG
GGGGAATGGCAAACCTGGACCCAGGACTCCGCCCTTTAAACACCCTGAACTTACTGGAATTGG
ACACCTTGTTTCCAACCTCCGTCAGACTGTTGCAGTAGAAGAATGATTTCTTTTGAACCTCC
AGTACTTTTGTGTTTTGTTTTTGGAACTGACAATTCCTCGGGAACCTGGCCTCTAATTAGT
TTTAGATGACAAGGTCTTAAGGAGAAATGAAATTATCGATTTGAGCAATTTGTACCTGTGATT
GTAAAGTCAATATCGGATTTTATTGTTGGGACCATGGACCTCTTTTGTGTTGTATGTTGTATTG
TCGTCCCAACGGAAGGAGAGCTCCTGACTCCAGGATGGGCTGCAGGTTGCAGTCAGGGCTTGA
AGTAGGAGCCCAGCAAAGAACCACCTGCTGGACAGTCCTTGACATGTGTTCTGTGTGTGCTG
TATAGCCTTAAGAAAAAGAATGGCTTCACTTTTCTGATTCTTCCCCCACCATGTGGCT
GGGAGGACTTGGGAGGGGGATGGGGACATTGGGAACCTGTCAAGAAGTGCTTTATCCAGAGAA
GCAAATTTTGCACGATTGGACTGCAATTTTTGTTTTGTATTGTTTGTGTTTTTTCTTGAAAAG
CTTTACTTTTCTTTCCACACTCAGCTCTCCCTCCTCAACCCCACTTTTATTTTTCTTGCTGGG
GTTGAGGAGAGAAAATATAGAATTCCTGGATAAGACCAAAACAAAACAAATATAAATACCT
GTATGTTTTGTTTTAGACGAGACCAAATAAACAAAAGTATCTGTTTATCAAAGTAAAAGTA
ACACAATGGACAATTCTGCTTATTCTCTCAAAGAGATTCTAAGATGCACCTTTAGAACTATTA
ATAGCAACCTGCATTTTTTTTTTAATTTATACTTCAGAATCCTTTAAGAACCTGGTGTTCTGA
GTGGTCCTGAATCATATAAGTTGGTAATGGAAGCTGTAATGACCAAGTCCCCTAAACATACTA
TGTCTTTGCCACGTGTGCTGTGACTTCTCTGTGGGTGATTTAATTTATTTGGATCCACCTCTG
AGTGAGCGCACAGTGATCAGGTGCTTCAAAGCCAACAGACCAGCTCCTCTTCTCCGGATCCT
CTTTTGATCTGCCCAGGAAAGGGATGCATTGACACTCTCCTGCATGCACCTGGCGAGAAGCCA
CCTGAAAGTCACTGTGGTTAAAGATATTGGTGGAGGTACCCAGGAGCACTGTTACAAATCCT
TCTTGTTTTGGCATCTCGTACAACATTATTAAGACACAGCTGAGAGTTGATGGGTGTGTAATG
CATATGCCAAGGAAATGTCATAATCCCAAAGCAATCAAAAAGGAGACCTCAAACCAGATGTT
AATTTGTTCTTTGTGTAACAATGTAACCAAAATATTGATGATAAAAGTCATAATTTAAGATTC
AGAATAAATGGGTTTGATGTCTGGCAAAAAAAAAAAAAA

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FIGURE 86

MQAPGRGPLGLRLMMPGRRGALREPGGCGSCLGVALALLLLLLPACCPVRAQNDTEPIVLEGK
CLVVCDSPPSADGAVTSSLGISVRSGSAKVAFSATRSTNHEPSEMSNRTMTIYFDQVLVNIGN
HFDLASSIFVAPRKGIYSFSFHVVKVYNRQTIQVSLMQNGYPVISAFAGDQDVTREAASNGVL
LLMEREDKVHLKLERGNLMGGWKYSTFSGFLVFPL

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation sites.

amino acids 53-57, 110-114

N-myristoylation sites.

amino acids 26-32, 27-33, 29-35, 33-39, 76-82, 205-211

Amidation site.

amino acids 16-20

Clq domain signature.

amino acids 117-148

Clq domain proteins.

amino acids 115-149

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FIGURE 87

AGGGCCCGCGGGTGGAGAGAGCGACGCCCCGAGGGG**ATG**GCGGCAGCGTCCCGGAGCGCCTCTG
GCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGGGCGGCTCCGGCGTCTTCC
AGCTGCAGCTGCAGGAGTTCATCAACGAGCGCGGCGTACTGGCCAGTGGGCGGCCTTGCGAGC
CCGGCTGCCGGACTTTCTTCCGCGTCTGCCTTAAGCACTTCCAGGCGGTTCGTCTCGCCCCGAC
CCTGCACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGCTGTCCGGGACG
ACAGTAGCGGCGGGGGGCGCAACCCCTCTCCAAGTGCCTTCAATTTACCTGGCCGGGTACCT
TCTCGCTCATCATCGAAGCTTGGCACGCGCCAGGAGACGACCTGCGGCCAGAGGCCCTTGCCAC
CAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCCTAGCTGTGGGTGCAAGTGGTTAT
TGGATGAGCAAACCAGCACCCCTCACAAGGCTGCGTACTCTTACCGGGTCATCTGCAGTGACA
ACTACTATGGAGACAACTGCTCCCGCCTGTGCAAGAAGCGCAATGACCACTTCGGCCACTATG
TGTGCCAGCCAGATGGCAACTTGTCTGCTGCGCGGTTGGACTGGGGAATATTGCCAACAGC
CTATCTGTCTTTCCGGCTGTCTATGAACAGAATGGCTACTGCAGCAAGCCAGCAGAGTGCCTCT
GCCGCCAGGCTGGCAGGGCGGCTGTGTAACGAATGCATCCCCACAATGGCTGTGCCACG
GCACCTGCAGCACTCCCTGGCAATGTACTTGTGATGAGGGCTGGGGAGGCCTGTTTTGTGACC
AAGATCTCAACTACTGCACCCACCACTCCCCATGCAAGAATGGGGCAACGTGCTCCAACAGTG
GGCAGCGAAGCTACACCTGCACCTGTGCGCCAGGCTACACTGGTGTGGACTGTGAGCTGGAGC
TCAGCGAGTGTGACAGCAACCCCTGTGCAATGGAGGCAGCTGTAAGGACCAGGAGGATGGCT
ACCACTGCCTGTGTCTCCGGGCTACTATGGCCTGCACTGTGAACACAGCACCTTGAGCTGCG
CCGACTCCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAACCAGGGGGCCAACATATGCTT
GTGAATGTCCCCCAACTTCACCGGCTCCAAGTGCAGAGAAGAAAGTGGACAGGTGCACCAGCA
ACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAAGCCGCATGTGCCGCTGCCGTC
CTGGATTACGGGCACCTACTGTGAAGTCCACGTCAGCGACTGTGCCCCGTAACCCCTTGCGCCC
ACGGTGGCACTTGCCATGACCTGGAGAATGGGCTCATGTGCACCTGCCCTGCCGGCTTCTCTG
GCCGACGCTGTGAGGTGCGGACATCCATCGATGCCTGTGCCTCGAGTCCCTGCTTCAACAGGG
CCACCTGCTACACCGACCTCTCCACAGACACCTTTGTGTGCAACTGCCCTTATGGCTTTGTGG
GCAGCCGCTGCGAGTTCCCCGTGGGCTTGCCGCCAGCTTCCCCTGGGTGGCCGTCTCGCTGG
GTGTGGGGCTGGCAGTGCTGCTGGTACTGCTGGGCATGGTGGCAGTGGCTGTGCGGCAGCTGC
GGCTTCGACGGCCGGACGACGGCAGCAGGGAAGCCATGAACAACTTGTTCGGAATCCAGAAGG
ACAACCTGATTCTTCCGCCCCAGCTTAAAAACACAAACCAGAAGAAGGAGCTGGAAGTGGACT
GTGGCCTGGACAAGTCCAAGTGTGGCAAACAGCAAAACCACACATTGGACTATAATCTGGCCC
CAGGGCCCCCTGGGGCGGGGGACCATGCCAGGAAAGTTTCCCCACAGTGACAAGAGCTTAGGAG
AGAAGGCGCCACTGCGGTTACACAGTGAAAAGCCAGAGTGTCCGATATCAGCGATATGCTCCC
CCAGGGACTCCATGTACCAGTCTGTGTGTTTGATATCAGAGGAGAGGAATGAATGTGTATTG
CCACGGAGGT**TAA**GGCAGGAGCCTACCTGGACATCCCTGCTCAGCCCCGCGGCTGGACCTTC
CTTCTGCATTGTTTACA

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FIGURE 88

MAAASRSASGWALLLLVALWQQRAAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFRVCLK
HFQAVVSPGPCTFGTVSTPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHAPG
DDLREALPPDALISKIAIQGSLAVGQNWLLDEQTSTLTRLRYSYRVICSDNYYGDNC SRLCK
KRNDHFGHYVCQPDGNSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGRLCNE
CIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYCTHHSPCKNGATCSNSGQRSYTCTCRPG
YTGVDCLELSECDSNPCRNGGSKDQEDGYHCLCPPGYGLHCEHSTLSCADSPCFNGGSCR
ERNQGANYACECPPNFTGSNCEKKVDRCTSNPCANGGQCLNRGPSRMCRCPGFTGT YCELHV
SDCARNPCA HGGTCHDLENGLMCTCPAGFSGRRC EVRTSIDACASSPCFN RATCYTDLSTDTF
VCNCPYGFVGSRCFPVGLPPSFPWVAVSLGVGLAVLLVLLGMVAVAVRQLRLRRPDDGSREA
MNNLSDFQKDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPGPLGRGTMPGK
FPHSDKSLGEKAPLRHLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIATEV

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 530-552

N-glycosylation sites.

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

Glycosaminoglycan attachment site.

amino acids 96-100

Tyrosine kinase phosphorylation site.

amino acids 340-347

N-myristoylation sites.amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631**Amidation site.**

amino acids 471-475

Aspartic acid and asparagine hydroxylation site.

amino acids 339-351

EGF-like domain cysteine pattern signature.amino acids 173-185, 206-218, 239-251, 270-282, 310-322, 348-360,
388-400, 426-438, 464-476, 506-518**Calcium-binding EGF-like:**amino acids 224-245, 255-276, 295-316, 333-354, 373-394, 411-432,
449-470

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FIGURE 89

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGAC
TTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTCAGAGATCCTGCAGC
CGCCCAGTCCCGGGCCCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTACTCC
TCCTTTTTCATTTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCC
GAGCGTGGAAGAATGGGGTTCCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCCCGATT
CAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCA
GAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAACAAAAACATATCCT
CCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTTGATAACTTGAACCTGCTAAAGGCA
ATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCACTTGATAAT
AAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGATTATGACTCT
ACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATCAACTAGACGGG
ACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAGAAAATGAC
AGAGCCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTATCACAGAAAGCCAA
GCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAAC
AATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCA
GAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACA
GTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGAC
AACTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAA
AAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAG
ATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTTCCTACCTTGAAAACCTGGAT
GAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAATGCTACTGACAATATAAGCAAG
CTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAAGCAGCT
AAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCACAAAAGATGATAACTCCAACCCAGGA
GGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTGGAAGCCATCAGAAAAAATATT
GAATGGTTGAAGAAACATGACAAAAAGGGAAATAAAGAAGATTATGACCTTTCAAAGATGAGA
GACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAAGAAGCC
GAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAAATGGCAAAAGATCCAGGAGTCTTTCAAC
TGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCC
AAGGGTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGC
TTTCTTCCCGTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAA
AAA

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FIGURE 90

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENK
PGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDDYSTKSG
LDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTL
EDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPKVTMAAIQDGLAKGENDETVSNT
LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVK
YGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEK
EYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFIN
KQADAYVEKGILDKEEAIAIKRIYSSL

Important features:**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

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FIGURE 91

TGCATCAGTGCCCAGGCAAGCCCAGGAGTTGACATTTCTCTGCCCAGCCATGGGCCTCACCCCT
GCTCTTGCTGCTGCTCCTGGGACTAGAAAGGTCAGGGCATAAGTTGGCAGCCTCCCTGAGGTGCT
GCAGGCACCCGTGGGAAGCTCCATTCTGGTGCAGTGCCACTACAGGCTCCAGGATGTCAAAGC
TCAGAAAGGTGTGGTGCCGGTTCTTGCCGGAGGGGTGCCAGCCCCTGGTGTCCTCAGCTGTGGA
TCGCAGAGCTCCAGCGGGCAGGCGTACGTTTCTCACAGACCTGGGTGGGGGCCTGCTGCAGGT
GGAAATGGTTACCCTGCAGGAAGAGGATGCTGGCGAGTATGGCTGCATGGTGGATGGGGCCAG
GGGGCCCCAGATTTTGCACAGAGTCTCTCTGAACATACTGCCCCAGAGGAAGAAGAAGAGAC
CCATAAGATTGGCAGTCTGGCTGAGAACGCATTCTCAGACCCTGCAGGCAGTGCCAACCCTTT
GGAACCCAGCCAGGATGAGAAGAGCATCCCCCTTGATCTGGGGTGCTGTGCTCCTGGTAGGTCT
GCTGGTGGCAGCGGTGGTGCTGTTTGCTGTGATGGCCAAGAGGAAACAAGAATCCCTCCTCAG
TGGTCCACCACGTCAGTGGACTCTGGACCGGCTGCTGAATTGCCTTTGGATGTACCACACATTA
GGCTTGACTCACCACCTTCATTTGACAATACCACCTACACCAGCCTACCTCTTGATTCCCCAT
CAGGAAAACCTTCACTCCCAGCTCCATCCTCATTGCCCCCTCTACCTCCTAAGGTCCTGGTCT
GCTCCAAGCCTGTGACATATGCCACAGTAATCTTCCCGGGAGGGAACAAGGTGGAGGGACCT
CGTGTGGGCCAGCCCAGAATCCACCTAACAAATCAGACTCCATCCAGCTAAGCTGCTCATCACA
CTTTAAACTCATGAGGACCATCCCTAGGGGTTCTGTGCATCCATCCAGCCAGCTCATGCCCTA
GGATCCTTAGGATATCTGAGCAACCAGGGACTTTAAGATCTAATCCAATGTCCTAACTTTACT
AGGGAAAGTGACGCTCAGACATGACTGAGATGTCTTGGGGAAGACCTCCCTGCACCCAACTCC
CCCACTGGTTCTTCTACCATTACACACTGGGCTAAATAAACCCCTAATAATGATGTGCAAAAAA
AA

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FIGURE 92

MGLTLLLLLLLLLGLEGQGIVGSLPEVLQAPVGSSILVQCHYRLQDVKAQKVWCRFLPEGCQPLV
SSAVDRRAPAGRRTFLTDLGGGLLQVEMVTLQEEDAGEYGCMVDGARGPQILHRVSLNILPPE
EEEETHKIGSLAENAFSDPAGSANPLEPSQDEKSIPLIWGAVLLVGLLVAAVVLFAVMAKRKQ
ESLLSGPPRQ

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 161-181

N-myristoylation sites.

amino acids 17-23, 172-178

Amidation site.

amino acids 73-79

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FIGURE 93

GGCGGCGTTGCCGGGCTCTCCGGAAGGAGACGTGGCGGCGGTTGGGCGGTTGATACCCGGGCG
CTTTATAGTCCCGCCGCTCCTCCTCCACCTCCTCCTCCTCCTCCTCCTCCTGGGGCAGAG
GAGGTTGTGGCGGTGGCTGGAGAAAAGCGGCGGCGGAGG**ATG**GAGGAAGGAGGCGGCGGCGTAC
GGAGTCTGGTCCCGGGCGGGCCGGTGTTACTGGTCCTCTGCGGCCTCCTGGAGGCGTCCGGCG
GCGGCCGAGCCCTTCCTCAACTCAGCGATGACATCCCTTTCCGAGTCAACTGGCCCCGGCACCG
AGTTCTCTCTGCCCACAACTGGAGTTTTATATAAAGAAGATAATTATGTCATCATGACAACTG
CACATAAAGAAAAATATAAATGCATACTTCCCCTTGTGACAAAGTGGGGATGAGGAAGAAGAAA
AGGATTATAAAGGCCCTAATCCAAGAGAGCTTTTGGAGCCACTATTTAAACAAAGCAGTTGTT
CCTACAGAATTGAGTCTTATTGGACTTACGAAGTATGTCATGGAAAACACATTCGGCAGTACC
ATGAAGAGAAAAGAACTGGTCAGAAAATAAATATTACGAGTACTACCTTGGGAATATGTTGG
CCAAGAACCTTCTATTTGAAAAAGAACGAGAAGCAGAAGAAAAGGAAAAATCAAATGAGATTC
CCACTAAAAATATCGAAGGTCAGATGACACCATACTATCCTGTGGGAATGGGAAATGGTACAC
CTTGTAGTTTGAACAGAACCGGCCCGAGATCAAGTACTGTGATGTACATATGTCATCCTGAAT
CTAAGCATGAAATTCTTTCAGTAGCTGAAGTTACAACCTTGTGAATATGAAGTTGTCATTTTGA
CACCCTCTTGTGCAGTCATCCTAAATATAGGTTTCAGAGCATCTCCTGTGAATGACATATTTT
GTCAATCACTGCCAGGATCTCCATTTAAGCCCCCTCACCTGAGGCAGCTGGAGCAGCAGGAAG
AAATACTAAGGGTGCCTTTTAGGAGAAATAAAGAGGGTGTGCGTTGGTGGAAATATGAATTCT
GCTATGGCAAACATGTACATCAATACCATGAGGACAAGGATAGTGGGAAAACCTCTGTGGTTG
TCGGGACATGGAACCAAGAAGAGCATATTGAATGGGCTAAGAAGAATACTGCTAGAGCTTATC
ATCTTCAAGACGATGGTACCCAGACAGTCAGGATGGTGTACATTTTATGGAAATGGAGATA
TTTGTGATATAACTGACAAACCAAGACAGGTGACTGTAAACTAAAGTGCAAAGAATCAGATT
CACCTCATGCTGTTACTGTATATATGCTAGAGCCTCACTCCTGTCAATATATTCTTGGGGTTG
AATCTCCAGTGATCTGTAAATCTTAGATACAGCAGATGAAAATGGACTTCTTTCTCTCCCA
ACTAAAGGATATTAAAGTTAGGGGAAAGAAAAGATCATTGAAAGTCATGATAATTTCTGTCCC
ACTGTGTCTCATTATAGAGTTCTCAGCCATTGGACCTCTTCTAAAGGATGGTATAAAATGACT
CTCAACCACTTTGTGAATACATATGTGTATATAAGAGGTTATTGATAAACTTCTGAGGCAGAC
ATTTGTCTCGCTTTTTTTCATTTTTGTTGTGTCTTATAAACTGACTGTTTTCTTTGCTTGG
TACTGTGATTCCAAAATAAATCTCATCCAAGCAAGTTAGAGTCCAGCCTAATCAAATGTCATA
ATTGTTGTACCTAFTGAAAGTTTTTAAATAATAGATTTATTATGTAAATTATAGTATATGTAA
GTAGCTAATGAAGTAAAGATCATGAAGAAAGAAATTGATAGGTGTAAATGAGAGACCATGTAA
AATATGTAAATTCTAGTACCTGAAATCCTTTCAACAGATTTTATATAGCAACTGCTCTCTGC
AAGTAGTTAACTAGAACTGGGCACATGGTAGAGGCTCACATGGGAGTTGTCCCTCACCTTG
TTAATCTCAAGAACTCTTATTTATAATAGGTTGCTTCTCTCTCAGAACTTTTATCTATTACT
TTTTTCTTCTTATGAGTATGTTTACTCTCAGAGTATCTATCTGATGTAGACAGTTGGTGTATGC
TTCTGAGACTCAGAATGGTTTACTCTAACAAAACACTGTGCTGTCTATCCCTTGTACTTGCCT
ACTGTAATATGGATTTCACTTCTGAACAGTTTACAGCACAATATTTATTTTAAAGTGAATAAA
ATGTCCACAAGCAAAA

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FIGURE 94

MEEGGGGVRS LVPGGPVLLVLCGLLEASGGGRALPQLSDDIPFRVNWPGTEFSLPTTGVLVLYKE
DNYVIMTTAHKEKYKCILPLVTSGDEEEEEKDYKGNPRELLEPLFKQSSCSYRIESYWTYEVC
HGKHIRQYHEEKETGQKINIHEY YLG NMLAKNLLFEKEREAEKEKSNEIPTKNIEGQMTPLY
PVG MNGT PCSLKQNRPRSSTVMYICHPE SKHEILSVAEVTTC EYEVVILTPLLCSHPKYRFR
ASPVNDIFCQSLPGSPFKPLTLRQLEQQEEILRVPFRRNKEGVGWKYEFCY GKHVHQYHEDK
DSGKTSVVVG TWNQEEHIEWAKKNTARAYHLQDDGTQTVRMVSHFYGN GDICDITDKPRQVTV
KLKCKESDSPHAVTVYMLEPHSCQYILGVESPVICKILDTADENGLLSLPN

Important features of the protein:**Signal peptide:**

amino acids 1-30

Glycosaminoglycan attachment site.

amino acids 28-32

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 337-341

N-myristoylation sites.amino acids 6-12, 23-29, 29-35, 49-55, 141-147, 152-158, 192-198,
196-202**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 54-60

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FIGURE 95

TTCCGTTTCTGGGAGGAGTGAGGGGCAACGGGTCTGGAGAAAAAGGAAAAAGAAGGGCTCAGC
GCCTCCCCGCCGGGCCGTGGACAGAGGGGCACAGTTTTCGGCAGGCGGGTGAGGTCTGAGGG
CCCGCCGGAGATGTTTTCTTGTCTGAGCACGGTGCAACCCAGGTTACAGTTCCTCTGAGTCA
TCTCATCAATGCCTTCCATACACCAAAAAACACTTCTGTTTCTCTCAGTGGAGTGTCTAGTTTC
TCAAACCAGCATCGAGATGTAGTTCTGAGCATGAGGCTCCCAGCAGTGAGCCTTCACTTAA
CTTAAGGGACCTTGGATTATCTGAACATAAAATTTGGACAGATTGATCAGCTGGTAGAAAATCT
ACTTCCTGGATTTTGTAAAGGCAAAAACATTTCTTCCCATTGGCATAACATCCCATGTCTCTGC
ACAATCCTTCTTTGAAAATAAATATGGTAACTTAGATATATTTAGTACATTACGTTCTCTTG
CTTGTATCGACATCATTCAAGAGCTCTTCAAAGCATTGTTCAGATCTTCAGTACTGGCCAGT
TTTCATACAGTCTCGGGGTTTTAAACTTTGAAATCAAGGACACGACGTCTCCAGTCTACCTC
CGAGAGATTAGCTGAAACACAGAATATAGCGCCATCATTCTGTAAGGGGTTTTCTTTGCGGGA
CAGAGGATCAGATGTTGAGAGTTTGGACAACTCATGAAAACCAAAAATATACCTGAAGCTCA
CCAAGATGCATTTAAACTGGTTTTGCGGAAGGTTTTCTGAAAGCTCAAGCACTCACACAAAA
AACCAATGATTCCTTAAGGCGAACCCGTCTGATTCTCTTCGTTCTGCTGCTATTCCGGCATTTA
TGGACTTCTAAAAAACCCATTTTTATCTGTCCGCTTCCGGACAACAACAGGGCTTGATTCTGC
AGTAGATCCTGTCCAGATGAAAAATGTCACCTTTGAACATGTTAAAGGGTGGAGGAAGCTAA
ACAAGAATTACAGGAAGTTGTTGAATTCTTGAAAAATCCACAAAATTTACTATTCTTGAGG
TAACTTCCAAAAGGAATTCTTTTAGTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCG
AGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTATGCTTCTGGATCCGAATTTGATGAGAT
GTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAGCAAAGGCGAATGCTCC
TTGTGTTATATTTATTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCAATGCA
TCCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCCAATGA
AGGAGTTATCATAATAGGAGCCACAACTTCCCAGAGGCATTAGATAATGCCTTAATACGTCC
TGGTCGTTTTGACATGCAAGTTACAGTTCCAAGGCCAGATGTAAAAGGTCGAACAGAAATTTT
GAAATGGTATCTCAATAAAATAAAGTTTGATCAATCCGTTGATCCAGAAATTATAGCTCGAGG
TACTGTTGGCTTTTTCCGGAGCAGAGTTGGAGAATCTTGTGAACCAGGCTGCATTAAGCAGC
TGTTGATGGAAAAGAAATGGTTACCATGAAGGAGCTGGAGTTTTCCAAAGACAAAATCTAAT
GGGGCCTGAAAGAAGAAGTGTGGAATTTGATAACAAAAACAAACCATCACAGCATATCATGA
ATCTGGTCATGCCATTATTGCATATTACACAAAAGATGCAATGCCTATCAACAAAGCTACAAT
CATGCCACGGGGGCCAACACTTGGACATGTGTCCCTGTTACCTGAGAATGACAGATGGAATGA
AACTAGAGCCCAGCTGCTTGCACAAATGGATGTTAGTATGGGAGGAAGAGTGGCAGAGGAGCT
TATATTTGGAACCGACCATATTACAAACAGGTGCTTCCAGTGATTTTGATAATGCCACTAAAAT
AGCAAAGCGGATGGTTACCAAATTTGGAATGAGTGAAAAGCTTGGAGTTATGACCTACAGTGA
TACAGGGAAACTAAGTCCAGAAACCAATCTGCCATCGAACAAGAAATAAGAATCCTTCTAAG
GGACTCATATGAACGAGCAAAACATATCTTGAAAACCTCATGCAAGGAGCATAAGAATCTCGC
AGAAGCTTTATTGACCTATGAGACTTTGGATGCCAAAGAGATTCAAATTGTTCTTGAGGGGAA
AAAGTTGGAAGTGAGATGATAACTCTCTTGATATGGATGCTTGCTGGTTTTATTGCAAGAATA
TAAGTAGCATTGCAGTAGTCTACTTTTACAACGCTTTCCCCTCATTCTTGATGTGGTGTAATT
GAAGGGTGTGAAATGCTTTGTCAATCATTTGTCACATTTATCCAGTTTGGGTTATTCTCATT
TGACACCTATTGCAAATTAGCATCCCATGGCAAATATATTTGAAAAATAAAGAACTATCAG
GATTGAAAACAAAAA

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FIGURE 96

MFSLSSTVQPQVTVPLSHLINAFTPKNTSVSLSGVSVSQNQHRDVVPEHEAPSSEPSLNLRD
LGLSELKIGQIDQLVENLLPGFCKGKNISSHWHTSHVSAQSFFENKYGNLDIFSTLRSSCLYR
HHSRALQSICSDLQYWPVFIQSRGFKTLKSRTTQLQSTSERLAETQNIAPSFVKGFLLRDRGS
DVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDLSLRTRLILFVLLLFGIYGLL
KNPFLSVRFRTTGLDSAVIDPVQMKNVTFEHVKGVEEAKQELQEVVEFLKNPQKFTILGGKLP
KGILLVGPPGTGKTLLARAVAGEADVPFYYASGSEFDEMFGVGASRIRNLFREAKANAPCVI
FIDELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKPNEGVIIGATNFPEALDNALIRPGRF
DMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDPEIIARGTVGFSGAELENLVNQAALKAADV
KEMVTMKELEFSKDKILMGPERRSVEIDNKNKTITAYHESGHAIAYYTKDAMPINKATIMPR
GPTLGHVSLLPENDRWNETRAQLLAQMDVSMGGRVAEELIFGTDHITTGASSDFDNATKIAKR
MVTKFGMSEKLGVMYSDTGKLSPETQSAIEQEIRILLRDSYERAKHILKTHAKEHKNLAEAL
LTYETLDAKEIQIVLEGKKLEVR

Important features of the protein:**Transmembrane domain:**

amino acids 238-259

N-glycosylation sites.amino acids 28-32, 90-94, 230-234, 278-282, 535-539, 584-588,
623-627**N-myristoylation sites.**

amino acids 35-41, 266-272, 286-292, 325-331, 357-363, 599-605

Amidation site.

amino acids 387-393, 709-713

ATP/GTP-binding site motif A (P-loop).

amino acids 322-330

AAA-protein family proteins

amino acids 315-336, 343-386, 405-451

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FIGURE 97

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAACCTTGTAATCTAGAAAGAGTGGCTAGGGGGGTATTTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 98

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNIDIR
ILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSLTIKKDLRLC
HAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE

Signal sequence:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 107-110, 140-143

N-myristoylation site.

amino acids 51-56

Interleukin 10:

amino acids 9-176

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FIGURE 99

[illegible]

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FIGURE 100

MRLLEWFLLLFGPWLLRKAVSAQIPESGRPQYLGLRPAAAGAGAPGQQLPEPRSSDGLGVGR
AWSAWPTNHTGALARAGAAGALPAQRTKRKPSIKAARAKKIFGWGDFYFRVHTLKFSLLVTG
KIVDHVNGTFSVYFRHNSSSLGNLSVSIVPPSKRVEFGGVWLPGPVPHPLQSTLALEGVLPGL
GPPLGMAAAAAGPGLGGSLLGGALAGPLGGALGVPGAKESRAFNCHVEYEKTNRARKHRPCLYD
PSQVCFTTEHTQSQAAWLCAKPFKVICIFVSFLSFDYKLVQKVC PDYNFQSEHPYFG

Important features of the protein:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 273-288

N-glycosylation sites.

amino acids 72-76, 133-137, 143-147, 149-153

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 93-97

N-myristoylation sites.amino acids 35-41, 58-64, 60-66, 81-87, 84-90, 184-190, 194-200,
203-209, 205-211, 206-212, 209-215, 217-223, 221-227, 224-230**Cytochrome b/b6 Qo site signature.**

amino acids 5-11

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FIGURE 101

AATGCCCCATGCGCACCCACAGCTCGCGCTCCTGCAAGTGTTCTTTCTGGTGTTCCCCGATG
GCGTCCGGCCTCAGCCCTCTTCCTCCCCATCAGGGGCAGTGCCCACGTCTTTGGAGCTGCAGC
GAGGGACGGATGGCGGAACCCTCCAGTCCCCTTCAGAGGCGACTGCAACTCGCCCCGGCCGTGC
CTGGACTCCCTACAGTGGTCCCTACTCTCGTGACTCCCTCGGCCCCTGGGAATAGGACTGTGG
ACCTCTTCCCAGTCTTACCGATCTGTGTCTGTGACTTGACTCCTGGAGCCTGCGATATAAATT
GCTGCTGCGACAGGGACTGCTATCTTCTCCATCCGAGGACAGTTTTCTCCTTCTGCCTTCCAG
GCAGCGTAAGGTCTTCAAGCTGGGTTTGTGTAGACAACTCTGTTATCTTCAGGAGTAATTCCC
CGTTTCCTTCAAGAGTTTTTCATGGATTCTAATGGAATCAGGCAGTTTTGTGTCCATGTGAACA
ACTCAAACCTTAACTATTTCCAGAAGCTTCAAAAGGTCAATGCAACCAACTTCCAGGCCCTGG
CTGCAGAGTTTGGAGGCGAATCATTCACTTCAACATTCCAAACCTCAATCACCACCATCTTTTT
ACAGGGCTGGGGACCCATTCTTACTTACTTCCCCAAGTGGTCTGTAATAAGCTTGCTGAGAC
AACCTGCAGGAGTTGGAGCTGGGGGACTCTGTGCTGAAAGCAATCCTGCAGGTTTCTTAGAGA
GTAAAAGTACAACCTGCACTCGTTTTTTCAAGAACCTGGCTAGTAGCTGTACCTTGGATTTCAG
CCCTCAATGCTGCCTCTTACTATAACTTCACAGTCTTAAAGGTCCAAGAAGCATGACTGATC
CACAGAATATGGAGTTCCAGGTTCTGTAACTTACCTCACAGGCTAATGCTCCTCTGTTGG
CTGGAAACACTTGTCAGAATGTAGTTTCTCAGGTCACCTATGAGATAGAGACCAATGGGACTT
TTGGAATCCAGAAAGTTTCTGTCAGTTTGGGACAAACCAACCTGACTGTTGAGCCAGGCGCTT
CCTTACAGCAACACTTCATCCTTCGCTTCAGGGCTTTTCAACAGAGCACAGCTGCTTCTCTCA
CCAGTCCTAGAAGTGGGAATCCTGGCTATATAGTTGGGAAGCCACTCTTGGCTCTGACTGATG
ATATAAGTTACTCAATGACCCTCTTACAGAGCCAGGGTAATGGAAGTTGCTCTGTTAAAAGAC
ATGAAGTGCAGTTTGGAGTGAATGCAATATCTGGATGCAAGCTCAGGTTGAAGAAGGCAGACT
GCAGCCACTTGCAGCAGGAGATTTATCAGACTCTTCATGGAAGGCCAGACCAGAGTATGTTG
CCATCTTTGGTAATGCTGACCCAGCCCAGAAAGGAGGGTGGACCAGGATCCTCAACAGGCACT
GCAGCATTTTCAGCTATAAACTGTACTTCCTGCTGTCTCATAACAGTTTCCCTGGAGATCCAGG
TATTGTGGGCATATGTAGGTCTCCTGTCCAACCCGCAAGCTCATGTATCAGGAGTTTCGATTCC
TATACCAGTGCCAGTCTATACAGGATTCTCAGCAAGTTACAGAAGTATCTTTGACAACCTCTTG
TGAACTTTGTGGACATTACCCAGAAGCCACAGCCTCCAAGGGGCCAACCCAAAATGGACTGGA
AATGGCCATTTCGACTTCTTTCCCTTCAAAGTGGCATTTCAGCAGAGGAGTATTCTCTCAAAAAT
GCTCAGTCTCTCCCATCCTTATCCTGTGCCTCTTACTACTTGGAGTTCTCAACCTAGAGACTA
TGTGAAGAAAAGAAAATAATCAGATTTTCAGTTTTCCCTATGAGAACTCTGAGGCAGCCACTT
ATCTTGGCTAAATAGAACCTCACCTGCTCATGACCAGAGAGCATTTAGGATAATAGATGACCT
AACTGAAGGAATCCTTGTATATGAAAGGAGTTATTTTAGAAAAGCAATAAAAATATTTTATTC
ATCNTAAAAA

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FIGURE 102

M RTPQLALLQVFFLVFPDGV RPQPSSSPSGAVPTSLELQRGTDGGTLQSPSEATATRPV PGL
PTVVPTLVTPSAPGNRTVDLFPVLPICVCDLTPGACDINCCDRDCYLLHPRTVFVSFCLPGSV
RSSSWVCVDNSVIFRSNSPFPSPRVFMD SNGIRQFCVHVNNNSNLNYFQKLQKVNATNFQALAAE
FGGESFTSTFQTQSPPSFYRAGDPILTYFPKWSVISLLRQPAGVGAGGLCAESNPAGFLESKS
TTCTRFFKNLASSCTLDSALNAASYYNFTVLKVPRSM TDPQNMEFQVPVILTSQANAPLLAGN
TCQNVVSQVTYE IETNGTFGIQKVS VSLGQTNLTVEPGASLQQHFILRFRAFQQSTAASLTSP
RSGNPGYIVGKPLLALTD DISYSMTLLQSQGN GSCSVKRHEVQFGVNAISGCKLRLKKADCSH
LQQEIYQTLHGRPRPEYVAIFGNADPAQKGGWTRILNRHCSISAINCTSCCLIPVSLEIQVLW
AYVGLLSNPQAHVSGVRFLYQCQSIQDSQQVTEVSLTTLVNFVDITQKPQPPRGQPKMDWKWP
FDFFPFKVAFSRGVFSQKCSVSPILILCLLLLGV LNLETM

Important features of the protein:**Signal peptide:**

amino acids 1-22

Transmembrane domains:

amino acids 484-505, 581-600

N-glycosylation sites:amino acids 78-82, 165-169, 179-185, 279-285, 331-337, 347-351,
410-414, 487-491**N-myristoylation sites:**

amino acids 30-36, 41-47, 124-130, 232-238, 236-242, 409-415

Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 420-431

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FIGURE 103

CCTAATTCTCAAGGTGATGCTATTTAGGAAGTCATAACTCATGTGAGTGGAGCCATGTGGGAT
TAAGAAGTGATAGGAGAGCTTGCTGTCTGTCTCTGCTCTCCACTGTGTGAGGATACAACAGGA
AGACAGCCATCTGGTGAGGAAGAGAGGGCCCTCGCCAGATACCGGACCTGCTGACACCTTGAT
CTTGGACTIONCCATCTTCCAGGAAGGCCTGACCTCAGTTGTTCCAGGGTAAAGAATTTGGGCA
GTGCCCACACCCACGCTGTTGGATAACATTTCTTCACCATAACAGTGAGGGTGAATGTGTACA
CGCCAGCTTCCTGCCTGTTACTCTCCACAGTATGCGAAGAATATCCCTGACTTCTAGCCCTG
TGCGCCTTCTTTTGTCTGTGCTACTAATAGCCTTGAGATCATGGTTGGTGGTCACT
CTCTTTGCTTCAACTTCACTATAAAATCATTGTCCAGACCTGGACAGCCCTGGTGTGAAGCGC
AGGTCTTCTTGAATAAAAATCTTTTCCTTCAGTACAACAGTGACAACAACATGGTCAAACCTC
TGGGCCTCCTGGGGAAGAAGGTATATGCCACCAGCACTTGGGGAGAATTGACCCAAACGCTGG
GAGAAGTGGGGCGAGACCTCAGGATGCTCCTTTGTGACATCAAACCCAGATAAAGACCAGTG
ATCCTTCCACTCTGCAAGTCGAGATGTTTTGTCAACGTGAAGCAGAACGGTGCCTGGTGCAT
CCTGGCAGTTCGCCACCAATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGA
CAGTAATTAATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAGACAGAGGGCTGGAAA
AGTATTTTCAGGAAGCTCTCAAAGGGAGACTGCGATCACTGGCTCAGGGAATTCTTAGGGCACT
GGGAGGCAATGCCAGAACCGACAGGCAGAAGATCCACCTAGAGGTGATACCACGGCGGCGCAG
AGTTGTTACCTGTGGTCCTCGATCGCTGACAGCCTGGCTCCCACTGCTGTGTGTTCCCTGA
GTCAAGTGGAGGCGGAGCCTGCAATGAGCGGAGATCGCGCCTCTGCATTCCAGTCTTGGCAAC
AGAGCAAGACTCCGTCTCAAAAAAAAAAATTTTTTTTCAGTACATATTTTTTAAAGATAGG
GCTGGGCACAGCAGCTCACATCTATAATCCCAACACTTTGGGAGGCCTAGGCAGGAGGATCAC
TTGAGCCCAGGAATCTGAAGCTGCAGTGAGCCTTTGCTCGTGAGATTGTGGACCTATGATCCT
ACCACCAGCCCACCTGGTTCTAACACCCCTCCTCTATGTGTGAGAGGGAGAGAAGAAAAGTG
AGGGAGAAAAGAGAGATAAGCAAAGAACAGAGAGGAAAATGGAAAATAAGAGGAAATTGGGG
GAATTAAACAGAGGGGAGGGCATGGATCCCCGGGAGTTAGAAGAGTAGCAGCTTGTGGATTAC
TACGCAGTGGAGGAAGAAGAGTTGTTGGAAATTATTTGAGAGGTAGTATAATCATTGTGAGG
CAGTTTTCTGCATTACCATTTCTCACAGACTAAGTTACTCATAAGCAAACGTGCAATTCACA
TTACACTGAAATTCTTCCCTAATACATCATTTGCATTGGAATAAAGTACGGTTTTCAAACAAC
CTGATATAGCAGAACTGACTGTATAAATTATGTGAGCACAGTGCAAGTAATTCTTTGTTTGT
TGTTTGTTTTTTTGAGACAGAGTCTCACTCTATCTCCAGGCTGGAGTGTAGTGGTGCGATCC
CGGCTCACTGCAACCTCGATCTCCAGGCTCAAGCGATTCCCCTGCCTCAGCCTCCTGAGTAG
CTGGGATTACAGGCATGAGCCACCACGCGGCTAATTTTTGTATTTTGTAGTAGACGGGGT
TTCACCTGTTGGCCAGGCTGGTCTCGAACTACGGACCTCAGGTGATCTGCCCCCTCAGCCT
CTCAAAGTGCTGGGATTATAGCATGAGCCACTGAGCCAGACACAAGTAGTTCTTTCTGATAA
ACACTTTAACTGAATGCA

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FIGURE 104

MRRISLTSSPVRLLLFLLLLLIALEIMVGGHSLCFNFTIKSLSRPGQPWCEAQVFLNKNLFLO
YNSDNNMVKPLGLLGKKVYATSTWGELTQTLGEVGRDLRMLLCDIKPQIKTSDPSTLQVEMFC
QREAERCTGASWQFATNGEKSLLFDAMNMTWTVINHEASKIKETWKKDRGLEKYFRKLSKGDC
DHWLREFLGHWAMPEPTGRRST

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 11-30 (possible type II protein)

N-glycosylation site.

amino acids 36-39, 154-157

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 2-5, 182-185, 209-212

Casein kinase II phosphorylation site.

amino acids 86-89, 93-96, 142-145, 185-188

N-myristoylation site.

amino acids 46-51

Amidation site.

amino acids 77-80, 207-210

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FIGURE 105

TTTTCCGAGTGACCTTCTTGATGCTGGCTGTTTCTCTCACCGTTCCCCTGCTTGGAGCCATGA
TGCTGCTGGAATCTCCTATAGATCCACAGCCTCTCAGCTTCAAAGAACCCCCGCTCTTGCTTG
GTGTTCTGCATCCAAATACGAAGCTGCGACAGGCAGAAAGGCTGTTTGAAAATCAACTTGTTG
GACCGGAGTCCATAGCACATATTGGGGATGTGATGTTTACTGGGACAGCAGATGGCCGGGTGC
TAAAACTTGAAAATGGTGAAATAGAGACCATTGCCCCGTTTGGTTCGGGCCCTTGCAAAACCC
GAGATGATGAGCCTGTGTGTGGGAGACCCCTGGGTATCCGTGCAGGGCCCAATGGGACTCTCT
TTGTGGCCGATGCATACAAGGGACTATTTGAAGTAAATCCCTGGAAACGTGAAGTGAAACTGC
TGCTGTCCTCCGAGACACCCATTGAGGGGAAGAACATGTCCTTTGTGAATGATCTTACAGTCA
CTCAGGATGGGAGGAAGATTTATTTACCGATTCTAGCAGCAAATGGCAAAGACGAGACTACC
TGCTTCTGGTGATGGAGGGCACAGATGACGGGCGCCTGCTGGAGTATGATACTGTGACCAGGG
AAGTAAAAGTTTTATTGGACCAGCTGCGGTTCCCGAATGGAGTCCAGCTGTCTCCTGCAGAAG
ACTTTGTCCTGGTGGCAGAAACAACCATGGCCAGGATACGAAGAGTCTACGTTTCTGGCCTGA
TGAAGGGCGGGGCTGATCTGTTTGTGGAGAACATGCCTGGATTTCAGACAACATCCGGCCCA
GCAGCTCTGGGGGGTACTGGGTGGGCATGTCGACCATCCGCCCTAACCCCTGGGTTTTCCATGC
TGGATTTCTTATCTGAGAGACCCTGGATTAAAAGGATGATTTTAAAGCTCTTTAGTCAAGAGA
CGGTGATGAAGTTTGTGCCGCGGTACAGCCTCGTCCTAGAACTCAGCGACAGCGGTGCCTTCC
GGAGAAGCCTGCATGATCCCGATGGGCTGGTGGCCACCTACATCAGCGAGGTGCACGAACACG
ATGGGCACCTGTACCTGGGCTCTTTCAGGTCCCCCTTCTCTGCAGACTCAGCCTCCAGGCTG
TTTAGCCCTCCCAGATAGCTGCCCCTGCCACGCAGGCCAGGAGTCTTCACACTCAGGCACCAG
GCCTGGTCCAGGAGGAGCTGTGGACACAGTCGTGGTTCAAGTGTCACATGCACCTGTTAGTC
CCTGAGAGGTGGTGGGAATGGCTGCTTCATTCTCGAGGATGCCCCGGGCCCCACCTGGGCTTG
TCTTTCTGTTTAGAGGGGAAGTGTAACATATCTGCCATGAGGAACATAAATTCATGTAAAGCCA
TTTTCTCTTAAACAAAACAAAACCTTTCTAAGTACAATCATTCTCTAGGATTTGGGAAGCTCCT
TGCACTTGGAACAGGGCTCAGGTGGGTGGAGCAGTAAGGCACTACCCAGAGAGCTTGCTGCTG
CGGCCCTGTCTGCGGCCTCAAAGTTCTTCTTTACTATATATAACGTGCGGTCATACCTTTCT
TCGTTGTGGTGGGGATGGAAGAGCAGAGGGAGCATGGCCCAGGGGTGTTGAGGCCAGCGGTGA
GAGCCGTGTTAGCCAAGACATGGAACCTGTGTTCTCAAGGGTTATGTGGGGCGTGGGCTCTCCA
TAGTGTGTATGAAAAGCTTGTTGACTCTAGCGGCTCAGAGAGGACTTTGCTGGGTTTCTTTCT
GTGAATATCTCCGTGCTGACCATGCTGGAATTGGATGATTCTGCAATTCGGGACCTACTGCAG
GGGTCCGTTTAGTAACGTCTTGTCTGTGATCTTTGTTCTTGACCTCTAGACCCCAAGATGTGA
ACAGTGCACGTGTTAATGTCATCTTTGCTCATGTGTTATAAGCCCCAAGTTGCTGTATATTTT
CACAAGTATGTCTACACACTGG

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FIGURE 106

MLAVSLTVPLLGAMMLLESPIDPQPLSFKEPPLLLGVLHPNTKLRQAERLFENQLVGPESIAH
IGDVMFTGTADGRVVKLENGEIETIARFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADAYK
GLFEVNPWKREVKLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEG
TDDGRLLLEYDVTVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIRRVYVSGLMKGGADL
FVENMPGFDPNIRPSSSGGYWGMSTIRPNPGFSMLDFLSERPWIKRMIFKLFSQETVMKFVP
RYSLVLELSDSGAFRRSLHDPDGLVATYISEVHEHDGHLYLGSEFRSPFLCRLSLQAV

Important features of the protein:**Signal peptide:**

amino acids 1-13

Transmembrane domain:

amino acids 1-21 (possible type II)

N-glycosylation sites.

amino acids 116-119, 152-155

Casein kinase II phosphorylation sites.

amino acids 19-22, 27-30, 98-101, 146-149, 221-224, 286-289, 332-335

N-myristoylation sites.

amino acids 71-76, 92-97, 189-194, 244-249, 338-343

Amidation site.

amino acids 164-167

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FIGURE 107

AACGAAGCGTGCGCGCTTTGGTAACCGGCTAGAAATCCCGCACGCGCGCCTGCCTCCTCTCCC
CAGGCCTGAGCTGCCCCCTCCCACTGCCTTTCCTTCTTCCCGCGAGTCAGAAGCTTCGCGAGGG
CCCAGAGAGGGCGGTGGGGTGGGCGACCCCTACGCCAGCTCCGGGCGGGAGAAAGCCACCCCTCT
CCCGCGCCCCAGGAAACCGCCGCGCTTCGGCGCTGCGCAGAGCCATGGAATTCTCCTGGCTGG
AGACGCGCTGGGCGCGGCCCTTTTACCTGGCGTTCGTGTTCTGCCTGGCCCTGGGGCTGCTGC
AGGCCATTAAGCTGTACCTGCGGAGGCAGCGGCTGCTGCGGGACCTGCGCCCCCTTCCAGCGC
CCCCACCCACTGGTTCCTTGGGCACCAGAAGTTTATTAGGATGATAACATGGAGAAGCTTG
AGGAAATTATTGAAAAATACCCCTCGTGCCTTCCCTTTCTGGATTGGGCCCTTTCAGGCATTTT
TCTGTATCTATGACCCAGACTATGCAAAGACACTTCTGAGCAGAACAGATCCCAAGTCCCAGT
ACCTGCAGAAATTCTCACCTCCACTTCTTGGAAGGACTAGCGGCTCTAGACGGACCCAAGT
GGTTCAGCATCGTCGCTACTAACTCCTGGATTCCATTTTAACATCCTGAAAGCATACTTG
AGGTGATGGCTCATTCTGTGAAAATGATGCTGGATAAGTGGGAGAAGATTGTCAGCACTCAGG
ACACAAGCGTGGAGGTCTATGAGCACATCAACTCGATGTCTCTGGATATAATCATGAAATGCG
CTTTCAGCAAGGAGACCAACTGCCAGACAAACAGCACCCATGATCCTTATGCAAAGCCATAT
TTGAACTCAGCAAAATCATATTTACCGCTTGTACAGTTTGTTGTATCACAGTGACATAATTT
TCAAACCTCAGCCCTCAGGGCTACCGCTTCCAGAAGTTAAGCCGAGTGTGAATCAGTACACAG
ATACAATAATCCAGGAAAGAAAGAAATCCCTCCAGGCTGGGGTAAAGCAGGATAAACTCCGA
AGAGGAAGTACCAGGATTTTCTGGATATTGTCTTTCTGCCAAGGATGAAAGTGGTAGCAGCT
TCTCAGATATTGATGTACACTCTGAAGTGAGCACATTCTGTTGGCAGGACATGACACCTTG
CAGCAAGCATCTCCTGGATCCTTTACTGCCTGGCTCTGAACCCTGAGCATCAAGAGAGATGCC
GGGAGGAGGTGAGGGGCATCCTGGGGGATGGGTCTTCTATCACTTGGGACCAGCTGGGTGAGA
TGTCGTACACCACAATGTGCATCAAGGAGACGTGCCGATTGATTCTGTCAGTCCCGTCCATTT
CCAGAGATCTCAGCAAGCCACTTACCTTCCCAGATGGATGCACATTGCCTGCAGGGATCACCG
TGGTTCTTAGTATTTGGGGTCTTACCACAACCCTGCTGTCTGGAAAAACCCAAAGGTCTTTG
ACCCCTTGAGGTTCTCTCAGGAGAATTCTGATCAGAGACACCCCTATGCCTACTTACCATTCT
CAGCTGGATCAAGGAAGTGCATTGGGCAGGAGTTTGCCATGATTGAGTTAAAGGTAACCATTG
CCTTGATTCTGCTCCACTTCAGAGTGACTCCAGACCCACCAGGCCTCTTACTTTCCCCAACCC
ATTTTATCCTCAAGCCCAAGAATGGGATGTATTTGCACCTGAAGAACTCTCTGAATGTTAGA
TCTCAGGGTACAATGATTAAACGTACTTTGTTTTTCGAAGTTAAATTTACAGCTAATGATCCA
AGCAGATAGAAAGGGATCAATGTATGGTGGGAGGATTGGAGGTTGGTGGGATAGGGGTCTCTG
TGAAGAGATCCAAAATCATTTCTAGGTACACAGTGTGTGCTAGATCTGTTTCTATATAACT
TTGGGAGATTTTTCAGATCTTTTCTGTTAACTTTCACTACTATTAATGCTGTATACACCAATA
GACTTTCATATATTTTCTGTTGTTTTTAAATAGTTTTTCAGAATTATGCAAGTAATAAGTGCA
TGTATGCTCACTGTCAAAAATTCCCAACACTAGAAAATCATGTAGAATAAAAATTTTAAATCT
CACTTCACTTAGCCGACATTCATGCCCTGACCAATCCTACTGCTTTTCTTAAAAACAGAATA
ATTTGGTGTGCATTCTTTCAGACTTTTCTTATACATTTTATATGTAGAAATGTAGCAATGTA
TTTGTATAGATGTGATCATTCCCTATATTGTTATTGATTTTTTCACTTAATAAAAATTCACCT
TATTCCTTAAAA

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FIGURE 108

MEFSWLETRWARPFYLA FVFC LALG LLQA IKLYLRRQRLRLRPF PAPP THWFLGHQKFIQD
DNMEKLEEIIEKY PRAFPFWIGPFQAFFCIYDPDYAKTLLSRTDPKSQYLQKFS PPLL GKGLA
ALDGP KW FQHRRL LTPGFHFNILKAYIEVMAHSV KMMLDKWEKICSTQDTSVEVYEHINSMSL
DIIMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLYHSDIIFKLS PQGYRFQKLSR
VLNQYTD TIIQERK KSLQAGVKQDNTPKRKYQDFLDIVLSAKDESGSSFSDIDVHSEVSTFLL
AGHDTLAASISWILYCLALNPEHQERCREEV RGILGDGSSITWDQLGEMSYTTMCIKETCR LI
PAVPSISRDL SKPLTFPDGCTLPAGITVVL SIWGLHHNPAVWKNPKVFDPLRFSQENS DQRHP
YAYLPFSAGSRNCIGQEFAMIELKVTIALILLHFRVTPDPTRPLTFPNHFILKPKNGMYLHLK
KLSEC

Important features of the protein:

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 310-330, 397-413, 459-473

N-glycosylation site.

amino acids 206-210

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 265-269, 504-520

N-myristoylation sites.

amino acids 25-31, 298-304, 353-359, 450-456, 456-462

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 447-457

Cytochrome P450 cysteine heme-iron ligand proteins.

amino acids 444-475

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FIGURE 109

GGCGTTCCGGGCCTCAACTTTGGCGTCGTGAGATTCTTGTGAGGCGTCTGCCTGGAAGCCGGC
AGCAATTTTGCTTCTTTAAAGAGAAAAAGAAGGCTAGGGACTCAGATTCCTGGATTCTGAGAT
CCAGACCAGCTCCTCCCAGACCTCTCCAGAAGAAGCCATGGGAACCCCTCGTATCCAGCATTT
GCTGATCCTCCTGGTCCTAGGAGCCTCCCTCCTGACCTCGGGCCTAGAGCTGTATTGTCAAAA
GGGTCTGTCCATGACTGTGGAAGCAGATCCAGCCAATATGTTTAACTGGACCACAGAGGAAGT
GGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCATACTAATAATTAAAGCAGGGACTGA
GACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGAAGGGGAGGAGGCCATAACAATTGTCCA
GCACTCTTCACCTCCCGGCCTGATCGTGACCTCCTACAGTAACTACTGTGAGGATTCCTTCTG
TAATGACAAAGACAGCCTGTCTCAGTTTTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTC
AACAAACCCTCCATTGTCCAACCTGTGTGGCTTTGGGGACCTGTTTCAGTGCTCCTTCTCTTCC
CTGTCCCAATGGTACAACCTCGATGCTATCAAGGAAACTTGAGATCACTGGAGGTGGCATTGA
GTCGTCTGTGGAGGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTT
AGCAGTAGGACCCATGTTTGTGAGGGAAGCGTGCCACATCAGCTGCTCACTCAACCTCGAAA
GACTGAAAATGGGGCCACCTGTCTTCCCATTCTGTTTGGGGGTACAGCTACTGCTGCCATT
GCTGCTGCCATCATTTATTTCACTTTTCCTAAGAAGGCACTTCTGGGCCTGGGTCTGAGGACAT
CTTTTTTGACTGGGAGCCTTCTTACTGTTGAGGTTCAACAAGCTGAGGAGTAGATGGGAATTT
GAGGGAGAATACAGAGATACTATGAACGTATTTGACATTTTAAATAACAATTTCTGCTATAATT
TTTGTATGCAGTAGGCGTTACTAATAAACATTTCTGCTGTGA

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FIGURE 110

MGTPRIQHLLILLVLGASLLTSGLELYCQKGLSMTVEADPANMFNWTTEEVEETCDKGALCQET
ILIIKAGTETAILATKGCIPEGEEAITIVQHSSPPGLIVTSYSNYCEDSFNDKDSLSQFWEF
SETTASTVSTTLHCPTCVALGTCFSAPSLPCPNGTTRCYQGKLEITGGGIESSVEVKGCTAMI
GCRLMSGILAVGPMFVREACPHQLLTQPRKTENGATCLPIPVGWLQLLLPLLLPSFIHFS

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 184-201

N-glycosylation sites.

amino acids 45-49, 159-163

N-myristoylation sites.amino acids 31-37, 70-76, 99-105, 147-153, 160-166, 174-180,
175-181

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FIGURE 111

CGAGAAGAGGACAGAGGAGACTGAGCAAAGGGGGGTGGGCTCCAGGCGACCCCTAGCCCAATTCTGCCCCTCCAT
CCCAAGGGGCAGAGAAATTGCTTTCTTTGCTGACTCCTACGAGGAAAAAAAAAAAAAAAAAAAAAACCATTAA
AGGGAAAGATAAACGGAGACGGAGGAAAGGTGGCAGCCAGATTACTTAGAGAGGCACAGAGGAGAGATCGGGG
TGAGTCGCCATGCGGACTCCCAGGGCCCAGCACCCGCCCTCCCCAGCTGCTGTTCTAATTCTGCTGAGCTGT
CCCTGGATCCAGGGTCTGCCCCGAAGGAGGAGGAGATATTGCCAGAGCCTGGAAGTGAGACCCCCACGGTGGCC
TCTGAGGCCCTGGCTGAAGTCTCATGGGGCCCTGCTGAGGAGGGGGCCAGAGATGGGCTACCTGCCAGGATCT
GATCCGGACCCACGCTAGCCACCCCTCCGGCCGGCCAGACTCTCGCAGTGCCCTCCCTGCCACGGGCCACTGAG
CCGGGACAGGGCCTCTGACAAACAGCCGTCAACCCCTAACGGGGTCAGGGGGCAGGCCCCACTGCGCCAGAAGT
CTGACCCCGCCCCAGGAACACAGCCCCACCCACCCAGCCCTGCCTCCCCAGGGCCTCCCTTGGGCCTGAG
GGAGGAGAGGAGGAGACGACACCACCATCATACCACGACAACTGTTACCACTACGGTGACCAGCCCAGTTCTG
TGTAATAACAACATCTCCGAGGGCGAAGGGTATGTGGAGTCTCCAGATCTGGGGAGCCCCGTCAGCCGACCCCTG
GGGCTCCTGGACTGCACTTACAGCATCCATGTCTACCCTGGCTACGGCATTGAGATCCAGGTGCAGACGCTGAAC
CTGTACAGGAAGAGGAGCTCCTGGTGTGGCTGGTGGGGGATCCCCAGGCCTGGCCCCCGACTCCTGGCCAAC
TCATCCATGCTTGGAGAAGGACAAGTCTTTCGGAGCCCAACCAACCGGCTGCTTCTGCACTTCCAGAGCCCACGG
GTCCCAAGGGCGGTGGCTTCAGGATCCACTATCAGGCCTACCTCCTGAGCTGTGGCTTCCCTCCCGGGCCGGCC
CATGGGGACGTGAGTGTGACGGACCTGCACCCCTGGGGGCACTGCCACCTTTCACTGTGATTTCGGGCTACCAGTG
CAGGGAGAGGAGACCCTCATCTGCCTCAATGGCACCCGGCCATCCTGGAACGGTGAAACCCCAAGCTGCATGCA
TCCTGTGGTGGCACCATCCACAATGCCACCCCTGGGCGCATCGTGTCCCCAGAGCCTGGGGGAGCCGTAGGGCCC
AACCTCACCTGCCGTTGGGTCAATTGAAGCAGCTGAGGGGCGCCGGCTGCACCTGCACTTTGAAAGGGTCTCGCTG
GATGAGGACAATGACCGGCTGATGGTGCCTCAGGGGGCAGCCCCCTATCCCCGTGATCTATGATTTCGGACATG
GACGATGTCCCGAGCGGGGTCTCATCAGTGACGCCCAGTCCCTCTACGTGGAGCTGCTGTGAGAGACACTGCC
AATCCCCTGCTGTTAAGCCTTCGATTTGAAGCCTTTGAGGAGGATCGTGCTTCGCCCCCTTCTGGCACATGGA
AATGTCACTACCACGGACCCTGAGTATCGCCCAGGGGCACTGGCAACCTTCTCGTGCCTCCCAGGATATGCCCTG
GAGCCCCCTGGGCCCCCAATGCCATCGAATGTGTGGATCCACAGAACCCCACTGGAACGACACAGAGCCGGCC
TGCAAAGCCATGTGTGGAGGGGAGCTGTGGAACCCAGCTGGCGTGGTCTCTCTCCGACTGGCCCCAGAGCTAT
AGCCCGGGCCAAAGACTGCGTGTGGGGCGTGACAGTCCAGGAAGAGAAGCGCATCTTGCTCCAAGTTGAGATATTG
AATGTGCGGGAAGGGGACATGCTGACGCTGTTCGACGGGGACGGTCCCAGCGCCCCGAGTCTTGGCCCCAGCTGCGG
GGACCTCAGCCGCGCCGCGCCTTCTCTCCTCTGGGCCCCGACCTCACACTGCAGTTTCAGGCACCGCCCCGGCCC
CCAAATCCAGGCCTGGGCGAGGGCTTCGTATTGCACTTCAAAGAGGTCCCGAGGAACGACACGTGCCCGGAGCTG
CCACCTCCGGAGTGGGGCTGGAGAACGGCATCCACGGGGACCTGATCCGGGGCACGGTGCTCACCTACCAGTGC
GAGCCTGGCTACGAGCTGCTAGGCTCCGACATTTCTCACTTGCCAGTGGGACCTGTCTTGGAGCGCCGCGCCGCC
GCCTGCCAAAAGATCATGACTTGTGCTGACCCCTGGCGAGATTGCCAACGGGCACCGCACCGCCTCGGACGCCGGC
TTCCCCGTTGGCTCCCAGTCCAGTACCGCTGCCTGCCAGGGTACAGCCTCGAGGGGGCAGCCATGCTCACCTGC
TACAGCCGGGACACAGGCACACCCAAGTGGAGCGATAGGGTCCCCAAATGCGCCTTGAAGTACGAGCCGTGCCTG
AACCCGGGGGTTCCCGAGAATGGCTACCAGACGCTGTACAAGCACCCTACCAGCGGGCGAGTCTCTGCGCTTC
TTCTGCTATGAGGGCTTTGAGCTTATCGGCGAGGTACCATCACCTGTGTGCGCCGGCCACCCCTCCCAGTGGACC
AGCCAGCCCCCACTCTGCAAAGTGACCCAGACCACAGATCCATCACGGCAGCTGGAAGGGGGGAACCTGGCCCTG
GCCATCCTGCTGCCTCTAGGCTTGGTCAATTGTCTCGGAGTGGCGTTTACATCTACTACACCAAGCTTCAGGGA
AAGTCCCTTTTTCGGCTTCTCGGGCTCCCACTCCTACAGCCCCATCACCGTGGAGTCCGACTTCAGCAACCCGCTG
TATGAAGCTGGGGATACGCGGGAGTATGAAGTTTCCATCTGAACCCCAAGACTACAGCTGCAGGACCCAGGACGC
CCCTCCCTCCTCATTCGGGCAGAGGGAAATACGGGACCCGGTCTCTGCCTCCTGGCTGCCCTCCTCCCTGGCTG
TGTAATAGTCTCCCTATCCACGAGGGGGCTTTGATGGCCCTGGAGATCCTACAGTAAATAAACAGCATCCTG
CCGCCCCAAAAA

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FIGURE 112

MGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEEEILPEPGSETPTVASEALAE LLHGALLRRG
PEMGYLPGSDPDPTLATPPAGQTLAVPSLPRATEPGTGPLTTAVTPNGVRGAGPTAPELLTTP
PGTTAPPPSPASPGPPLGPEGGEEETTTTIIITTTVTITVTSPVLCNNNISEGEGYVESPD
GSPVSR TLGLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAPRLLANSSMLG
EGQVLRSP TNRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFPPRPAHGDVSVTDLHPGGTATFH
CDSGYQLQGEETLICLNGTRPSWNGETPSCMASCGGTIHNATLGRIVSPEPGGAVGPNLTCRW
VIEAAEGRRLLH LHFERVSLDEDNDRMLMVRSGGSPSPVIYDSMDVPERGLISDAQSLYVEL
LSETPANPLLLSLRFEAFEEEDRCFAPFLAHGNVTTTDPEYRPGALATFSCLPGYALEPPGPPN
AIECVDPTEPHWNDTEPACKAMCGGELSEPAGVVLS PDWPQSYSPGQDCVWGVHVQEEKRILL
QVEILNVREGDMLTLFDGDGPSARVLAQLRGPQPRRLLSSGPD LTLQFQAPPGPPNPGLGQG
FVLHFKEVPRNDTCPELPPPEWGWRTASHGDLIRGT VLT YQCEPGYELLGSDILTQWDLWS
AAPPACQKIMTCADPGEIANGHRTASDAGFPVGS HVQYRCLPGYSLEGAAMLTCYSRDTGT PK
WSDRVPKCALKYEPCLNPGVPENGYQTLYKH HYQAGESLRFFCYEGFELIGEVTITCVPGHPS
QWTSQPPLCKVTQT TDP SRQLEGGNLALAILLPLGLVIVLGSGVYIYYTKLQKSLFGFSGSH
SYSPITVESDFSNPLYEAGDTREYEVSI

Important features of the protein:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 842-864

N-glycosylation sites.amino acids 176-180, 222-226, 247-251, 332-336, 355-359, 373-377,
473-477, 517-521, 641-645**Tyrosine kinase phosphorylation site.**

amino acids 61-69

N-myristoylation sites.amino acids 2-8, 84-90, 111-117, 114-120, 190-196, 198-204,
235-241, 309-315, 333-339, 351-357, 472-478, 484-490, 528-534,
626-632, 665-671, 775-781, 842-848**Amidation site.**

amino acids 384-388

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

CUB domain proteins profile.

amino acids 202-218, 376-392, 553-569

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FIGURE 113

GCCGCGGGCGGAGCTGCCTGCCGGTCCCGCGCCGCGCGTCCGCACTCCTCGGCCCTCGGGCGGTTCGATGGGACGG
GGCGCCGCGGAGCAGGAGGCGCGCCCGTCCGGGTGCTCGGGCCGCGCGGGAGCCCACTGTGGGGCTCGGGCATG
GCGGGCCGAGGACCTGAGCTCTCCTCAGGGGAGCGGGAGGCAGCTGCTGGCCGGCGATGGGGACGGAGTGGGG
CCGTGCGCGCCGCGCGGAGCCGTGAGCGCCGAGCCACCGCCGCGCTACCTCAGCCCTTCGCGAAGCGCCGGCA
GCTCGGGAACATGGCCCTGGAGCGGCTCTGCTCGGTCCCTCAAAGTGTTGTTAATAACAGTACTGGTAGTGGAAGG
GATTGCCGTGGCCCAAAAACCAAGATGGACAAAATATTGGAATCAAGCATATTCTGCAACCCAGTGTGGCAT
TTGGGTTTGAACCCAGCAATGGAGGTCATTTTGCTTCGCCAAATTATCCTGACTCATATCCACCAACAAGGAGTG
TATCTACATTTTGAAGCTGCTCCAGTCAAAGAATAGAGTTGACCTTTGATGAACATTATTATATAGAACCATC
ATTTGAGTGTGGTTTGATCACTTGAAGTTTCGAGATGGGCCATTTGGTTTTCTCTCTCTTATAGATCGTTACTG
TGGCGTGAAAAGCCCTCCATTAAATAGATCAACAGGGAGATTTCATGTGGATTAAAGTTTAGTTCTGATGAAGAGCT
TGAAGGACTGGGATTTTCGAGCAAAATATTCAATTTATCCAGATCCAGACTTTACTTACCTAGGAGGTATTTTAAA
TCCCATTCAGATTGTGAGTCTCGGAGCTCTCGGAGCTGATGGAATAGTGCGCTCTAGTCAGGTAGAACAAGAGGA
GAAAACAAAACCCAGGCCAAGCCGTTGATTGCATCTGGACCATTAAAGCCACTCCAAAAGCTAAGATTTATTTGAG
GTTCTAGATTATCAAATGGAGCACTCAAATGAATGCAAGAGAACTTCGTTGCAGTCTATGATGGAAGCAGTTT
TATTGAAAACCTGAAGGCCAAGTTTTCGAGCACTGTGGCCAATGATGTAATGCTTAAACAGGAATTGGAGTGAT
TCGAATGTGGGCAGATGAAGGTAGTGGCTTAGCAGGTTTCGAATGCTCTTTACTTCTTTGTGGAGCCTCCCTG
CACAAGCAGCACTTTCTTTTGGCATAGCAACATGTGCATCAATAATTCTTTAGTCTGTAATGGTGTCCTCAAAATG
TGCATACCTTGGGATGAAAATCATTGTAAGAAAAGTAGTTACACTTTCAAACAGGGACATGAGTGCCCTGAGCAGGCCCTGGA
TGGAACAATTATTGGCATTACTTCAGGGATTGTCTTGGTCTTCTCATTATTTCTATTTTAGTACAAGTGAAACA
GCCTCGAAAAAAGGTTCATGGCTTGCAAAACCGCTTTTAAATAAAACCGGGTTCCAAGAAGTGTTTGATCCTCCTCA
TTATGAAGTGTTCCTAAGGGACAAAGAGATTTCTGCAGACCTGGCAGACTTGTGGAAGAATTGGACAACCTA
CCAGAAGATGCGCGCTCCTCCACCGCTCCCGCTGCATCCACGACCACCACTGTGGGTGCGAGGCCCTCAGCGT
CAAACAAAGCAGGACCAACCTCAGTTCCATGGAACCTTCTTCCGAAATGACTTTGCACAACCACAGCCAATGAA
AACATTTAATAGCCTTCAAGAAAAGTAGTTACACTTTCAAACAGGGACATGAGTGCCCTGAGCAGGCCCTGGA
AGCCGAGTAATGGAGGAGATTCCCTGTGAAATTTATGTGAGGGGGCGAGAAGATTCTGCACAAGCATCCATATC
CATTGACTTCTAACTCTCTGCTAATGGTGATGTGAATTCCTTAGGGTGTGTACGTACGCAGCCTCCAGGGCACCAT
ACTGTTTCCAGCAGCCAACCTTTTCTCCCATCACAACCTACGAAGACCTTGATTTACCGTTAACCTATTGTATGG
TGATGTTTTTATCTCTCAGGCAGTCTATATATGTTAAACCAATCAAGGAACCTTACTCTATTAGTGGAACAAT
AATCATCTCTATTGCTTGGTGTCAATTTATAGGAAGCACTGCCAGTTAAAGAGCATTAGAAGAGGTGGTTGGATGG
AGCCAGGCTCAGGCTGCCTCTTCTGTTTAGCAACAAGAAAGACTGCTCTTGACTGATAACAGCTCTGTCAATATTT
TGATGCCACAATAAACTTGATTTTTTTTTTACATTCCTTTTATTTTTCTCTTCTAAATTTAATTTGTTTTATAA
GCCTATCGTTTTACCATTTCAATTTCTTACATAAGTACAAGTGGTTAATGTACCACATACTTCAGTATAGGCATT
TGTTCTTGAGTGTGCAAAATACAGCTAGTTACTGTGCCAATTAAGACCCAGTTGATTTACCCATCTGTTTCT
TCTTGGCTAATCTCTGACTTCTGCCTTTTAAATTAAGTGGGCCCTTATTCCTTATTTTCTGTGAGAAATAATAGAT
GATATGATTTATTACCTTTCAATTATATTTTCTCAGTTATACTAGAAAATTTCAATAATCCTGGGATATATGTAC
CATTGTGAGCTATGACTAAAAATTTGAAAAGATAAAAAATTTCTAGCAAGCCTTTGAAGTTTACCAAGTATAGTC
ACATTCAGTGACAGCCCATTCATTCCAGTAAAGAATCATTTCATTCACTTTGGGAGAGGCCTATAATTACATTTA
TTTGCAATGTTTCTCTCGCTAGATTGTTACATAGCTCCCATTCGTGGTGGTTTGCTTACAGCATATGGTAACCA
AGGTTAGATGCCAGTTAAATTCCTTAGAAATTTGGATGAGCCTTGAGATTGCTTCTTAAGTGGGACATGACATTT
TTCTAGCTCTTATCAAGAATAACAACCTCCACTTTTTTTTAACTGCACCTTTGACTTTTTTTATGGTATAAAAA
CAATAATTTATAAACATAAAAGCTCATTGTGTTTTTTTAGACTTTTGATATTATTTGATACTGTACAACTTTATT
AAATCAAGATGAAAGACCTACAGGACAGATTCCTTTTCACTGTTTACATCAGTGGCTTTGATGCAAAATATGCTGT
GTTGGACCTGGACGCTATAACTTATTGTAAAGACCTTGGAATGTGGACATAAGCTCTTTCTTTCTTTTGTAC
TGTATTTAGTTTGTGATAAATTTTCACTGTGTGATATTTATGCTCTAAATCACTACACAAATCCCATATTTAAA
TATACATTGTACCTGAAAAAAA

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FIGURE 114

MALERLCSVLKVLITVLVVEGIAVAQKTQDGQNIQIKHIPATQCGIWVRTSNGGHFASPNYP
DSYPPNKECIYILEAAPRQRIELTFDEHYIIEPSFECRFDHLEVRDGPFGFSPLIDRYCGVKS
PPLIRSTGRFMWIKFSSDEELEGLGFRAKYSFIPDPDFTYLGGILNPIPDQFELSGADGIVR
SSQVEQEEKTKPGQAVDCIWTIKATPKAKIYLRLDYQMEHSNECKRNFVAVYDGSSSIENLK
AKFCSTVANDVMLKTGIGVIRMWADEGSRLSRFRMLFTSFVEPPCTSSTFFCHSNMCINNSLV
CNGVQNCAYPWDENHCKEKKKAGVFEQITKTHGTIIGITSGIVLVLLIISILVQVKQPRKKVM
ACKTAFNKTGFQEVFDPFHYELFSLRDKEISADLADLSEELDNYQKMRRSSTASRCIHDHHC
SQASSVKQSRTNLSSMELPFRNDFAQPQPMKTFNSTFKKSSYTFKQGHECPEQALEDRVMEEI
PCEIYVRGRED SAQASISIDF

Important features of the protein:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 348-369

N-glycosylation sites.

amino acids 311-315, 385-389, 453-457, 475-479

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 426-430, 479-483

N-myristoylation sites.amino acids 22-28, 32-38, 54-60, 186-192, 279-285, 318-324,
348-354, 352-358, 441-447

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FIGURE 115

GGTCTCTGTCCTTGGCTGTGGCTCCTGCGCTCTGGCTGAGCCATGTTTCCTTCTCCTCGCCCTC
CTCACTGAGCTTGGAAAGACTGCAAGCCCACGAAGGTTCTGAAGGAATATTTCTGCATGTCACA
GTTCCACGGAAGATTAAGTCAAATGACAGTGAAGTTTCAGAGAGGAAGATGATTACATCATT
ACAATTGATGGACAACCTTACACTCTACATCTCGGAAAACAATCATTCTTACCCCAAGACTTT
TTGGTTTATACATATAATGAAACTGGATCTTTGCATTCTGTGTCTCCATATTTTATGATGCAT
TGCCATTACCAAGGATATGCTGCCGAATTTCCAAATTCATTTGTGACACTCAGTATATGTTCT
GGTCTCAGGGGATTTCTCCAGTTTGAAAATATCAGTTATGGAATTGAACCAGTAGAATCTTCA
GCAAGATTTGAGCATATAATTTATCAAATGAAAAATAATGATCCAAATGTATCCATTTTAGCA
GTAAATTACAGTCATATTTGGCAGAAAGACCAGCCCTACAAAGTTCCTTTAAACTCACAGATA
AAAAATCTTTCAAAACTATTACCCCAATATCTGGAAATATACATTATAGTGGA AAAAGCTTTG
ATGTTTACCCAGTTCAAATTGACTGTTATACTGTCTTCCTTGGAATTGTGGTCAAATGAAAAC
CAGATTTCCACCAGTGGGGATGCTGATGATATATTACAAAGATTTTGGCATGGAAACGGGAC
TATCTCATCCTACGGCCCCATGACATAGCATACTTACTTGTTTACAGGAAACATCCTAAATAT
GTGGGAGCAACATTTCTGCGACCGTATGCAATAAAAGCTATGATGCAGGTATTGCTATGTAT
CCAGATGCAATAGGTTTGGAGGGATTTTCGGTTATTATAGCTCAACTGCTTGGCCTTAATGTA
GGATTAACATATGATGACATCACTCAGTGTTTCTGTCTGAGAGCTACATGCATCATGAATCAT
GAAGCAGTGAGTGCCAGTGGTAGAAAGATTTTAGCAACTGCAGCATGCACGACTATAGATAT
TTTGTTTCAAATTTGAGACTAAATGCCTTCAGAAGCTTTCAAATTTGCAACCATTACATCAA
AATCAACCAGTGTGTGGTAATGGGATTTTGAATCCAATGAAGAATGTGACTGTGGTAATAAA
AATGAATGTCAATTTAAGAAGTGCTGTGATTATAACACATGTAAACTGAAGGGCTCAGTAAAA
TGTGGTTCTGGACCATGTTGTACATCAAAGTGAGTTGTCAATAGCAGGCACTCCATGTAGA
AAGAGTATTGATCCAGAGTGTGATTTTACAGAGTACTGCAATGGAACCTCTAGTAATTGTGTT
CCTGACACTTATGCACTGAATGGCCGTTTGTGCAAGTTGGGAACTGCCTATTGCTATAACGGA
CAATGTCAAACCTACTGATAACCAGTGTGCCAAGATATTTGGAAAAGGTGCTCAAGGTGCTCCA
TTTGCCCTGTTTTAAAGAAGTTAATTCTCTGCATGAAAGATCTGAAAACCTGTGGTTTTAAAAAT
TCACAACCATTACCTTGTGAACGGAAGGATGTTCTCTGTGGAAAATTAGCTTGTGTTTCAGCCA
CATAAAAATGCTAATAAAAAGTGACGCTCAATCTACAGTTTATTTCATATATTCAAGACCATGTA
TGTGTATCTATAGCCACTGGTTCCTCCATGAGATCAGATGGAACAGACAATGCCTATGTGGCT
GATGGCACCATGTGTGGTCCAGAAATGTACTGTGTAAATAAAACCTGCAGAAAAGTTTCAATTA
ATGGGATATAACTGTAATGCCACCACAAAATGCAAAGGGAAAGGGATATGTAATAATTTTGGT
AATTGTCAATGCTTCCCTGGACATAGACCTCCAGATTGTAAATTCAGTTTGGTTCCCCAGGG
GGTAGTATTGATGATGGAATTTTCAGAAATCTGGTGACTTTTATACTGAAAAGGGCTACAAT
ACACACTGGAACAACCTGGTTTATTCTGAGTTTCTGCATTTTCTGCCGTTTTTCATAGTTTTC
ACCACTGTGATCTTTAAAGAAATGAAATAAGTAAATCATGTAACAGAGAGAATGCAGAGTAT
AATCGTAATTCATCCGTTGTATCAGAAAGCGATGACGTGGGACATTAAATATTGCACAGA ACTT
CCATAGCAAATAACCTAAAGGAACGAATGTGCTTTATTTATAACCTTACGTTATCCCCAATGC
ATTGTAAATGTCAAACCTTTGGAAAATAAAGCCTGCGTGCCCTCCC

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FIGURE 116

MFLLLALLTELGRQLQAHEGSEGI FLHVTVP RKIKSNDSEV SERKMIYIITIDGQPYTLHLGKQ
SFLPQNFLVYTYNETGSLHSVSPYFMMHCHYQGYAAEFNSFVTL SICSGLRGFLQFENISYG
IEPVESARFEHIIYQMKNNDPNV SILAVNYSHIWQKDQPYKVPLNSQIKNLSKLLPQYLEIY
IIVEKALMFTQFKLT VILSSLELWSNENQISTSGDADDILQRFLAWKRDY LILRPHDIAYLLV
YRKHPKYVGATFP GTVCNKSYDAGIAMYPDAIGLEGFSVIIAQLLGLNVGLTYDDITQCFCLR
ATCIMNHEAVSASGRKIFSNCSMHDYRYFVSKFETKCLQKLSNLQPLHQNPVCGNGILESNE
ECDCGNKNECQFKKCCDYNTCKLKGSVKCGSGPCCTSKCELSIAGTPCRKSIDPECDFTTEYCN
GTSSNCVPTDYALNGRLCKLGTAYCYNGQCQT TDNQCAKIFGKGAQGAPFACFKEVNSLHERS
ENCGFKNSQPLPCERKDVLCGKLACVQPHKNANKSDAQSTVYSYIQDHVCVSIATGSSMRSDG
TDNAYVADGTMC GPEMYCVNKT CRKVHLMGYNCNATTKCKGKGICNNFGNCQC FPGHRPPDCK
FQFGSPGGSIDDGNFQKSGDFYTEKGYNTHWNNWFILSFCIFLPFFIVFTTVIFKRNEISKSC
NRENAEYNRNSSVSESDDVGH

Important features of the protein:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 665-684

N-glycosylation sites.amino acids 36-39, 76-79, 122-125, 149-152, 156-159, 177-180,
270-273, 335-338, 441-444, 537-540, 587-590, 601-604, 703-706**Casein kinase II phosphorylation sites.**amino acids 74-77, 208-211, 221-224, 304-307, 337-340, 346-349,
376-380, 415-418, 499-502, 639-642, 708-711**Tyrosine kinase phosphorylation site.**

amino acids 243-249

N-myristoylation sites.amino acids 53-58, 79-84, 266-271, 298-303, 372-377, 403-408,
408-413, 442-447, 462-467, 469-474, 488-493, 567-572, 610-615,
616-621, 634-639**Amidation site.**

amino acids 328-331

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FIGURE 117

CCCACGCGTCCGCGGACGCGTGGGGCTCAGTGGGCGTCGCGGAAGGCTAAGGGAGTGTGGCG
GGCGGCTCCGGGAGCCAACATGCCCTCGGTATGCGCAGCTGGTCATGGGCCCCGCGGGCAGCGG
GAAGAGCACCTACTGTGCCACCATGGTCCAGCACTGTGAAGCCCTCAACCGGTCTGTCCAAGT
TGTAACCTGGATCCAGCAGCAGAACACTTCAACTACTCCGTGATGGCTGACATCCGGGAAGT
GATCGAGGTGGATGATGTAATGGAGGATGATTCTCTGCGATTCCGTCCCAACGGAGGATTGGT
ATTTTGCATGGAGTACTTTGCCAATAATTTTGGCTGGGAGAACTGTCTTGGCCATGTAGA
GGACGACTATATCCTTTTTGATTGTCCAGGTCAGATTGAGTTGTACACTCACCTGCCTGTGAT
GAAACATCTGGTCCAGCAGCTCGAGCAGTGGGAGTTCCGAGTCTGTGGAGTTTTTCTTGTTGA
TTCTCAGTTCATGGTGGAGTCATTCAAGTTTATTTCTGGCATCTTGGCAGCCCTGAGTGCCAT
GATCTCTCTAGAAATTCGCAAGTCAACATCATGACAAAATGGATCTGCTGAGTAAAAAAGC
AAAAAAGGAAATTGAGAAATTTTAGATCCAGACATGTATTCTTTATTAGAAGATTCTACAAG
TGACTTAAGAAGCAAAAATTCAGAACTGACTAAAGCTATATGTGGACTGATTGATGACTA
CAGCATGGTTCGATTTTTACCTTACGATCAGTCAGATGAAGAAAGCATGAACATTGTATTGCA
GCATATTGATTTTGCCATTCAATATGGAGAAGACCTAGAATTTAAAGAACCAAAGGAACGTGA
AGATGAGTCTTCCTCTATGTTTGACGAATATTTTCAAGAATGCCAGGATGAATGAAGAGTTTA
CTAAAAGTAACCATCTAAAGAGCTTGTGGCCAAACCAGCAGAACATTCTTCTCTTCAAAGGAT
GCAATAGTAGAAAGCTACTTATTTTAATGAAAAAAGTAAACTTCGTTCTTTATCAGCCTCA
TGCCTGAATCAAATTTTAAATTATTCTGAACTGCTGCTGTTTAAAGTGGAATCTTTTAGTAT
TATAACAGCATCACTTTAGATTTTGTAAGTCAAATTGAAATGAATGCACATAGATTTATATA
TAAATTAGCACCTGAGCTAAGGTTAAGGCCGGTCTAAACTTATTTTCACTTTTTGTATTATTT
TTGAGATGCAGGAATTACTGTAACAAAATATGTATGTCCGAAGGGAAAAAGCTGCAAGGATAT
ATATAAGACCACTGCTTATCTGTATCTTCCATTTTCCTATATTGAAAATGTATATTATTTAT
ATAACTTAAAAAGTAAAAATAACTATGTTTTGAGAT

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FIGURE 118

MPRYAQLVMGPAGSGKSTYCATMVQHCEALNRSVQVVNLDPAAEHFNYSVMADIRELIEVDDV
MEDDSLRFPGNGGLVFCMEYFANNFDWLENCLGHVEDDYILFDCPGQIELYTHLPVMKHLVQQ
LEQWEFRVCGVFLVDSQFMVESFKFISGILAALSAMISLEIPQVNIMTKMDLLSKKAKKEIEK
FLDPDMYSLLEDSTSDLRSKKFKKLTKAICGLIDDYSMVRFLLPYDQSDEESMNIVLQHIDFAI
QYGEDLEFKEPKEREDESSSMFDEYFQECQDE

Important features of the protein:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 151-170

N-glycosylation sites.

amino acids 31-35, 47-51

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 212-216

Tyrosine kinase phosphorylation site.

amino acids 189-197

N-myristoylation sites.

amino acids 13-19, 76-82, 154-160

ATP/GTP-binding site motif A (P-loop).

amino acids 10-18

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FIGURE 119

GGGCGCTGGGAGACACCGGACGCCCCGCTCGGCTGCGCTGCGGCTCAGGCCCCCGCTCGGGCCC
GACCCGCTCGGTACCGCCGGCTCGGGCGCGCACCTGCCGGCTGCGGCCCCAGGGCCATGCGG
AGGCCCACGAGGAGGCCGGCGGCCACGCGCATCCCGTAGCCCAGGTGGCCCAGGTCTGCACCG
CGGCGGCCTCGGCGGCC**ATGG**AGCCCCCGTATTGCTGACGGCGCACTACGATGAGTTCCAAGA
GGTCAAGTACGTGAGCCGCTGCGGCGCGGGGGGCGCGCGGGGCCTCCCTGCCCCCGGGCTT
CCCGTTGGGCGCTGCGCGCAGCGTCACCGGGGCCCGGTCCGGGCTGCCGCGCTGGAACCGGCG
CGAGGTGTGCTGCTGTGCGGGCTGGTGTTCGCCGCCGGCCTCTGCGCCATTCTGGCGGCTAT
GCTGGCCCTCAAGTACCTGGGCCCCGGTCGCGGCCGGCGGCGGCGCCTGTCCCGAGGGCTGCCC
TGAGCGCAAGGCCTTCGCGCGCGCCGCTCGCTTCCTGGCCGCCAACCTGGACGCCAGCATCGA
CCCATGCCAGGACTTCTACTCGTTGCGCTGCGGCGGTTGGCTGCGGCGCCACGCCATCCCCGA
CGACAAGCTCACCTATGGCACCATCGCGGCCATCGGCGAGCAAAACGAGGAGCGCCTACGGCG
CCTGCTGGCGCGGCCCGGGGGTGGGCTGGCGGCGCGGCCAGCGCAAGGTGCGCGCCTTCTT
CCGCTCGTGCTCGACATGCGCGAGATCGAGCGACTGGGCCCCGCGACCCATGCTAGAGGTCAT
CGAGGACTGCGGGGGCTGGGACCTGGGCGGCGCGGAGGAGCGTCCGGGGGTGCGGCGCGATG
GGACCTCAACCGGCTGCTGTACAAGGCGCAGGGCGTGTACAGCGCCGCCGCGCTCTTCTCGCT
CACGGTCAGCCTGGACGACAGGAACCTCTCGCGCTACGTTCATCCGCATTGACCAGGATGGGCT
CACCCCTGCCAGAGAGGACCCTGTACCTCGCTCAGGATGAGGACAGTGAGAAGATCCTGGCAGC
ATACAGGGTGTTCATGGAGCGAGTGCTCAGCCTCCTGGGTGCAGACGCTGTGGAACAGAAGGC
CCAAGAGATCCTGCAAGTGGAGCAGCAGCTGGCCAACATCACTGTGTGAGAGTATGACGACCT
ACGGCGAGATGTCAGCTCCATGTACAACAAGGTGACGCTGGGGCAGCTGCAGAAGATCACCCC
CCACTTGCGGTGGAAGTGGCTGCTAGACCAGATCTTCCAGGAGGACTTCTCAGAGGAAGAGGA
GGTGGTGCTGCTGGCGACAGACTACATGCAGCAGGTGTGCGAGCTCATCCGCTCCACACCCCA
CCGGTCTCTGCACAACTACCTGGTGTGGCGCGTGGTGGTGGTCTGAGTGAACACCTGTCCCC
GCCATTCCGTGAGGCACTGCACGAGCTGGCACAGGAGATGGAGGGCAGCGACAAGCCACAGGA
GCTGGCCCCGGTCTGCTTGGGCCAGGCCAATCGCCACTTTGGCATGGCGCTTGGCGCCCTCTT
TGTACATGAGCACTTCTCAGCCGCCAGCAAAGCCAAGGTGCAGCAGCTAGTGAAGACATCAA
GTACATCCTGGGCCAGCGCCTGGAGGAGCTGGACTGGATGGACGCCGAGACCAGGGCTGCTGC
TCGGGCCAAGCTCCAGTACATGATGGTGTGCTGGCTACCCGGACTTCTGCTGAAACCCGA
TGCTGTGGACAAGGAGTATGAGTTTGAGGTCCATGAGAAGACCTACTTCAAGAACATCTTGAA
CAGCATCCCCCTCAGCATCCAGCTCTCAGTTAAGAAGATTGCGCAGGAGGTGGACAAGTCCAC
GTGGCTGCTCCCCCACAGGCGCTCAATGCCTACTATCTACCCAACAAGAACCAGATGGTGT
CCCCGCGGGCATCCTGCAGCCACCCCTGTACGACCCTGACTTCCACAGTCTCTCAACTACGG
GGGCATCGGCACCATCATTGGACATGAGCTGACCCACGGCTACGACGACTGGGGGGGCCAGTA
TGACCGCTCAGGGAACCTGCTGCACTGGTGGACGGAGGCCTCCTACAGCCGCTTCTGCGAAA
GGCTGAGTGCATCGTCCGTCTCTATGACAACCTCACTGTCTACAACCAGCGGGTGAACGGGAA
ACACACGCTTGGGGAGAACATCGCAGATATGGGCGTCCCTCAAGCTGGCCTACCACGCCTATCA
GAAGTGGGTGCGGGAGCACGGCCAGAGCACCCACTTCCCCGGCTCAAGTACACACATGACCA
GCTCTTCTTCATTGCCTTTGCCCAGAACTGGTGCATCAAGCGGCGGTGCGAGTCCATCTACCT
GCAGGTGCTGACTGACAAGCATGCCCTGAGCACTACAGGGTGTGGGCAGTGTGTCCAGTT
TGAGGAGTTTGGCCGGGCTTTCCACTGTCCCAAGGACTCACCCATGAACCCTGCCACAAAGTG
TTCCGTGTGG**TG**AGCCTGGCTGCCCCGCTGCACGCCCCCACTGCCCCCGCACGAATCACCTCC
TGCTGGCTACCGGGGACGGCATGCACCCGGTGCCAGCCCCGCTCTGGGCAACCACCTGCCTTCC
AGCCCCCTCCAGGACCCGGTCCCCCTGCTGCCCCCTCACTTCAGGAGGGGCCTGGAGCAGGGTGA
GGCTGGACTTTGGGGGGCTGTGAGGGAAATATACTGGGGTCCCCAGATTCTGCTCTAAGGGGG
CCAGACCCTCTGCCAGGCTGGATTGTACGGGCCACCTTCGCTGTGTCTTGCTGCAAAGTC
TGGTCAATAAATCACTGCACTGTTAAAAA

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FIGURE 120

MEPPYSLTAHYDEFQEVKYVSRGAGGARGASLPPGFPLGAARSVTGARSGLPRWNRREVCLL
 SGLVFAAGLCAILAAMLALKYLGPVAAGGGACPEGCPERKAFARAARFLAANLDASIDPCQDF
 YSFACGGWLRRAIPDDKLTGTIAAIGEQNEERLRLLARPGGGPGGAAQRKVRAFFRSCLD
 MREIERLGPRPMLEVEDCGGWDLGGAERPGVAARWDLNRLLYKAQGVYSAAALFSLTVSLD
 DRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKILAAAYRVFMERVLSLLGADAVEQKAQEILQ
 VEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITPHLRWKWLLDQIFQEDFSEEEEVLLA
 TDYMQQVSQILIRSTPHRVLHNYLVWRVVVLSEHLSPPFREALHELAQEMEGSDKPQELARVC
 LGQANRHFGMALGALFVHEHFAASKAKVQQLVEDIKYIILGQRLEELDWMADAETRAAARAKLQ
 YMMVMVGYPDFLLKPDADVKEYEFVHEKTYFKNILNSIPFSIQLSVKKIRQEVDKSTWLLPP
 QALNAYYLPNKNQMVFPAGILQPTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGN
 LLHWWTEASYSRFLRKAECIVRLYDNFTVYNQRVNGKHTLGENIADMVGLKLAYHAYQKWVRE
 HGPEHPLRLKYTHDQLFFIAFAQNWCIRRSQSIYLQVLTDKHAPEHYRVLGVSVSQFEEFGR
 AFHCPKDSMPNPAHKCSVW

Important features of the protein:**Transmembrane domain:**

amino acids 64-88

N-glycosylation sites.

amino acids 255-259, 322-326, 656-660

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 722-726

N-myristoylation site.amino acids 24-30, 26-32, 27-33, 40-46, 47-53, 65-71, 148-154,
169-175, 170-176, 237-243, 450-456, 604-610, 607-613**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 85-96

Prenyl group binding site.

amino acids 772-777

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 609-619

Neutral zinc metallopeptidases, zinc-binding region proteins.

amino acids 609-619

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FIGURE 121

CGGACTGCCCCGACCGCGCGATGGAGTCGACCGGCAGCGTCGGGGAGGCCCCGGGCGGACCCC
GGGTGCTGGTGGTGGGCGGCGGCATCGCGGGGCTGGGCGCGGCGCAGAGGCTCTGCGGCCACT
CCGCCTTCCCGCACCTGCGGGTCCTGGAGGCCACGGCCCCGCGCCGGGGGCCGCATCCGCTCGG
AGCGCTGCTTCGGTGGCGTGGTGGAGGTGGGCGCGCACTGGATCCATGGGCCCTCCCGGGGTA
ACCCCGTCTTCCAGCTGGCTGCTGAGTACGGGCTGCTGGGGGAGAAGGAGCTGTCCCAGGAGA
ACCAGCTGGTGGAGACCGGGGGTCACGTGGGCCTGCCCTCCGTGAGCTACGCCAGCTCCGGGG
CCAGCGTGAGCCTCCAGCTGGTGGCGGAGATGGCGACTCTGTTCTACGGCCTGATAGACCAGA
CCCCGGAGTTCCTGCACGCTGCAGAGACCCCGGTGCCAGCGTCGGGGAGTACCTCAAGAAGG
AGATTGGCCAGCACGTGGCCGGCTGGACAGAGGATGAGGAGACCAGGAAGCTGAAGCTGGCCG
TCCTGAACTCCTTCTTCAACCTGGAATGCTGTGTGAGCGGCACCCACAGCATGGACCTGGTGG
CCCTGGCACCCCTTTGGGGAGTATACCGTGCTGCCGGGGCTGGACTGCACCTTTTCTAAGGGCT
ATCAAGGACTCACAACTGCATGATGGCCGCCCTGCCGGAGGACACTGTAGTTTTTTGAGAAGC
CTGTGAAGACCATCCACTGGAACGGGTCTTCCAGGAGGCAGCCTTTCCCGGGGAGACCTTTC
CAGTGTGCGTAGAGTGTGAGGATGGAGACCGGTTCCCGGCGCACCATGTCATCGTCACCGTGC
CCTTAGGTTTTCTTAGGGAACATTTGGACACCTTCTTTGACCCTCCCCTGCCGGCTGAGAAGG
CAGAAGCAATCAGGAAGATAGGCTTTGGGACCAACAACAAAATCTTCCTGGAGTTTGAGGAGC
CCTTCTGGGAGCCAGACTGCCAGCTGATCCAGCTGGTGTGGGAGGACACGTCGCCCCCTGGAGG
ATGCTGCCCCCTGAGCTACAGGACGCCTGGTTCCGGAAGCTCATTGGCTTTGTGGTCTGCCTG
CCTTTGCGTCTGTCCACGTTCTCTGTGGGTTTATTGCCGGACTTGAGTCTGAGTTCATGGAGA
CTCTGTGCGATGAAGAAGTACTTCTGTGTCTCACCCAAGTGCTCCGGAGAGTGACAGGAAACC
CACGGCTCCCCGCGCCCAAGAGCGTCTGCGGTCTCGCTGGCACAGCGCCCCGTACACTAGGG
GGTCTACAGCTACGTGGCCGTGGGCAGTACTGGGGGCGACCTGGACCTGCTGGCTCAGCCCC
TCCCTGCAGACGGCGCCGGCGCCAGCTCCAGATCCTGTTTGCGGGGAAGCCACACATCGCA
CGTTTTACTCCACGACGCACGGGGCTCTGCTGTGCGGATGGAGGGAGGCCGACCGCCTCCTCA
GTCTGTGGGCCCCGCAGGTGCAGCAGCCCAGGCCGAGGCTCTAGCTGGGCCCAGCCTACTCTG
TTCCACCCGTGTCGGGGGTAGGCTGGGACCGTCATTTCTTCTGACAGATTTAGTCTGGCTTG
AAATTTGGGGATGTTAATGAGGGTCTCTGGTTTTTGGTAACAGGGCCACCTTCTCAGTTCT
TGTGTCTGTTATTGGAGTCTGGCCAGGGTTGACTTGAGCTGAGACACCAGATGCTCACGGAGA
TGCTGGACACATAAAGCAAGTTACAGCCACAAAAA

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FIGURE 122

MESTGSVGEAPGGPRVLVVGGGIAGLGAAQRLCGHSAFPHLRVLEATARAGGRIRSERCFGV
VEVGAHWIHGPSRGNPVFQLAAEYGLLGEKELSQENQLVETGGHVGLPSVSYASSGASVSLQL
VAEMATLFYGLIDQTREFLHAAETPVPSVGEYLLKKEIGQHVAGWTEDEETRKLKLAVLNSFFN
LECCVSGTHSMDLVALAPFGEYTVLPGLDCTFSKGYQGLTNCMMAALPEDTVVFEKPVKTIHW
NGSFQEAAPGETFPVSVECEDGDRFPAHHVIVTVPLGFLREHLDTFFDPPLPAEKAEAIRKI
GFGTNNKIFLEFEFPFWEPCQLIQLVWEDTSPLEDAAPELQDAWFRKLIGFVVLPAFASVHV
LCGFIAGLESEFMETLSDEEVLLCLTQVLRRTGNPRLPAPKSVLRSRWHSAPYTRGSYSYVA
VGSTGGDLDLLAQPLPADGAGAQLQILFAGEATHRTFYSTTHGALLSGWREADRLLSLWAPQV
QQPRPRL

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 364-385

N-glycosylation site.

amino acids 253-257

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 408-412

N-myristoylation sites.amino acids 20-26, 21-27, 25-31, 105-111, 119-125, 164-170,
216-222, 227-233, 443-449, 484-490**Aminooxidase Flavin containing amine oxidase:**

amino acids 23-497

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FIGURE 123

CGGACGCGTGGGGGAAGATGGATAAATAATTCTGTACACGTGCCCTGGCCTCTGGAGCTCAGCTGCCAGTCCAC
GTCTAGGGAATCTTAGCATCTGGGACCAAGACACTTTACAGCAATCATCACCCTTTGCAGAGGAGGTGAGCTCAC
CAGGACTCATCTGCCATTTAGACCTTTTGTCTACCTGCCAGGTGGCCCCCACTGCTGACGAGAGATGGTGA
TCTCTCAGTCTCCCCGGACTCCTTGAAGCCAGTATCGCTGACCAGCAGTCTTGTCTTCCTCATGCACCTCCTCCT
CCTTACGCTTGGGAGCCGAGCTCAGAGGTCAAGGTGCTAGGCCCTGAGTATCCCATCCTGGCCCTCGTCGGGGA
GGAGGTGGAGTTCCCGTGCCACCTATGGCCACAGCTGGATGCCAGCAAATGGAGATCCGCTGGTTCCGGAGTCA
GACCTTCAATGTGGTACACCTGTACCAGGAGCAGCAGGAGTCCCTGGCAGGCAGATGCCGGCGTTCGGGAACAG
GACCAAGTTGGTCAAGGACGACATCGCCTATGGCAGCGTGGTCTGCAGCTTACAGCATCATCCCCTCTGACAA
GGGCACATATGGCTGCCGCTTCCACTCCGACAACCTTCTCTGGCGAAGCTCTCTGGGAACCTGGAGGTAGCAGGGCT
GGGCTCAGACCCTCACCTCTCCCTTGAGGGCTTCAAGGAAGGAGGCATTAGCTGAGGCTCAGATCCAGTGGCTG
GTACCCCAAGCCTAAGGTTCACTGGAGAGACCACAGGGACAGTGCCTGCCTCCAGAGTTTGAAGCCATCGTCTG
GGATGCCCAGGACCTGTTCACTGTGGAAACATCTGTGGTTGTCCGAGCGGGAGCCCTCAGCAATGTGTCCGTCTC
CATCCAGAATCTCCTCTTGAGCCAGAAGAAAGAGTTGGTGGTCCAGATAGCAGACGTGTTCTGTTACCCGGAGCCTC
TGCGTGGAAAGAGCGCGTTCCGTGCGGACCCCTGCCGCTGCTGTGGTCTCGCGGCGCTGGCGCTGGCGCTCCTCCG
GAAGCAGCGGAGAAGCCGAGAAAAGCTGAGGAAGCAGGCGGAGAAGAGACAAGAGAACTCACTGCAGAGCTGGA
AAAGCTTACAGACAGAGCTTGACTGGAGACGGGCTGAAGGCCAGGCTGAGTGGAGAGCAGCCAAAAATATGCACT
GGATGTGACGCTGGACCCGGCCTCGGCGCACCCACAGCCTGGAGGTGTGAGGATGGCAAGAGCGTGTCTTCCCG
CGGGGCGCGCCAGGCCCCGGCGCCTGGCCACCCGACGCGGTTCTCGGAGCAGACGTGCGCGCTGAGCCTGGAGCG
GTTCTCCGCGCGCCGCACTACTGGGAGGTGCACGTGGGCGCGCGCAGCCGCTGGTTCCTGGGCGCCTGCCTGGC
CGCGGTGCGCGCGCGCGGGGCTGCGCGCCTGAGCCCTGCGGCGGCTACTGGGTGCTGGGGCTGTGGACGGCTG
CGAGTACTTCGTCTGGCCCCGACCCGCTGCGGCTCACCTGCGCGTGCCCCGCGCGCCTGGGCGTCTTCTCT
GGACTACGAGGCGGAGAGCTGTCTTCTTCAACGTGTCCGACGGCTCCACATCTTACCTTCCACGACACCTT
CTCGGGCGCGCTGTGTGCTACTTACAGGCCAGGCCCCACGACGGCGCGAACATCCGGATCCCCCTGACCATCTG
CCCCGTGCCGTTAGAGGGACGGGCGTCCCCGAAGAGAAACGACAGTACACCTGGCTACAGCCCTATGAGCCCGC
GGACCCCGCCTGGACTGGTGGTGAAGGCGCCCTCGTGGCGCGGGACTGGCCCCGGGGGGCCCCCTGGATCCAG
GCCAGCGCTTTGCTCTCTCTGCTCTGAAGGGAGCAGGTGCACCAGCCAAATGTGAGCGAGGGGGACAAAGA
GAGGGACCTTTGCCCTACGTAGATGTGTATGTGTAGTGCGATTTTCTTCAAGGAAAGGAGACAAGTCCAAAGCTCG
TTTGTGGATTGTGGGACTGAGCGAAGGAGTACAAATATATCCACGTGCTCAGAGCTGGGGTGTCTACGGTGGC
GGTGGGCAAGAAGCCAGCATGGAAGAAAGAAGGGAGAAAACCTTTGGTACTGCCTTAGAGGGATCAGTTAATTTG
TATAGTTTTATATTTTTGTATATGTTTGTAGCTTAAAAAGGTGAGATGCAATAACACTTCGTAAGCAACGA
GTTACCTAAGTAAGGCTCAGATCCTAGTTTTTAAAAACCATTTCCCATTAATGAAGTTGGAGGAACAGCTGCT
TCTGAGCCGGGGCAAAAATTTCAAGGTGAGCCTGGAGCATTGTGTGTGGTGAAGTAAAAATAAGGCTCAAAACGT
GACGGCAACCCGGCAAAAGGGTAGGGAGCCAGGCCGAAGGGGCGCTCACTGACCAATTGTGGGACAATTTGAACAT
CAGGATGAATAATGACAGGAGAGATTATAACACACTGAATAAAAAACATAATCCATGAGTTCATGCTGATACTCAA
ATTTCTTTTTTAAAAAGGAGAAACAGGAAGGTTTCTTTTGAGGTGAAATCTAATTATTGGTGAGAGTCTTGAGGA
ACAGGCTGTTTCCAGTCTCAAAGCAGTAACCTTATACACTACTTATAAGTTTGAAAGGGGAAAGGTTACCTTTAC
AATGGAGACATCTACCAGATCATCCAAGTGATTAATTTAACATCATCAATGATGGGACCAAGGACATTATTAGT
TTGACAACCTGGGGAAGAAGTGTCTTACCCCCCTACCCCAAGACATTCTCTGTGCGCCAGGCTGGAGTGCA
GCCTCAACCTCCTGGGCCCCAAGTGATCCTCCACCTCAGCACACAACACCATGCCCAATTTAAGTGCGTTATAG
AGACGGGGGTCTCACTTTGTACCCAGGCTGGTCTCAACTCCTGCGCTCAAGCAATCCTCCACCTGGGCGCTCC
CAAAATGCTGGGTGTACAGGCATGAGCCGCTGTGCTGGCTTATTTTCAAGAGTGAGACATTTGTACTGTGGCTA
TGTAAGGAGAACATTCTTGTCTTAGCAAAACATACTGAAGTTTTTAGATATTAATTACCACAGTGTCTGCCACTGA
ATTTCCAGTGACTAAGTGGAATAATATAAAACATATGAATATAAAGAAAGAAAGAGACAAGTCAAATGTAGTAAA
ATGACAACACTTGGTGAATCTAGGTGACTGGTGCAGAGATGTTCAATGTACTATCAATGTGGCTTTGCTGTGGGT
TTGAAATTTGCAAACTAAGAGTTGGGTGGCGGGGAGAAGGATACCAAAAACTAAGTGATTATCTTTGGATG
GGAAATGTTTGGTAATTGCATTCTAAAAATGTCTTCTTGTATTTTTAATGTTCAATAATGTATATGTATCAG
TTCTGTAATAAAGGGGAAAACACTTTTCA

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FIGURE 124

MVDLSVSPDSLKPVS LTSSLVFLMHLLLLQPGEPSSEVKVLGPEYPILALVGEEVEFPCHLWP
QLDAQQMEIRWFRSQTFNVVHLYQEQQELPGRQMPAFRNRTKLVKDDIAYGSVVLQLHSIIPS
DKGTYGCRFHS DNFSGEALWELEVAGLGSDPHLSLEGFKEGGIQLRLRSSGWYPKPKVQWRDH
QGQCLPPEFEAIVWDAQDLFSLETSVVVRAGALSNVSVSIQNLLLSQKKELVVQIADVFPVGA
SAWKSAFVATLPLLLVLAALALGVLRKQRRSREKLRKQAEKRQEKLTAELEKLQTELDWRRAE
GQAEWRAAQKYAVDVTLDPASAHPSLEVSEDGKSVSSRGAPPGPAPGHPQRFSEQTCALSLE
FSAGRHYWEVHVGRRSRWFLGACLAAPRAGPARLSPAAGYWVLGLWNGCEYFVLAPHRVALT
LRVPPRRLGVFLDYEAGELSFNFVSDGSHIFTFHDTFSGALCAYFRPRAHDGGEHPDPLTICP
LPVRGTGVPEENDSDTWLQPYEPADPALDWW

Important features of the protein:**Signal peptide:**

amino acids 1-34

Transmembrane domain:

amino acids 247-272

N-glycosylation sites.

amino acids 102-106, 139-143, 224-228, 464-468, 516-520

Tyrosine kinase phosphorylation site.

amino acids 105-114

N-myristoylation sites.

amino acids 129-135, 220-226, 399-405, 423-429, 480-486

Amidation site.

amino acids 390-394

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FIGURE 125

TATAGTCCCAGCTACTCATGGGGCTGATGCAGGTTGAGGCAGGAGGTTTCATGAGCCCAGGAGGTTGGAGCTGTAA
TGAGCTAGGATTCTGCCTCTGCACTCCTAGCTGGATGACAGAGCAAGACCCTGTCTCAAAAAAGAAAAA
AAAAAGAATGCATGAACCAGACATGACAGTTCCTGGCCTCAAAGATCTTCCAAAGGAAATGATTTTTTTTAAAC
ACCAATGCTGCAGGAAAAAGCAACATATTTAAGTTATCCAATAACACCTATCCAATAATTGTAAATCATTATCAT
GACATGGTAGAGTTGTTTATATTTCTTTTCTTTTAGGTGAAACACCATTCAAAGTCGTAGTCAAATCTCTTTCA
CCTAAAGAGTTGGTCCGGATACATGTCCCTAAACCTTTGGACAGGAATGATGGAACATTTTTTGATGAGATATAGG
ATGTATGAAACTGTCGATGAAGGCCTGAAGATAGAGGTCCTTTATGGTGATGAACATGTGGCTCAGTCTCCCTAT
ATTTTGAAGGACCAGTGATACCATGAGTACTGTGAGTGTCCGGAAGATCCTCAGGCCTGGCAGAAGACTCTTTCT
TGTCACCAAGGAACCACAGATTGCAAAAGATTTTGCTTCTTTCCAGCATCAATCTCCAGCAAATGCTAAAA
GAAGTCCCCAAAAGGTTTGGGGATGAGAGAGGTGCCATTGTTTATTACACGATTCTCAATAACCATGTTTACCGG
AGATCTTTAGGGAAATACACAGACTTCAAGATGTTCTCTGATGAGATTTGTTATCATTGACAAGAAAGGTCCTT
CTCCAGATTTAGAAATTTATGTTAATCTTGGAGATTGGCCCTTGGAGCATCGAAAAGTCAATGGAACCCCTAGC
CCCATACCTATCATTTCATGGTGTGGCTCTCTGGATTCAAGAGATGTTGTCTCTTCCAACGTATGACATACCCAC
TCCATGCTTGAAGCCATGCGGGGTGTACAAATGATCTCCTCTCTATTTCAGGGAAATACAGGCCTTCTGGATC
AATAAAACAGAGAGAGCTTTCTTCAGAGGTAGAGACAGCCGAGAGGAGAGGCTCCAGTTGGTACAGCTGTCCAAA
GAAATCCTCAGCTACTAGATGCAGGAATTACAGGATATTTCTTTTCCAAGAGAAAGAAAGGAGCTTGGAAAA
GCCAAGTTGATGGGTTTTCTTTGATTTCTTTAAGTACAAGTATCAAGTAAATGTGGATGGGACCGTGGCTGCTTAC
AGATATCCATATCTCATGCTGGGCGACAGTCTGGTTTTAAAGCAGGACTCGCCATATTATGAACATTTCTCATG
GCACTAGAACCTTGAAGCATTATGTTCCAATTAAAGAAATCTGAGTGATTTATTAGAGAAAGTTAAATGGGCT
AAGGAAAATGATGAAGAAGCCAAGAAGATTGCAAAAGAAGGACAGTTGATGGCTAGGGACCTACTACGCCACAC
AGGCTTTACTGCTACTATTACCAAGTACTGCAGAAATATGCCGAGCGCCAGTCCAGCAAACCCGAAGTACGTGAT
GGAATGGAACCTGTTCTCAGCCAGAAGATAGCACAGCCATCTGCCAGTGCCACAGGAAAAAGCCTTCAAGAGAA
GAACCTTTGAGTCTAGCCCAGAATCACACTCCTGTGTATCCCGGCTACACTTTAAGGAAAGATTGAATCTAAGCTGT
GAAGGACAGTATAGAAGACTGCACCAAGTGGACTAGTTCTCCCGTGGCTTTATATATGTAGATGGATATAGCAG
TACTGGTTGAGTATCCCTCATCTGAAATGCTTAGGACAGGAGTGTTCAGGCTTCAGATTTTTTAAGATTTGGG
AATATTTGCATGTACATAATGAGGTATCTTGGGGATGAGATCCAAGTCTAAACACAAAATTCATTTATATTTAT
ATATACCTTGTTCACATACCCTGAAGGTAATTTTATATAATATTTTTTAATAATTTGTGCATGAACAAAGTTTGT
ATACATTGAACTGTCAGAAAGCAAAGGTGTCACTATCTTAGCGACCCAAGTGGTGGTGTGAGCACTCAAAAGTT
TTGGATTTTGGGGTATTTTCAAGTTTTAGATTTTGTATGAGGAATGTTCAACCTGTATTTGAACAAGCATTACCA
AATATCATTGAATATTAATATCTTTTGCCTAAAACTGCTATTATCAGCATCATAGTTTCTCTAAAAAGAAAAT
TGGGGATCATAGCCGATAGAGAGACTTGCTAAAAATATAAATCAGCCTCTGCAAACTGTTTACATATTTATTGGT
TTACATATTTTATTGGTTTATTTCTATCCCTGTTCACTTTTTCTCTTCCACTTCCAATTATGAAGAGAAAATAT
TTGTTTCAAGGTTGTCCCCCGCCCCCGTCACTGCATAATTTCTCCTCTTACAGCTGCTTTTGGCTTTTATTAA
TAACAGCTTCCCTTTAGAAAGGTCTGATAAGGATATTTAAGGAAGAAGAGAAATGACTCTGTTATTAAGGTGGCAT
GGAGACTGTGGAGGGAATATTTTTTAAAGCACTACTCATATCTTTAACTAAATTTTGCCAAAGCCCGAGACAA
CATTAAAGGAGAAATGTACCTTAAGTTAGTAATTTCCAAATCTATCTGAGTTGTATACCCATCAAAGACAATACAG
TTATTAACATAGATGAAGGTATGCTATAGGCATCATTATTATCTCTATATTGAATAGGTGAAAGATAACTGTAG
TCAGGTGAAAGGCATTTCATCATTTTTAAGCTGAAAAGGGGATCCTTGAAAACACTGAAAACCTCTACAACAATCT
TCAGGAAGCCTGCTATCTTGGGATTCACTAATAATAGGCCAAGAACAAGGCAAGCATCCATTCTCACTCCACC
ACTTTTCTATTTTCACTGGGTGTCTTGGTACGATGAAGACTTTGGAAATTTCTTTCTTTTAGGACAGGGTCA
GGATTTAGGACTCATAGCCTGAAAGCTCATTACATACTCCTTGTAACCATCAGTCCAGGTTTCAAGTTCACTAAAG
TGCATGTTCTAAAAACAAGAGCTATCCTCATTCCAAATTTTAAATATGTACTCTGGCCGGTTGCAGTGGCTCAGG
CCTGTAATCCCAGCACTTTGGCAGGCCGAGATGGGCGGATCTTTGAGGTGAGGAGTTGAGACCAGCCTGGCCA
ACATGGTGAACCCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGCATTTGCCTGTAATCCCAGCT
ACTCGGGAGGCTGAGGCAGGAGAAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTACACCCTG
CACTCCAGCCTGGGTGACAGAGTGAGACTCCATCTCAAAAACGAAAATAAAAAATATGTAATCTCCTTAA
CTGAAATATTTACTTAATCTGGAAAAACAATGTAATTTTTTAAAGTGGTTACATCTATTCTTGCTGAAGAACA
TAAACAGAATTTTTTGACTAAGCATAACCAAATTTTCAAGACAGTCTAATCAATGCCAAGTATCCAAGGCAAACTC
TAATACCCATCCATTGTGCAAAACCACAAGCAGCGAAGTATTAATAAGAGCAAGCTGTCTGAGCCCATACCTA
ATGAATTTGTGTCTTAAATATTGTACATTGTGTTTGGGCTTGTCAAACTGGGATTATGGCAAGAAAGGTTGCC
TAACTCATACCTTTCTGCCTCAAATTCAGGTGCTAAAGGCTAATGGCATTTTAAACATCTTACATTTTTAAAA
TTTATATTGCCTCTGCCAAACAGGCCTAATAGTTAAAGCAAGTTGAGACAAACCAGGCAGATTCAAGTGTGTGGA
ACAGGAAGGATGTGCTTTAAAAAAGGTGGAATCCCTCAAAAATTTCTATAGGGAGACAGCAGCCTTAATCTACA
TAATCTTCTATCTCGCAATTCAGCCGACGCTTTAAAGAGTTAGTGTTAATGGCTTTCTGGTTTGAACAAAAA
ATGCATCTATGTGGTTGAAAGTTTGGGAGGAGATTACCAATATCTGAGGAGAAGATGGAGTGAAGGGAATTTCT
ACTTTTTGCTTTTATACCTTTCTATAATATTTAGATTTTTTTTTTACTGTAAGTATGGATCAATTTGCAAAATAAG
AAAAATGCCAACCTTAGAAAAGACAATAAATGCACAAAAGATATAAACAGGAACAGCAAATATTTATTTTTTTC
CATTTTGTCTTTTTTAAATCTATGTTTAGAATTTATATCTTGGGACTTATGTATATATATACCTTTTAAATAAA
ATAAATTTTCTAAATAAAAAGTTG

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FIGURE 126

MVELFIFLFLLLGETPFKVVVKSLSPKELVRIHVPKPLDRNDGTFLMRYRMYETVDEGLKIEVL
YGDEHVAQSPYILKGPVYHEYCECPEDPQAWQKTLSCPTKEPQIAKDFASFPSINLQQMLKEV
PKRFGDERGAIVHYTILNNHVYRRSLGKYTDFKMFSDEILLSLTRKVLLPDLEFYVNLGDWPL
EHRKVNGTPSPIPIISWCGSLDSRDVVLPTYDITHSMLEAMRGVTNDLLSIQGNTGPSWINKT
ERAFFRGRDSREERLQLVQLSKENPQLLDAGITGYFFFQEKELGKAKLMGFFDFFKYKYQV
NVDGTVAAARYPYLMLGDSLVLKQDSPYYEHFYMALEPWKHYVPIKRNLSDLLEKVKWAKEND
EEAKKIAKEGQLMARDLLQPHRLYCYYYQVLQKYAERQSSKPEVRDGMELVPQPEDSTAICQC
HRKKPSREEL

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 250-254, 363-367

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 444-448

N-myristoylation site.

amino acids 208-214, 319-325, 388-394

Endoplasmic reticulum targeting sequence.

amino acids 448-453

Mitochondrial energy transfer proteins signature.

amino acids 25-34

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FIGURE 127

AGCCGTCGGAGGGAGCCGGAGCGCTTCTCCCGAGTTGGTGATAGATTGGTGGTCATCCAACAT
GCAGAAATGAATGAGCAGTGAAAAGCAGCAGAGCCGATGGGTCATGAGGATGTAAGTGCGTTT
GAAGGCTTCCACACCCTCTACTCCAGGAATCATGAATAAACTGGAGGATAAGCAGGACCAGAT
GATACCA**ATGA**AGAGAAGTTTACAGGCCCTCTATTGCCAACTGTTAAGTTTCCTGCTGATCTTG
GCACTGACCGAAGCGCTGGCATTGTCATCCAGGAACCATCTCCCAGGGAATCTCTTCAGGTC
CTCCCTTCAGGCACTCCCCCGGGAACCATGGTGACAGCACCCACAGCTCTACCAGACATACT
TCTGTGGTGATGCTGACCCCCAATCCCGATGGACCCCCCTCACAGGCTGCAGCTCCCATGGCA
ACACTGACACCCCGTGACAGAGGGGCACCCTCCTACGCACACCATCTCCACCATCGCTGCGACA
GTAACCGCCCCCTATTCTGAAAGCTCCCTGTCCACAGGGCCCGCTCCAGCAGCCATGGCAACC
ACATCCTCCAAGCCAGAGGGCCGCCCTCGAGGGCAGGCTGCCCCCACCATCCTGCTGACAAAG
CCACCGGGGGCCACCAGCCGCCCCACCACAGCGCCCCCCCCGCACTACCACACGCAGGCCCCC
AGGCCCCCAGGCTCTTCCCGAAAAGGGGCTGGTAATTATCATACGCCCTGTCCCGCCTGCACCT
GGTGGCCACTCCAGGAGTAAAGAAGGACAGCGAGGACGAAATCCAAGCTCCACACCTCTGGGG
CAGAAGCGGGCCCCCTGGGGAATCTTTAGATCTACAAGGGCAACTTCACAGGGTCTGTGGAA
CCAGAGCCCTCTACCCTCACCCCCAGGACCCCACTCTGGGGCTACTCCTCTTCACCACAGCCC
CAGACAGTGGCTGCGACCACAGTGCCCAGCAATACCTCATGGGCACCCACCACCACCTCCCTG
GGGCTGCAAAGGACAAGCCAGGCCTTCGCAGAGCAGCCAGGGGGGTGGTTCTACCTTCACC
AGCCAAGGAGGGACACCAGATGCCACAGCAGCCTCAGGTGCCCTGTGAGTCCACAAGCTGCC
CCAGTGCCTTCTCAGCGCCCCCACCACGGTGACCCACAGGATGGCCCCAGCCATAGTGACTCT
TGGCTTACTGTTACCCCTGGCACCAGCAGACCTCTGTCTACCAGCTCTGGGGTCTTCACGGCT
GCCACGGGGCCCCACCCAGCTGCCTTCGATACCAGTGTCTCAGCCCCCTCCCAGGGGATTCTT
CAGGGAGCATCCACAACCCCAAGCTCCAACCCATCCCTCCAGGGTCTCAGAAAGCACTATT
TCTGGAGCCAAGGAGGAGACTGTGGCCACCCTCACCATGACCGACCGGGTGCCAGTCTCTC
TCCACAGTGGTATCCACAGCCACAGGCAATTTCTCAACCGCTGGTCCCCGCCGGGACCTGG
AAGCCTGGGACAGCAGGGAACATCTCCCATGTGGCCGAGGGGGACAAACCGCAGCACAGAGCC
ACCATCTGCCTGAGCAAGATGGATATCGCCTGGGTGATCCTGGCCATCAGCGTGCCCATCTCC
TCCTGCTCTGTCCTGCTGACGGTGTGCTGCATGAAGAGGAAGAAGAAGACCGCCAACCCGGAG
AACAACCTGAGCTACTGGAACAACACCATCACCATGGACTACTTCAACAGGCATGCTGTGGAG
CTGCCCAGGGAGATCCAGTCCCTTGAAACCTCTGAGGACCAGCTCTCAGAGCCCCGCTCCCCA
GCCAATGGCGACTATAGAGACACTGGGATGGTCTTGTTAACCCTTCTGTCAAGAAACACTG
TTTGTGGGAAACGATCAAGTATCTGAGATCT**TAA**CTACAGCAGGCATCACTTTGCCATTCGGTA
TTTTTCGTCTCTAAATTATAAATATACAAATATATATTATAAATATAACCTTGTGTAACCC
TGACTTAATGAGAAACATTTTCAGCTTTTTTTCCTATGAATTGTCAACATCTTTTTTACAAGT
GTGGTTTAAAAAAAAAAAAAACTTTACAGAATGATCTGTGGCTTTATAAAATAAAGGTATTTCT
AAGCAAAAAAAAAAAAAAAAAA

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FIGURE 128

MKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESLQVLPSGTPPGTMVTAPHSSTRHTSV
VMLTPNPDGPPSQAAAPMATLTPRAEGHPPTHISTIAATVTAPYSESSLSTGPAPAAMATTS
SKPEGRPRGQAAPTILLTKPPGATS RPTTAPPRTTTTRRPPRPPGSSRKAGNSSRPVPPAPGG
HSRSKEGQRGRNPSSTPLGQKRPLGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQT
VAATTVPNTSWAPTTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDATAASGAPVSPQAAPV
PSQRPHHGDPQDGPSHSDSWLTVTPGTSRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPOG
ASTTPQAPTHPSRVSESTISGAKEETVATLTM TDRVPSPLSTVVSTATGNFLNRLVPAGTWKP
GTAGNISHVAEGDKPQHRATICLSKMDIAWVILAI SVPISSCSVLLTVCCMKRKKKTANPENN
LSYWNNTITMDYFNRHAVELPREIQSLETSEDQLSEPRSPANGDYRDTGMVLVNPFCQETLFV
GNDQVSEI

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 469-487

N-glycosylation sites.

amino acids 178-182, 223-227, 261-265, 446-450, 504-508, 509-513

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 495-499

N-myristoylation sites.amino acids 44-50, 48-54, 175-181, 222-228, 279-285, 286-292,
288-294, 296-302, 351-357, 374-380, 427-433, 442-448**TonB-dependent receptor proteins signature 1.**

amino acids 1-44

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FIGURE 129

AGGCGAGGCGCGGCGCCGCTGCACACACGCACACGGAGCT**ATG**GGGTGCCATGTTGCCACCAG
CTGCCACGTGGCCTGGCTTTTGGTGCTGATCTCTGGATGCTGGGGCCAGGTGAACCGGTGCC
CTTCTTCACCAACCACTTCTTTGATACATACTGCTGATCAGCGAGGACACGCCTGTGGGTTC
TTCTGTGACCCAGTTGCTGGCCCAAGACATGGACAATGACCCCTGGTGTTTGGCGTGTCTGG
GGAGGAGGCCTCTCGCTTCTTTGCAGTGGAGCCTGACACTGGCGTGGTGTGGCTCCGGCAGCC
ACTGGACAGAGAGACCAAGTCAGAGTTTACCGTGGAGTTCTCTGTCTCAGCGACCACCAGGGGGT
GATCACACGGAAGGTGAACATCCAGGTGCGGGATGTGAATGACAACGCGCCACATTTACAA
TCAGCCCTACAGCGTCCGCATCCCTGAGAATACACCAGTGGGGACGCCCATCTTCATCGTGAA
TGCCACAGACCCCGACTTGGGGGCAGGGGGCAGCGTCTCTACTCCTTCCAGCCCCCTCCCA
ATTCTTCGCCATTGACAGCGCCCGCGGTATCGTCACAGTGATCCGGGAGCTGGACTACGAGAC
CACACAGGCCTACCAGCTCACGGTCAACGCCACAGATCAAGACAAGACCAGGCCTCTGTCCAC
CCTGGCCAACTTGGCCATCATCATCACAGATGTCCAGGACATGGACCCCATCTTCATCAACCT
GCCTTACAGCACCAACATCTACGAGCATTCTCCTCCGGGCACGACGGTGGCATCATCACCGC
CATAGACCAGGATAAAGGACGTCCCCGGGGCATTGGCTACACCATCGTTTCAGGGAATACAA
CAGCATCTTTGCCCTGGACTACATCAGCGGAGTGCTGACCTTGAATGGCCTGCTGGACCGGGA
GAACCCCTGTACAGCCATGGCTTCATCTGACTGTGAAGGGCACGGAGCTGAACGATGACCG
CACCCCATCTGACGCTACAGTCACCACGACCTTCAATATCCTGGTTATTGACATCAATGACAA
TGCCCCGGAGTTCAACAGCTCCGAGTACAGCGTGGCCATCACTGAGCTGGCACAGGTGGGCTT
TGCCCTTCCACTCTTCATCCAGGTGGTGGACAAGGATGAGAATTGGGCCTGAACAGCATGTT
TGAGGTGTACTTGGTGGGGAACTCCACCACTTCATCATCTCCCCGACCTCCGTCCAGGG
GAAGGCGGACATTCGTATTTCGGGTGGCCATCCCCTGAGCTACGAGACCGTGGACCGCTACGA
CTTTGATCTCTTTGCCAATGAGAGTGTGCCTGACCATGTGGGCTATGCCAAGGTGAAGATCAC
TCTCATCAATGAAAATGACAACCGGCCCATCTTCAGCCAGCCACTGTACAACATCAGCCTGTA
CGAGAACGTCACCGTGGGGACCTCTGTGCTGACAGTCCTGGTGAGTCCCCGCTTCACTGCAGG
GCCACTGAGCTCTCCAGGGCCGACTGTGGTGAGGCACCCAGAGGGATTTTGTCCAAGGGACCT
CAGCAATCAGGGAAGGAGGCACCCCCAAATCCCTGAGCTGTGTTTGGTGTAT**TAA**ATAAA
GTTTTTGGACTCTTCAGGAAGGGGCTCCCTTGACCTAGGTTGCAATATGGAAAAGGAGCCAAC
CTGAGGGGTGACGAGACTGAGCTGAGGACACTGGTTTTCTGCCTTTCCTGAGAGAGACTCAG
TGAGGGTGGGCTGGGAGCCCTGGAAGCCCCCTCAAATGGGTGGGAAGGTGCCAGCCATCCTTG
AGAAGGGCAACCCTCTCCATGTGAGCACAGGCACCCAGAGAGGGGCAGGCGCCTGGAGGGTACC
GGGGCACCCCCAGCTGCCCATGGCTGGACTTGCCCTTTGACAAGGGGCCCTCCAGTGTCAAT
TGTATCTGTCACTACTCTTGGTTGCAAGGGACAGAAACCCTTAAGTAGTTCAAGCAAAAAGG
ATCCAACACCTTGAGAAAGCCGAGGTGGGCGGATCACTTGAGGTGGGAGTTTGAGACCAGCC
TGGCCAACATGGCAAAACCCCGTCTCTACTAAAAAATACAAAAATTAGCCGGGTGTGGTGGCAC
ACGCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCGG
AGGTTGCAGTGAGCCGAGATTGTGTCACTGCCCTCCAGCCTGGGCGACAGAGCCAGATTCTGT
CTC

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FIGURE 130

MGCHVATSCHVAWLLVLISGCWGQVNRLPFFTNHFFDTYLLISEDTPVGSSVTQLLAQDMDND
PLVFGVSGEEASRFFAVEPDTGVVWLRQPLDRETKSEFTVEFSVSDHQGVITRKVNIQVGDVN
DNAPTFHNQPYSVRIPENTPVGTPIFIVNATDPDLGAGGSVLYSFQPPSQFFAIDSARGIVTV
IRELDYETTQAYQLTVNATDQDKTRPLSTLANLAIITDVQDMDPIFINLPYSTNIYEHSPPG
TTVRIITAIDQDKGRPRGIGYTIVSGNTNSIFALDYISGVLTLNGLLDRENPLYSHGFILTVK
GTELNDDRTPSDATVTTTTENILVIDINDNAPEFNSSEYSVAITELAQVGFALPLFIQVVDKDE
NLGLNSMFEVYLVGNNSHHFIISPTSVQ GKADIRIRVAIPLDYETVDRYDFDLFANESVPDHV
GYAKVKITLINENDNRPIFSQPLYNISLYENVTVGTSVLTVLVSPRFTAGPLSSPGPTVVRHP
EGFCPRDLSNQRRHPQIPELCLLVY

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 355-374

N-glycosylation sites.amino acids 155-159, 206-210, 349-353, 393-397, 434-438, 466-470,
472-476**N-myristoylation sites.**

amino acids 2-8, 49-55, 162-168, 270-276, 278-284, 316-322

Amidation site.

amino acids 515-519

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

Leucine zipper pattern.

amino acids 298-320

PTS HPR component serine phosphorylation site signature.

amino acids 377-393

Cadherins extracellular repeated domain signature.

amino acids 120-131, 336-347

Cadherins extracellular

amino acids 120-144, 336-360

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FIGURE 131

GTGGGCCGCCCCTGCTGCTGCCGTCCATGCTGATGTTTGCGGTGATCGTGGCCTCCAGCGGGC
TGCTGCTCATGATCGAGCGGGGCATCCTGGCCGAGATGAAGCCCCTGCCCCTGCACCCGCCCCG
GCCGCGAGGGCACAGCCTGGCGCGGGAAAGCCCCAAGCCTGGGGGCCTGTCCCTCAGGGCTG
GGGACGCGGACTTGCAAGTGCGGCAGGACGTCCGGAACAGGACCCTGCGGGCGGTGTGCGGAC
AGCCAGGCATGCCCCGGGACCCCTGGGACTTGCCGGTGGGGCAGCGGCGCACCCCTGCTGCGCC
ACATCCTCGTAAGTGACCGTTACCGCTTCCTCTACTGCTACGTCCCCAAGGTGGCCTGCTCTA
ACTGGAAGCGGGTGATGAAGGTGCTGGCAGGCGTCCTGGACAGCGTGGACGTCCGCCTCAAGA
TGGACCACCGCAGTGACCTGGTGTTCCTGGCCGACCTGCGGCCTGAGGAGATTCGCTACCGCC
TGCAGCACTACTTTAAGTTCCTGTTTGTGCGGGAGCCCTTGGAACGCCTCCTCTGCTTACC
GCAACAAGTTTGGCGAGATCCGAGAGTACCAGCAACGCTATGGGGCTGAGATAGTGAGGCGGT
ACAGGGCTGGAGCGGGGCCAGCCCTGCAGGCGACGATGTCACATTCCCCGAGTTCCTGAGAT
ACCTGGTGGATGAGGACCCTGAGCGCATGAATGAGCATTGGATGCCCCTGTACCACCTGTGCC
AGCCTTGTGCCGTGCACTATGACTTTGTGGGCTCCTATGAGAGGCTGGAGGCTGATGCAAATC
AGGTGCTGGAGTGGGTACGGGCACCACCTCACGTCCGATTTCCAGCTCGCCAGGCCTGGTACC
GGCCAGCCAGCCCCGAAAGCCTGCATTACCACTTGTGCAGTGCCCCCGGGCCCTGCTGCAGG
ATGTGCTGCCTAAGTATATCCTGGACTTCTCCCTCTTTGCCTACCCACTGCCTAATGTCACCA
AGGAGGCGTGTGAGCAGTGAAGCCATGGGTGTGGGGCCAGCAGCTGGTGGGGACTGGTTTCAACG
CCAGCTTTCTGTGCTTCTGCCTGTCATTCCGAGAACTCTGGCTCTGGGGCTTGGGGCTTCTC
AGGATCCTGGATGGCAGAGACTGCCCTCAGAAGTTCCTTGTCAGGGTGGGCACCCACAGTGA
CTCAGAGGACAGGGCTAGGCAGGAGACCTGCTGCTCCTCATTTGGGGGGATCTCTTGGGGGGCA
GACACCAGTTTGCCAATGAAGCAACACATCTGATCTAAAGACTGGCTCCAGACCCCGGGCTGC
CAGGATTATGCAGTCCACTTGGTCTACCTTAATTTAACCTGTGGCCAAACTCAGAGATGGTAC
CAGCCAGGGGCAAGCATGACCAGAGCCAGGGACCCTGTGGCTCTGATCCCCCATTTATCCACC
CCATGTGCCTCAGGACTAGAGTGAGCAATCATACCTTATAAATGACTTTTGTGCCTTTCTGCT
CCAGTCTCAAATTTCCCTACACCTGCCAGTTCTTTACATTTTCCAAGGAAAGGAAAACGGAA
GCAGGGTTCTTGCTGGTAGCTCCAGGACCCAGCTCTGCAGGCACCCAAAGACCCTCTGTGCC
CAGCCTCTTCCTTGAGTTCTCGGAACCTCCTCCCTAATTCTCCCTTCCTTCCCCACAAGGCCT
TTGAGGTGTGACTGTGGCTGGTATATCTGGCTGCCATTTTCTGATGCATTTATTTAAAATT
TGTACTTTTTGATAGAACCCTTGTAAGGGCTTTGTTTTCTAATAGCTGACTTTTTAATAAAG
CAGTTTTATATAT

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FIGURE 132

MLMFAVIVASSGLLLMIERGILAEMKPLPLHPPGREGTAWRGKAPKPGGLSLRAGDADLQVRQ
DVRNRTLRAVCGQPGMPRDPWDLVPGQRRRTLLRHILVSDRYRFLYCYVPKVACSNWKRVMKVL
AGVLDSVDVRLKMDHRSDLVFLADLRPEEIYRLQHYFKFLFVREPLERLLSAYRNKFGEIRE
YQORYGAEIVRRYRAGAGPSPAGDDVTFPEFLRYLVDEDPERMNEHWMPVYHLCQPCAVHYDF
VGSYERLEADANQVLEWVRAPPHVRFPARQAWYRPASPESLHYHLC SAPRALLQDVL PKYILD
FSLFAYPLPNVTKEACQQ

Important features of the protein:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 67-71, 325-329

Tyrosine kinase phosphorylation sites.

amino acids 152-159, 183-183

N-myristoylation sites.

amino acids 89-95, 128-134

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FIGURE 133

CGGCAGTTCTGGCCCCTGCAGCTGGAGGTACCCTGAGTTCTGAGGGTCGTAGTGCTGTTTCTG
GTATTCTCATCGCGGTACCTCTACCGGTGTGGACAAGTAAAGTTTGAATCAGCTTCTCCATG
GCCTGGGCACCAGTTCCCGGCTGAGCCATTTTCCTTTTGGCTAAAAGTCCCCGCCAGAGGCC
AATTCGTCGCGGCGGCGGTGGAGATCGCAGGTCGCTCAGGCTTGCAGATGGGTCAAGGGTTGT
GGAGAGTGGTCAGAAACCAGCAGCTGCAACAAGAAGGCTACAGTGAGCAAGGCTACCTCACCA
GAGAGCAGAGCAGGAGAATGGATGCGAGCAACATTTCTAACACCAATCATCGTAAACAAGTCC
AAGGAGGCATTGACATATATCATCTTTTGAAGGCAAGGAAATCGAAAGAACAGGAAGGATTCA
TTAATTTGGAAATGTTGCCTCCTGAGCTAAGCTTTACCATCTTGTCCTACCTGAATGCAACTG
ACCTTTGCTTGGCTTCATGTGTTTGGCAGGACCTTGCGAATGATGAACTTCTCTGGCAAGGGT
TGTGCAAATCCACTTGGGGTCACTGTTCCATATACAATAAGAACCCACCTTTAGGATTTTCTT
TTAGAAAATTGTATATGCAGCTGGATGAAGGCAGCCTCACCTTTAATGCCAACCCAGATGAGG
GAGTGAACACTACTTTATGTCCAAGGGTATCCTGGATGATTCGCCAAAGGAAATAGCAAAGTTTA
TCTTCTGTACAAGAACTAAATTGGAAAAACTGAGAATCTATCTTGATGAAAGGAGAGATG
TCTTGGATGACCTTGTAACATTGCATAATTTTAGAAATCAGTTCTTGCCAAATGCACTGAGAG
AATTTTTTCGTCATATCCATGCCCCCTGAAGAGCGTGGAGAGTATCTTGAAACTCTTATAACAA
AGTTCTCACATAGATTCTGTGCTTGCAACCCTGATTTAATGCGAGAACTTGGCCTTAGTCCTG
ATGCTGTCTATGTACTGTGCTACTCTTTGATTCTACTTTCCATTGACCTCACTAGCCCTCATG
TGAAGAATAAAATGTCAAAAAGGGAATTTATTGAAATACCCGTCGCGCTGCTCAAAATATTA
GTGAAGATTTTGTAGGGCATCTTTATGACAATATCTACCTTATTGGCCATGTGGCTGCAATAAA
AAGCACAATTGCTAGGACTTCAGTTTTTACTTCAGACTAAAGCTACCCAAGGACTTAGCAGAT
ATGGGGGTTACATCAGTGCTGGTCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGCAAC
CTTTTTTCTTTTGCCATTTTCTATTTTAGTAATTTCTTGGGGAATAAATAATTTGCAGA
ATTTTTCTTAATTTGTTTATCACGTTTTGCACAAAGCAGAGCCACTGTCTAACACAGCTGTT
AACGAATGATAAACTGACATTATACTCTAAAAGATGGTGTATTTGTGCATTAGATTTGCCTGA
AAAACCTTATCCATTTCCATTCTTTATACAAATACCATGTAATGTGTACATATTTAACTAAAG
AGATTTATAGTCATAATTATTTTATTGTAAAGATTTTAACTAAAGTTTTCTTTCTCTC

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FIGURE 134

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRRMDASNISNTNHRKQVQGGIDIYHLLKARKSK
EQEGFINLEMLPPELSFTILSYLNATDLCLASCVWQDLANDELLWQGLCKSTWGHCSIYNKNP
PLGFSFRKLYMQLDEGSLTFNANPDEGVNYFMSKGILDDSPKEIAKFIFCTRTLWKKLRIYL
DERRDVLDLVTLHNFRNQFLPNALREFFRHIHAPEERGEYLETLITKFSHRFCACNPDLMRE
LGLSPDAVYVLCYSLILLSIDLTSPHVKNKMSKREFIRNTRRAAQNISEDFVGHLYDNIYLG
HVAA

Important features of the protein:**Transmembrane domain:**

amino acids 253-272

N-glycosylation sites.

amino acids 37-41, 87-91, 298-302

N-myristoylation site.

amino acids 110-116

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FIGURE 135

GGCACGAGGGAGCCTCCGTTAGGGGGTGGGAAAGGACTTTGCCATAGGTCGCTGAGGCCACCA
TCTGCTCTCTTACTGGCCAAGGGCGTAAAAAGATAGTCTTCCCATTAGCTAGAGAGCAAACCC
CAGAAAGCCTATTGGCTGCGCCGTCCGCGGGCCTTGGTCCGCTTTGAAGGCGGGCTGCGGCTG
CGAGAGGAGGGCGGGCGGGAGGCTAGCTGTTGTGCTGGTTGCTCGGAGGCACGTGTGCAGTCC
CGGAAGCGGCGAGGGGAAACTGCTCCGCGCGCGCCGCGGGAGGAGGAACCGCCCGGTCTTTTA
GGGTCCGGGGCCCGGCCGGGGCCATGGATTCAATGCCTGAGCCCGCGTCCCGCTGTCTTCTGCTT
CTTCCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCCGGCCCCGGAGCTGGGCCCCGAGCCAGGCC
GGAGCTGAGGAGAACGACTGGGTTTCGCCTGCCAGCAAATGCGAAGTGTGTAAATATGTTGCT
GTGGAGCTGAAGTCAGCCTTTGAGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGGCTAT
GGCATCCTGGACCAGAAGGCCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAA
GTCACTGAGACCATTTGCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGAGGACCGGCAGC
AATCGATTTGCCAAGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGG
GTCAAGGTGGTGTATGGACATCCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGAC
CTCAAGAAGCAGTGTGATGTGCTGGTGGAAGAGTTTGAGGAGGTGATCGAGGACTGGTACAGG
AACCACCAGGAGGAAGACCTGACTGAATTCCTCTGCGCCAACCACGTGCTGAAGGGAAAAGAC
ACCAAGTTGCCTGGCAGAGCAGTGGTCCGGCAAGAAGGGAGACACAGCTGCCCTGGGAGGGAAG
AAGTCCAAGAAGAAGAGCAGCAGGGCCAAGGCAGCAGGCGGCAGGAGTAGCAGCAGCAAACAA
AGGAAGGAGCTGGGTGGCCTTGAGGGAGACCCAGCCCCGAGGAGGATGAGGGCATCCAGAAG
GCATCCCCTCTCACACACAGCCCCCCTGATGAGCTCTTGAGCCCCACCCAGCATCCTCTGTCTCTG
AGACCCCTGATTTTGAAGCTGAGGAGTCAGGGGCATGGCTCTGGCAGGCCGGGATGGCCCCGC
AGCCTTCAGCCCCTCCTTGCCCTTGGCTGTGCCCTCTTCTGCCAAGGAAAGACACAAGCCCCAG
GAAGAACTCAGAGCCGTCATGGGTAGCCACGCCGTCCTTTCCCCTCCCCAAGTGTTTCTCTC
CTGACCCAGGGTTCAGGCAGGCCTTGTGGTTTCAGGACTGCAAGGACTCCAGTGTGAACTCAG
GAGGGGCAGGTGTCAGAACTGGGCACCAGGACTGGAGCCCCCTCCGGAGACCAAACCTACCAT
CCCTCAGTCCTCCCCAACAGGGTACTAGGACTGCAGCCCCCTGTAGCTCCTCTCTGCTTACCC
CTCCTGTGGACACCTTGCACTCTGCCTGGCCCTTCCCAGAGCCCAAAGAGTAAAAATGTTCTG
GTTCTGATTTCTGAAAAAAAAAAAAAAAAAAATTCCT

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FIGURE 136

MDSMPEPASRCLLLLPLLLLLLLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAF
EETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSNRFAGM
SETFETLHNLVHKGVKVMDIPYELWNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDL
TEFLCANHVLKGKDTSCLAEQWSGKKGDTAALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGL
EGDPSPEEDEGIQKASPLTHSPDEL

Important features of the protein:**Signal peptide:**

amino acids 1-26

N-glycosylation site.

amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 227-231, 228-232

Tyrosine kinase phosphorylation site.

amino acids 142-150

N-myristoylation sites.amino acids 36-42, 74-80, 86-92, 125-131, 222-228, 237-243,
250-256, 263-269**Amidation sites.**

amino acids 212-216, 222-226

ATP/GTP-binding site motif A (P-loop).

amino acids 62-70

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FIGURE 137

CACGCCTCCCGCTGCCAGCCCGGCACCGGGATCTTAATCAGTCACTATGAAAACCTCATTAGCT
CCACAGCAATGAGTCCTCCACTGCTGAAGCTTGGCGCTGTGCTTAGTACCATGGCAATGATCT
CAAACCTGGATGTCCCAAACCTCTCCCATCCTTGGTGGGACTGAACACCACGAGGCTGTGACTC
CGGATACCTTAACCTCAGATTAGTCCTAAAGAAGGGTGGCAGGTGTACAGCTCAGCTCAGGATC
CTGATGGGCGGTGCATTTGCACAGTTGTTGCTCCAGAACAAAACCTGTGTTCCCGGGATGCCA
AAAGCAGGCAACTTCGCCAACTACTGGAAGAGGTTTCAAGACATGTCCAGTCTATTGAAGTCT
TAAACTTGAGAACTCAGAGAGATTTCCAATATGTTTTAAAAATGGAACCCAAATGAAAGGGC
TGAAGGCCAAAATTTCCGGCAGATTGAAGATGATCGAAAGACACTTATGACCAAGCATTTCAGG
AGTTGAAAGAGAAAATGGACGAGCTCCTGCCTTTGATCCCCGTGCTGGAACAGTACAAAACAG
ATGCTAAGTTAATCACCCAGTTCAGGAGGAAATAAGGAATCTGTCTGCTGTCCTCACTGGTA
TTCAGGAGGAAATTGGTGCCTATGACTACGAGGAACACACCAAGAGTGCTGAGCTTGGA
CAAGACTTCGTGACTGCATGAAAAGCTAACATGTGGCAAACCTGATGAAAATCACAGGCCAG
TTACAGTCAAGACATCTGGAACCCGATTTGGTGTCTGGATGACAGACCTTTAGCATCTGAGA
AAAACAACAGAGTCTGGTACATGGACAGTTATACTAACAATAAAATTGTTTCGTGAATACAAAT
CAATTGCAGACTTTGTCTAGTGGGGCTGAATCAAGGACATACAACCTTCCTTTCAAGTGGGCAG
GAACTAACCATGTTGTCTACAATGGCTCACTCTATTTTAAACAAGTATCAGAGTAAATCATCA
TCAAATACAGCTTTGATATGGGGAGAGTGCTTGCCCAACGAAGCCTGGAGTATGCTGGTTTTTC
ATAATGTTTACCCCTACACATGGGGTGGATTCTCTGACATCGACCTAATGGCTGATGAAATCG
GGCTGTGGGCTGTGTATGCAACTAACCGAATGCAGGCAATATTGTCATCAGCCAACCTTAACC
AAGATACCTTGGAGGTGATGAAGAGCTGGAGCACTGGCTACCCCAAGAGAAGTGCAGGGGAAT
CTTTCATGATCTGTGGGACACTGTATGTCACCAACTCCCACTTAACTGGAGCCAAGGTGTATT
ATTCTATTCCACCAAAACCTCCACATATGAGTACACAGACATTCCTTCCATAACCAATACT
TTCACATATCCATGCTTGACTACAATGCAAGAGATCGAGCTCTCTATGCCTGGAACAATGGCC
ACCAGGTGCTGTTCAATGTCACCCTTTTCCATATCATCAAGACAGAGGATGACACATAGGCAA
ATGTGACATGTTTTTCAATTGATTTAAACAGTGTGATTTGTGATAAACTCTATAAGACCCCTTCC
GTTTTTTTCTTCACTATTATTTTTTTCATCATTCTCCAAAGCAAAGCATTTTTTATTGTAAAGTT
GGTGTTCAAAAACATAGCTGAGCTTGTCTAACTTACCATGTTGGAACACATCTTAACTTCT
AAATTTACAAGGCCTATCATGTCCTTGTGATGAAAAGCACTAAAAAAAAAAAAAGAGTTTAAAGT
GGCTAAAGTCATAGTTTTTGCAAGAGATTAATGATCTGCCTTATATTAGAGTCAGAGACTAATG
GTGGCTTAAATGCACGAATGTCTTTTTTTTTTAAACTGTCAATTTTTTTACTGTCTTTTGCTCCA
TCTCAGGAAATATTTTGGTAGGAATTAGGAGAACAAAAGCACTTTTATCCCATTTATTTCTT
TAAAAATGTAAGGATTTTCAATTTATATTGAAAAATAATATTAATCATTTTGTGTTAACACAA
TTCTCTGATGCGGTGCTGTACAGTCATTTTTTAAATCTCTTGCTAACATTTTATTGGCAGTATG
TATTTCTACCATTTGTAACCACCATTTGTGCTATTGTATCTCTTCACTTCTGTGAAAGTAATATT
TTTTATAAANACACTGNAATTTTAAAAAAAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAAA

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FIGURE 138

MSPPLLKLGAVLSTMAMISNWMSTLPSLVGLNTTRLSTPDTLTQISPKEGWQVYSSAQDPDG
RCICTVVAPEQNLCSDAKSRQLRQLLEKVQNMSQSIEVLNLRTQRDFQYVLKMETQMKGLKA
KFRQIEDDRKTLMTKHFQELKEKMDLPLIPVLEQYKTDAKLITQFKEEIRNLSAVLTG IQE
EIGAYDYEELHQRVLSLETRLRDCMKKLTGKLMKITGPVTVKTSGTRFGAWMTDPLASEKNN
RVWYMSYTNKIVREYKSIADFVSGAESRTYNLPFKWAGTNHVVYNGSLYFNKYQSNIIKY
SFDMGRVLAQRSLEYAGFHNVPYTWGGFSDIDLMADEIGLWAVYATNQAGNIVISQLNQDT
LEVMSWSTGYPKRSAGESFMICGTLYVTNSHLTGAKVYYSYSTKTSTYEYTDIPFHNQYFHI
SMLDYNARDRALYAWNNGHQVLFNVTLEFHIKTEDDT

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 33-37, 95-99, 179-183, 299-303, 465-469

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 215-219

Tyrosine kinase phosphorylation site.

amino acids 106-114

N-myristoylation sites.

amino acids 9-15, 31-37, 235-241, 239-245

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FIGURE 139

GAAGCAGTGCAGAGAGGAGAGCGGAGCGGAGCTGCCGCTGAGCAAAGGCCTTCACCA**ATG**GCCG
AGTCCCCCGGCTGCTGCTCCGTCTGGGCCCCTGCCTCCACTGCCTGTATAGCTGCCACTGGA
GGAAATGCCCCAGAGAGAGGATGCAAACCAGCAAGTGC GACTGTATCTGGTTTGGCCTGCTCT
TCCTCACCTTCCTCCTTTCCCTGAGCTGGCTGTACATCGGGCTCGTCCTTCTCAATGACCTGC
ACAACTTCAATGAATTCCTCTTCCGCCGCTGGGGACACTGGATGGACTGGTCCCTGGCATTCC
TGCTGGTCATCTCTACTGGTCACATATGCATCCTTGCTATTGGTCCTGGCCCTGCTCCTGC
GGCTTTGTAGACAGCCCCTGCATCTGCACAGCCTCCACAAGGTGCTGCTGCTCCTCATTATGC
TGCTTGTTGGCGGCTGGCCTTGTTGGGACTGGACATCCAATGGCAGCAGGAGTGGCATAGCTTGC
GTGTGTCAGTGCAGGCCACAGCCCCATTCTTCATATTGGAGCAGCCGCTGGAATTGCCCTCC
TGGCCTGGCCTGTGGCTGATACCTTCTACCGTATCCACCGAAGAGGTCCCAAGATTCTGCTAC
TGCTCCTATTTTTTGGAGTTGTCCTGGTCATCTACTTGGCCCCCTATGCATCTCCTCACCTT
GCATCATGGAACCCAGAGACTTACCACCCAAGCCTGGGCTGGTGGGACACCGAGGGGGCCCCA
TGCTGGCTCCCGAGAACACCCTGATGTCCTTGCGGAAGACAGCTGAATGCGGAGCTACTGTGT
TTGAGACTGATGTGATGGTCAGCTCCGATGGGGTCCCCTTCCTCATGCATGATGAGCACCTCA
GCAGGACCACGAATGTAGCCTCTGTATTCCCAACCCGAATCACAGCCCACAGCAGTGACTTCT
CCTGGACTGAACTGAAGAGACTCAATGCTGGATCCTGGTTCCCTAGAGAGGCGACCCTTCTGGG
GGGCCAAACCGCTGGCAGGCCCTGATCAGAAAGAGGCTGAGAGTCAGACGGTACCAGCATTAG
AAGAGCTATTGGAGGAAGCTGCAGCCCTCAACCTTTCCATCATGTTGACTTGCGCCGACCCC
CACAGAACCACACATACTATGACACTTTTGTGATCCAGACATTGGAGACTGTGCTGAATGCAA
GGGTGCCCCAAGCCATGGTCTTTTGGCTACCAGATGAAGATCGGGCTAATGTCCAACGACGGG
CACCTGGAATGCGCCAGATATATGGACGTCAGGGAGGCAACAGAACGGAGAGGGCCCCAGTTTC
TTAACCTCCCCTATCAAGATCTGCCACTATTGGATATCAAGGCATTGCATAAGGATAATGTCT
CGGTGAACCTATTTGTAGTGAACAAGCCCTGGCTCTTCTCTCTGCTTGGTGTGCAGGGGTGG
ATTCGGTCACCACCAACGACTGCCAGCTGCTGCAGCAGATGCGTTACCCTATCTGGCTTATTA
CCCCTCAAACCTACCTAATCATATGGGTCATTACCAATTGTGTTTCCACCATGCTGCTTTTGT
GGACCTTCCTCCTCCAAAGGAGATTTGTTAAGAAGAGAGGGGAAACTGGCTTAGAAACAGCAG
TGCTGCTGACAAGGATCAACAATTTTCATGATGGAG**TGA**ATGCCCTGCCCTGCTTCCCCACCCA
AGCCAGTCTACATTGCCCAAACAGCAAGGGTTGGAGAGTGGCTTAAGTGGAATGCTTCAGGGG
TGGTGGGTTGCAAGTGGGGGGAGCTTTGCCAACAGGAGGTTTTGAACCATGAGGGCCCTCTGC
CCAGGTGATGGGCATTCCCTAAGCTGCTATGGAATCTGCTCCCTTTGGGGTTTTGACCTGAGA
TGTTTGGGAAGAGAGTGAGTAATGAGAAGTTTCTCCTCAAATGAACTAGAACAGAGGAAGTA
AAAGGGAGATTGCTCGGA

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FIGURE 140

MAESPGCCSVWARCLHCLYSCHWRKCPRERMQTSKDCIWFGLLFLTFLLSLSWLYIGLVLLN
DLHNFNEFLFRRWGHWMDSLAFLLVISLLVTYASLLLVLALLLRRCRQPLHLHSLHKVLLLL
IMLLVAAGLVGLDIQWQQEWHSRLRVSLQATAPFLHIGAAAGIALAWPVADTFYRIHRRGPKI
LLLLLFFGVVLVIYLAPLCISSPCIMEPRDLPPKPGLVGHRGAPMLAPENTLMSLRKTAECGA
TVFETDVMVSSDGVFPLMHDEHLSRTTNVASVFPTRIAHSSDFSWEKRLNAGSWFLERRP
FWGAKPLAGPDQKEAESQTVPALEELLEEEAALNLSIMFDLRRPPQNHTYYDTFVIQTLETVL
NARVPQAMVFWLPDEDRAVQRRAPGMRQIYGRQGGNRTERPQFLNLPYQDLPLLDIKALHKD
NVSVNLFVVKPWLFSLWCAGVDSVTTNDCQLLQQMRYPIWLITPQTYLIIWVITNCVSTML
LLWTFLLQRRFVKRGKTGLETAVLLTRINNFMM

Important features of the protein:**Transmembrane domains:**

amino acids 38-60, 83-107, 122-138, 156-173, 189-210, 484-506

N-glycosylation sites.

amino acids 349-353, 362-366, 415-419, 442-446

N-myristoylation sites.

amino acids 163-169, 413-419, 523-529

Leucine zipper pattern.

amino acids 93-115, 109-131

Glutamine amidotransferases class-II active site.

amino acids 1-13

[illegible]

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FIGURE 142

MYLVAGDRGLAGCGHLLVSLGLLLLLLARSSTRALVCLPCDESKCEEPRNCPGSIVQGVCGCC
 YTCASQRNESCGETFGIYGTCDRGLRCVIRPPLNGDSLTEYEAGVCEDENWTDDQLLGFKPCN
 ENLIAGCNIINGKCECNTIRTCNPFEPFSQDMCLSALKRIEEKPDCKARCEVQFSRCPE
 DSVLIEGYAPPGECCPLPSRCVCNPAGCLRKVCQPGNLNLSKASGKPGECCLYECKPVFG
 VDCRTVECPVQQTACPPDSYETQVRLTADGCCTLPTRCECLSGLCGFPVCEVGSTPRIVSRG
 DGTGPKCCDVFECVNDTKPACVFNNVEYYDGMFRMDNCRFCRCQGGVAICFTAQCGEINCER
 YYVPEGECCPVCEDPVYPFNNPAGCYANGLILAHGDRWREDDCTFCQCVNGERHCVATVCGQT
 CTNPVKVPGEECPVCEEPTIITVDPPACGELSNTLTGKDCINGFKRDHNGCRTCQCINTEEL
 CSERKQGCTLNCPPFGFLTDAQNCEICECRPRPKCRPIICDKYCPLGLLKNKHGCDICRCKKC
 PELSCSKICPLGFQQDSHGCLICKCREASASAGPPILSGTCLTVDGHHHKNEESWHDGCRECY
 CLNGREMCALITCPVPACGNPTIHPGCCPSCADDFVQKPELSTPSICHAPGGEYFVEGETW
 NIDSCTQCTCHSGRVLCETEVCPPLLQNPSTQDSQCTDQPFPSLSRNNVSNYPNYCKND
 EGDIFLAAESWKPDVCTSCICIDSVISCFSESCPSVSCERPVLKRGQCCPYCIEDTIPKKVVC
 HFSGKAYADEERWDLDSCTHCYCLQGQTLCTVSCPPLPCVEPINVEGSCCPMCPEMYVPEPT
 NIPIEKTNRGERVDLEVPWPTPSENDIVHLPRDMGHLQVDYRDNRLLHPSSEDSSLDSIASVVV
 PIIICLSIIIAFLFINQKKQWIPLLCWYRTPTKPSLNNQLVSVDCCKGTRVQVDSSQRMRLRI
 AEPDARFSGFYSMQKQNLQADNFYQTV

Important features of the protein:**Signal peptide:**

amino acids 1-34

Transmembrane domain:

amino acids 940-962

N-glycosylation sites.

amino acids 71-75, 113-117, 330-334, 474-478, 746-750

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 992-996

N-myristoylation site.

amino acids 9-15, 58-64, 61-67, 75-81, 79-85, 362-368, 402-408, 407-413,
 439-445, 492-498, 511-517, 551-557, 558-564, 586-592, 606-612, 625-631,
 845-851

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 52-63, 844-855

Cell attachment sequence.

amino acids 314-317

Leucine zipper pattern.

amino acids 3-25

Eukaryotic thiol (cysteine) proteases cysteine active site.

amino acids 57-69

VWFC domain proteins.

amino acids 448-456, 382-390

C-terminal cystine knot proteins

amino acids 60-86

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FIGURE 143

GACGTCTGGCCGGCTCCCGGCGAAGGGCAGCGGAGGAGCGGCCAGAGCGCGCAGCTAGGGCA
CTGGCGAAACCCCGGGACAGTCCCTCTCCGTGCGGGGGCGGCGCAGAGCAGTCCCATCCCCG
GGTCCCGGGCGCGGCTGACTGCCGGCTGGTTCCCTGCGCGCAGTAGCTCCCCGAGCCGGGCTG
CACCGGAGGCGGCGAGATGGTGCGCGCGCTCGGCCTCCTGCTGCGCGCCCTGCAGCTGCTACT
GTGGGGCCACCTGGACGCCCAGCCCGCGGAGCGCGGAGGCCAGGAGCTGCGCAAGGAGGCGGA
GGCATTTCCTAGAGAAGTACGGATACCTCAATGAACAGGTCCCCAAAGCTCCCACCTCCACTCG
ATTACGCGATGCCATCAGAGCGTTTCAGTGGGTGTCCCAGCTACCTGTCAGCGGCGTGTGGA
CCGCGCCACCCTGCGCCAGATGACTCGTCCCCGCTGCGGGGTACAGATACCAACAGTTATGC
GGCCTGGGCTGAGAGGATCAGTGACTTGTTTGCTAGACACCGGACCAAAATGAGGCGTAAGAA
ACGCTTTGCAAAGCAAGGTAACAAATGGTACAAGCAGCACCTCTCCTACCGCCTGGTGAAGTG
GCCTGAGCATCTGCCGGAGCCGGCAGTTCGGGGCGCCGTGCGCGCCGCCTTCCAGTTGTGGAG
CAACGTCTCAGCGCTGGAGTTCTGGGAGGCCCCAGCCACAGGCCCGCTGACATCCGGCTCAC
CTTCTTCCAAGGGGACCACAACGATGGGCTGGGCAATGCCTTTGATGGCCCAGGGGGCGCCCT
GGCGCACGCCTTCCTGCCCCGCGCGGCGAAGCGCACTTCGACCAAGATGAGCGCTGGTCCCT
GAGCCGCCGCGCGGGCGCAACCTGTTTCGTGGTGCTGGCGCACGAGATCGGTACACGCTTGG
CCTCACCCACTCGCCCGCGCGCGCGCTCATGGCGCCCTACTACAAGAGGCTGGGCGCGA
CGCGCTGCTCAGCTGGGACGACGTGCTGGCCGTGCAGAGCCTGTATGGGAAGCCCCTAGGGGG
CTCAGTGGCCGTCCAGCTCCCAGGAAAGCTGTTCACTGACTTTGAGACCTGGGACTCCTACAG
CCCCAAGGAAGGCGCCCTGAAACGCAGGGCCCTAAATACTGCCACTCTTCCTTCGATGCCAT
CACTGTAGACAGGCAACAGCAACTGTACATTTTTAAAGGGAGCCATTTCTGGGAGGTGGCAGC
TGATGGCAACGTCTCAGAGCCCCGTCCACTGCAGGAAAGATGGGTCTGGGCTGCCCCCAACAT
TGAGGCTGCGGCAGTGTCATTGAATGATGGAGATTTCTACTTCTTCAAAGGGGGTTCGATGCTG
GAGGTCCGGGGCCCCAAGCCAGTGTGGGGTCTCCACAGCTGTGCCGGGCAGGGGGCCTGCC
CCGCCATCCTGACGCCGCCCTCTTCTTCCCTCCTCTGCGCCGCCTCATCCTCTTCAAAGGTGC
CCGCTACTACGTGCTGGCCCCAGGGGGACTGCAAGTGGAGCCCTACTACCCCCGAAGTCTGCA
GGACTGGGGAGGCATCCCTGAGGAGGTACGCGCGCCCTGCCGAGGCCCGATGGCTCCATCAT
CTTCTTCCGAGATGACCGCTACTGGCGCCTCGACCAGGCCAACTGCAGGCAACCACCTCGGG
CCGCTGGGCCACCGAGCTGCCCTGGATGGGCTGCTGGCATGCCAACTCGGGGAGCGCCCTGTT
CTGAAGGCACCTCCTCACCTCAGAACTGGTGGTGCTCTCAGGGCAAATCATGTTCCCCACC
CCCGGGGCAGAACCCTCTTAGAAGCCTCTGAGTCCCTCTGCAGAAGACCGGGCAGCAAAGCC
TCCATCTGGAAGTCTGTCTGCCTTTGTTCTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 144

MVARVGLLLRALQLLLWGHLDQAERGGQELRKEAEAFLEKYGYLNEQVPAKPTSTRFSDAI
RAFQWVSQLPVSGVLDRATLRQMTRPRCGVTDNTNSYAAWAERISDLFARHRTKMRRKKREFAKQ
GNKWKQHL SYRLVNWPEHLPEPAVRGAVRAAFQLWSNVSALEFWEAPATGPADIRLTFFQGD
HNDGLGNAFDGPGGALAHAFLLPRRGEAHFDQDERWSLSRRRGRNLFVFLAHEIGHTLGLTHSP
APRALMAPYYKRLGRDALLSWDDVLAVQSLYKPLGGSVAVQLPGKLFTDFETWDSYSPQGRR
PETQGPKYCHSSFDAITVDRQQQLYIFKGSHFWEVAADGNVSEPRPLQERWVGLPPNIEAAAV
SLNDGDFYFFKGGRCWRFRGPKPVWGLPQLCRAGGLPRHPDAALFFPPLRRLILFKGARYYVL
ARGGLQVEPYYPRLQDWGGIPEEVSGALPRPDGSIIFRDDRWRDLQAKLQATTSGRWATE
LPWMGCWHANSGSALF

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 355-359

N-myristoylation sites.amino acids 92-98, 153-159, 193-199, 202-208, 288-294, 368-374,
509-515**Amidation site.**

amino acids 312-316

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 237-247

Matrixins cysteine switch

amino acids 231-262, 271-284

Hemopexin domain protein

amino acids 66-108, 231-262

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FIGURE 145

GCCGGCTAGGGCGCCGGAGCCGCACGCAGCCGCGGGGCTCCGAGAGGCGCGCACTGGGGCTGGGACTGCGCGGCG
CCGCCGCTGCGAGCGCCACTGAGCGGTGCGCGCAACTTCGGAGGCACAGCGCCGGAGCCAGGCGAGCGCTCAGAGA
CCCGGAGCCAGAGGGGCGCGCCGGAGCCTCGTTCGAGAGCCGGCGCCAGGCACCCACCGCGCTCCGAGTGCCAGG
CGGCCCTCCGCGCAGCGTGGCTTCCGCTGCCCCACGGAAGGCACGGGCTGGCGCTGCCGGGCGCCGGGGAGGAC
GGCGAGGAGGAGGCGGCGGCGGCGGAGACGGCGGCGGCGAGACTGGGGCCAGGGAGACAGCCCTGGGGGAGAGGC
GCCCCAACCAGGCGCGGGAGC**ATG**GGGGCCCCGAGCGGAGCTCGGGGCGCGCTGCTGCTGGCACTGCTGCTCTG
CTGGGACCCGAGGCTGAGCCAAGCAGGCACTGATTCTGGCAGCGAGGTGCTCCCTGACTCCTTCCCGTCAGCGCC
AGCAGAGCCGCTGCCCTACTTCCCTGACGAGCCACAGGACGCCCTACATTGTGAAGAACAAGCCTGTGGAGCTCCG
CTGCCGCGCCTTCCCCGCCACACAGATCTACTTCAAGTGCAACGGCGAGTGGGTGAGCCAGAACGACCACGTAC
ACAGGAAGGCCTGGATGAGGCCACCGGCTGCGGGTGCAGGAGTGCAGATCGAGGTGTGCGGGCAGCAGGTGGA
GGAGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCCTGGCTGGAGCTCCGCGAGGCACCAAGAGTCGCGG
AGCCTAGCTCCGCATCGCCTACCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCA
TGAGGTTCTCCTGCAGTGCCGCCCGCGGAGGGGCTGCTGGCCGAGGTGGAATGGCTCAAGAAATGGATGT
CATCGACCCACCCAGGACACCAACTTCTGCTCACCATCGACCACAACCTCATCATCGCCAGGCCCCGCTGTC
GGACACTGCCAACTATACCTGCGTGGCCAAAGACATCGTGGCCAAACGCCGGAGCACCCTGCCACCGTCATCGT
CTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGGTCACCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAA
GCGCACCCGACCTGCACCAACCCCGCTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAGAC
CGCCTGCACCACCATCTGCCAGTCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTGAGTG
TGCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCACCCAGAAACGGAGGCCGTGACTGCAGCGGGACGCTGCT
CGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATAAGAAAATCTAAGCGACCCCAACAGCCACCTGCT
GGAGGCTCAGGGGATGCGGCGCTGTATGCGGGGCTCGTGGTGGCCATCTTCGTGGTCTGTGGCAATCCTCATGGC
GGTGGGGTGGTGGTGTACCGCCGCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGAC
TGGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGCAACCCGAGCTCCTACACCCCTCTGTGCCCTCC
TGACCTGACAGCCAGCGCGGCATCTACCGCGACCCGTGTATGCCCTGCAGGACTCCACCCAGCAAAATCCCCAT
GACCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCACGGGCTCTGG
GCCAGGCTGGCAGATGGGGCTGACCTGCTGGGGGCTTGGCGCCTGGCACATACCCTAGCGATTTGCCCGGGA
CACCCACTTCTGCACTGCGCAGCGCCAGCCTCGGTTCCAGCAGCTCTTGGGCTGCCCGAGACCCAGGGAG
CAGCGTCAGCGGCACCTTTGGCTGCCTGGGTGGGAGGCTCAGCATCCCCGCGCAGGGGTGAGCTTGCTGGTGCC
CAATGGAGCCATTCCCCAGGGCAAGTCTACGAGATGTATCTACTCATCAACAAGGCAGAAAGTACCCTCCGCT
TTCAGAAGGGACCCAGACAGTATTGAGCCCTCGGTGACCTGTGGACCCACAGGCTCCTGCTGTGCCGCCCGCT
CATCCTCACCATGCCCCACTGTGCCGAAGTCACTGCCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCACCA
GGGCCACTGGGAGGAGGTGGTGACCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGCCAG
GGCCTGTACATCCTGCTGGACCAGCTGGGCACCTACGTGTTACGGGCGAGTCCCTATTCCCGCTCAGCAGTCAA
GCGGCTCCAGCTGGCCGTCTTCGCCCCCGCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGTCTACTGCCTGGA
GGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAA
ACCGCTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGGGAGGAG
CAAGCTGCTGGCCAAATACCAGGAGATCCCCCTTCTATCACATTTGGAGTGGCAGCCAGAAGGCCCTCCACTGCAC
TTTACCCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCACCTGCAAGATCTGCGTGCGGCAAGTGGAAGGGGA
GGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCC
TGGCAGCACTGTACCAACCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATATGCAA
CAGCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGCTCTCTATGGACCGGTACCT
GAATTACTTTGCCACCAAGCGAGCCCCACGGGTGTGATCCTGGACCTCTGGGAAGCTCTGCAGCAGGACGATGG
GGACCTCAACAGCCTGGCGAGTGCCCTTGGAGGAGATGGGCAAGAGTGAGATGCTGGTGGCTGTGGCCACCGACGG
GGACTGCT**GA**GCCTCCTGGGACAGCGGGCTGGCAGGAGTGGCAGGAGGCAGGTGCAGGGAGGCCTGGGGCAGCC
TCCTGATGGGGATGTTTGGCCTCTGCTTCCCTCCAGTTCACAGCCAGAGTTCCTCTCCTCCTCTTCCCCAA
CCCCAGACCATGACCAGCCTTAGAAAATCCATGTAATCTGTTGTTAGAGGGCCAGAGTTCCTTCTCCACCCC
GCTCTCTCTCTTGGCCTGAGATCTCTGTGCAGGAACCAAGATGGGGCTGAAGCCTCTGGAGGCAGTTGGTTGG
GGGCGGGCAGGCAGGAGGCCCTCCCTCCACCCCCCACCCTCAGCCCGGCAACTTCTGGGTTCCGTGGGTTTAG
TTCCGTTCTCGTTTCTTCTTCCGTTATTGATTCTCCTTTCTCCCTAAGCCCCCTCTGCTTCCACGCCCTTT
TCCTCTTTGAAGAGTCAAGTACAATTACAGACAACTGCTTTCTCCTGTCCAAAAGCAAAAGGCAAGGAAAGAA
AGAAAGCTTCAGACCGCTAGTAAGGCTCAAAGAAGAGAAAAACACCAAAACCAAGGGAAAAAGAAAAACCCAG
TTTCTTAGGAAACGCAACGATTTATTATCCAGATTATTTGGATAAGTCCTTTTAAAA

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FIGURE 146

MGARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPDSFPSAPAEPLPYFLQEPQDAYIVKNK
 PVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLEATGLRVREVQIEVSROQVEELFGLEDY
 WCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPEGVPVAEVEWLK
 NEDVIDPTQDTNFLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTTATVIVYVNGGWSSW
 AEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTTICPVDGAWTEWSKWSACS
 TECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKKTLSDPNSHLLEASGDAALYA
 GLVVAIFVVAAILMAVGVVVYRRNCRDFDITDSSAALTGGFHPVNFKTARPSNPQLLHPSV
 PPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLPSLVKVYSSSTTGSGPGLADGADLLG
 VLPPGTYPSPDFARDTHFLHLSASLGSQQLLGLPRDPGSSVSGTFCGLGGRLSIPGTGVSLLV
 PNGAIPQKGKFYEMYLLINKAESTLPLSEGTQTVLSPSVTCGPTGLLLCRPVILTMPHCAEVSA
 RDWIFQLKTOAHQGHWEVVTLDEETLNTPCYQCQLEPRACHILLDQLGTYVFTGESYSRSAVK
 RLQLAVFAPALCTSLEYSRLVYCLEDTPVALKEVLELERTLGGYLVEEPKPLMFKDSYHNRL
 SLHDLPHAHWRSKLLAKYQEI PFYHIWSGSQKALHCTFTLERHSLASTEELTKICVRQVEGEG
 QIFQLHTTLAETPAGSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRM
 LAQKLSMDRYLNYFATKASPTGVILDLWEALQDDGDLNSLASALEEMGKSEMLVAVATDGDC

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 374-395

N-glycosylation sites.

amino acids 222-225, 347-350

Glycosaminoglycan attachment site.

amino acids 492-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 233-236, 234-237

Casein kinase II phosphorylation sites.

amino acids 30-33, 87-90, 251-254, 341-344, 359-362, 629-632, 651-654, 706-709, 757-760, 827-830, 925-928, 941-944

Tyrosine kinase phosphorylation sites.

amino acids 216-223, 773-780

N-myristoylation sites.

amino acids 2-7, 6-11, 27-32, 96-101, 137-142, 179-184, 247-252, 281-286, 334-339, 379-384, 491-496, 495-500, 509-514, 542-547, 547-552, 550-555, 553-558, 560-565, 611-616, 785-790, 834-839, 844-849

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 541-551

ATP/GTP-binding site motif A (P-loop).

amino acids 926-933

Growth factor and cytokines receptors family signature 2.

amino acids 306-312

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FIGURE 147

GAGAGGGACAGAGGCTGGAGAAGGATGTATGGCCTGCCCTGGGCTTGTCTGTTCCCTCCTGAGCCTGAGCCCCTT
ACCTTCCTGACCCCATGAAGCACACACTGGCTCTGCTGGCTCCCCTGCTGGGCCTGGGCCTGGGGCTGGCCCTGA
GTCAGCTGGCTGCAGGGGCCACAGACTGCAAGTTCCTTGGCCCCGAGAGCACCTGACATTCACCCCAGCAGCCA
GGGCCCCGGTGGCTGGCCCCCTCGAGTTCGTGCGCCAGGACTCCTGGACTCCCTCTATGGCACCGTGCGCCGCTTCC
TCTCGGTGGTGCAGCTCAATCCTTTCCCTTCAGAGTTGGTAAAGGCCCTACTGAATGAGCTGGCCTCCGTGAAGG
TGAATGAGGTGGTGGGTACGAGGCGGGCTACGTGGTATGCGCTGTGATCGCGGGCCTCTACCTGCTGCTGGTGC
CCACTGCCGGGCTTTGCTTCTGCTGCTGCCGCTGCCACCGCGCTGCGGGGACGAGTGAAGACAGAGCACAAGG
CGCTGGCCTGTGAGCGCGCGGCCCTCATGGTCTTCTGCTGCTGACCACCCTCTTGTGCTGATTGGTGTGGTCT
GTGCCCTTTGTACCAACCAGCGCACGCATGAACAGATGGCCCCAGCATCGAGGCCATGCCTGAGACCCTGCTCA
GCCTCTGGGGCCTGGTCTCTGATGTCCCCAAGAGCTGCAGGCCGTGGCACAGCAATTCTCCCTGCCCCAGGAGC
AAGTCTCAGAGGAGCTGGATGGTGTGGTGTGAGCATTTGGGAGCGGATCCACACTCAGCTCAGGAGCTCCGTGT
ACCCCTTGCTGGCGGCCGTGGGCAGTTTGGGCCAGGTCTGCAAGTCTCCGTGCACCACCTGCAAACTTTGAATG
CTACAGTGGTAGAGCTGCAGGCCGGGCAGCAGGAGATTGTGAGGGGCCCTGAGCTGGGCCCGCACCTTGAGCTGGGTG
AGCTGCTGAGGAGGCCAGGTGCCAGGGAGATTGTGAGGGGCCCTGAGCTGGGCCCGCACCTTGAGCTGGGTG
CTGACTTCAGCCAGGTGCCCTCTGTGGACCATGTCTGCACCAGCTAAAAGGTGTCCCCGAGGCCAACTTCTCCA
GCATGGTCCAGGAGGAGAACAGCACCTTCAACGCCCTTCCAGCCCTGGCTGCCATGCAGACATCCAGCGTGGTGC
AAGAGCTGAAGAAGGCAGTGGCCCCAGCAGCCGGAAGGGGTGAGGACACTGGCTGAAGGGTTCGCGGCTGGAGG
CAGCTTCCCCGCTGGGCCCAGGCACTGCAGGAGGTGGAGGAGAGCAGCCGCCCTACCTGCAGGAGGTGCAGAGAT
ACGAGACCTACAGGTGGATCGTGGGCTGCGTGTCTGCTCCGTGGTCTTATTCGTGGTGTCTGCAACCTGCTGG
GCCTCAATCTGGGCATCTGGGGCCTGTCTGCCAGGACGACCCCCAGCCACCCAGAAGCCAAGGGCGAGGCTGGAG
CCCCGCTTCTCATGGCAGGTGTGGGCCCTCAGCTTCTCTTTGCTGACCCCTCATCCTCCTGGTGTTCGCCACCT
TCCTGGTGGGTGGCAACGTGCAGACGCTGGTGTGCCGGAGCTGGGAGAACGGCGAGCTCTTTGAGTTTGACAGCA
CCCCAGGGAACCTGCCCCCGTCCATGAACCTGTGCAACTTCTTGGCCTGAGGAAGAATACAGCATCCACCAAG
CCTATCAGCAGTGCAAGGAAGGGGCAGCGCTCTGGACAGTCTGCACTACCTGAAAGGAGAGCTGCCTGCCTGGGCAGCCA
ACCTGGATATCAACAGTATACCAACAAGCTACGGCAGGAGTTGCAGAGCCTGAAAGTAGACACACAGAGCCTGG
ACCTGCTGAGCTCAGCCGCGCGCGGGACCTGGAGGCCCTGCAGAGCAGTGGGCTTCAGCGCATCCACTACCCCG
ACTTCTCGTTTCAGATCCAGAGGCCCGTGGTGAAGACCAGCATGGAGCAGCTGGCCCCAGGAGCTGCAAGGACTGG
CCCAGGCCCAAGACAATTCTGTGCTGGGGCAGCGGCTGCAGGAGGAGGCCCAAGGACTCAGAAACCTTCACCAGG
AGAAGGTCTCCCCCAGCAGAGCCTTGTGGCAAAGCTCAACCTCAGCGTCAGGGCCCTGGAGTCTCTGCCCGGA
ATCTCCAGCTGGAGACCTCAGATGTCTAGCCAATGTCACTACCTGAAAGGAGAGCTGCCTGCCTGGGCAGCCA
GGATCCTGAGGAATGTGAGTGAGTGTTCCTGGCCCCGGGAGATGGGCTACTTCTCCAGTACGTGGCCTGGGTGA
GAGAGGAGGTGACTCAGCGCATTTGCCACCTGCCAGCCCCCTCTCCGGAGCCCTGGACAACAGCCGTGTGATCCTGT
GTGACATGATGGCTGACCCCTGGAATGCCTTCTGTTCTGCTGGCATGGTGCACCTTCTTCTGATCCCCAGCA
TCATCTTTGCGCTCAAGACCTCCAATACTTCCGTCTATCCGGAAACGCCTCAGCTCCACCAGCTCTGAGGAGA
CTCAGCTCTTCCACATCCCCCGGGTTACCTCCCTGAAGCTGTTAGGGCCTTGTGGGGTGAGGTGACCTGAGGCTG
CCTGTCTCTCCCTTTGATTTAGCCTGGGCCACAGGACTTCGGTAGCTCTTGCCCCAGAGCCCAGGCTGGCATCCA
GGCCTGGACTGTCCCCAGTTCCGGCTTACCTGGCCCCACCTTGCCTGCTCCTTTCCACCCCTTTCTGCTCACGAC
CCCCATCATTACGCTCAGAATCACATGGGACTTCTGTGAGCTGCAGAGCCAGCAAGTCCCTACAGGTGTCAAC
CGTTACCCCCATGCTGGTGGCATCCTCACAGGAAGAGCCTGTTCTCCACCTGCTGGAGCCTGGACCCTGGGGTGG
GACAGAGGCCTCGTCCAACCCCACTCCCTTCCCGTGTGTCTTCCCCCTGCCAAGCCTCCCCCTGCCAAGCCTCC
CCCTGCCCCCTCTCTGAGCCCCCTCGCCCCCACACCGTCTCATCTGGCCTCCCCCTGGCCCCCACTTCCCTCTT
ATGCCCTTCTTGGCCCTTTGCTTCTCTTGTAGTCCCTTGTCCCTCTTACCATATCTCCACTGCTACCTTGTGGCCCCA
GAGACACCCCTGCCCAACCAACCACTCAGGTAACGCCACTAATCAGGCAGGGGCCACCATGGCCTAGGTCTGGG
CTGGCTGCAGGCCCTGCCTCATGGCCTCTGAGCCCTCACTGCCCCAGGGCCTTGGGCCCTCTGCAGATCTCATC
CAGGATTTATTGTTGTCCAGTGGGGTGAGGGAGGCTGTCTGAAGGCCGAGCCTCCCTGCCTGCACCCAAGTTAG
AAATGGGGGTACCAGCACTTAGCTTCTCTGTGAGTGTGGCTQCCAAGGAAGGGACCTGGGACCTGGGCCACAGT
GGGGGCTTGCCCTTACCTCTTCAAGGAAGCATCTTCCACAGCCCCACCAACTTCTTAGGAGTGATCTGGT
GGCCAGAACAGGATTTTGCACGGCCCCCTTTTATCTGCGCATGTGGCCTAGGGTCATCCCCAGCCCATCCCTGTG
TCAGCCCTGAGTGTCTGGACACTGCGTTCCAGAAATGAGGAAGAGGAGAGAGAAGAGATGGACAGACCTCAGATCC
ATTAAAGTGTTCTCACTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 148

MKHTLALLAPLLGLGLGLALSQLAAGATDCKFLGPAEHLTFTPAARARWLAPRVRAPGLL
 DSLYGTVRRFLSVVQLNPFPSSELVKALLNELASVKVNEVVRYEAGYVVCVAVIAGLYLLL
 PTAGLCFCCCRCHRRRCGRVKTEHKALACERAALMVFLLLTLLLLIGVVCAVVTNQRTH
 EQMGPSIEAMPETLLSLWGLVSDVPQELQAVAQQFSLPQEQVSEELDGVGVSIGSAIHTQ
 LRSSVYPLLAAGVSLGQVLQVSVHHLQTLNATVVELQAGQQDLEPAIREHRDRLELLQE
 ARCQGDCAAGALSWARTLELGADFSQVPSVDHVLHQLKGVPEANFSSMVQEENSTFNALPA
 LAAMQTSSSVQELKKAVAQQPEGVRTLAEGFPGLEAASRWAQALQVEESSRPLYQEVQR
 YETRWIVGCVLCSVVLFFVLCNLLGLNLGIWGLSARDDPSHPEAKGEAGARTLMAGVGL
 SFLFAAPLILLVFATFLVGGNVQTLVCRSWENGELFEFADTPGNLPPSMNLSQLLGLRKN
 ISIHQAYQQCKEGAALWTVLQLNDSYDLEEHLDINQYTNKLRQELQSLKVDTSQSLDLLSS
 AARRDLEALQSSGLQRIHYPDFLVQIQRPVVKTSMEQLAQELQGLAQADNSVLGQRLQE
 EAQGLRNLHQEKVVPQQSLVAKLNLVRALESSAPNLQLETSDVLANVTYLGELPAWAA
 RILRNVSECFLAREMGYFSQYVAWVREEVTQRIATCQPLSGALDNSRVILCDMMADPWNA
 FWFCLAWCTFFLIPSIIFAVKTSKYFRPIRKRLSSTSSEETQLFHIPRVTSCLK

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 105-125, 153-173, 428-449, 476-500, 778-797

N-glycosylation sites:amino acids 270-273, 343-347, 352-356, 530-534, 540-546, 563-567,
684-688, 707-711, 725-729**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 811-815

Tyrosine kinase phosphorylation site.

amino acids 95-103

N-myristoylation sites.amino acids 13-19, 15-21, 17-23, 26-32, 58-64, 124-130, 168-174,
228-234, 230-236, 320-326, 338-344, 393-399, 429-435, 446-452,
477-483, 500-506, 536-542, 644-650, 761-767**Phospholipase A2 histidine active site.**

amino acids 129-137

4Fe-4S ferredoxins, iron-sulfur binding region signature.

amino acids 126-138

Mitochondrial energy transfer proteins signature.

amino acids 80-89

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FIGURE 149

CACAGCTCCCTTCCCAGGACGTGAAAATCTGCCTTCTCACCATGAGGCTTCTAGTCCTTTCCA
GCCTGCTCTGTATCCTGCTTCTCTGCTTCTCCATCTTCTCCACAGAAGGGAAGAGGCGTCCTG
CCAAGGCCTGGTCAGGCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAA
CAAACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGAGCCAGAGCCCCGCC
TTTGGGTGGTGCCTGGGGCACTCCCACAGGTGTAGCACTCCCAAAGCAAGACTCCAGACAGCG
GAGAACCTCATGCCTGGCACCTGAGGTACCCAGCAGCCTCCTGTCTCCCCTTTCAGCCTTCAC
AGCAGTGAGCTGCAATGTTGGAGGGCTTCATCTCGGGCTGCAAGGACCCTGGGAAAGTTCCAG
AACTCCACGTCCTTGTCTCAATTGTGCCATCAACTTTCAGAGCTATCATGAGCCAACCTCACC
CCACAGGGCCTCAGTCGCCACCATGTGGGCCTCTCCAGTGCAAACCACCGAGCATTCCACCAT
GACCGGTCACAGCTACAAATCCAGAGACCATCAATCCTGCTAGAGTGCAGGGTGGCAAGCACC
CAAGGGTGGCTGACCAAGACTGCAGAGTCTCCTCCATCTTCAGGTCCATTAGCCTCCTGGCA
TTTAACTACCAGCATCCAGTGGTCCCCAAGGAATCCCTTCCTAGCCTCCTGACATGAGTCTGC
TGGAAAGAGCATCCAAACAAACAAGTAATAAATAAATAAATAAACTCA

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FIGURE 150

MRLLVLSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNSTNLKGHHVRLCKPC
KLEPEPRLWVVP GALPQV

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 48-52

Amidation sites.

amino acids 23-27, 33-37

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FIGURE 151

CACCGGAGGGCACGCAGCTGACGGAGCTGCGCTGCGTTGCGCTCGTTTGCCTCGCGCCCTCCA
CTGGAGCTGTTTCGCGCCTCCCGGCTCCCACCGCAGCCCACCGGCAGAGGAGTCGCTACCAGC
GCCCAGTGCGCTCTGTCAAGTCCGCAAACCTCCTTGCCGCCCCGCCCCGGGCTGGGCACCAAATAC
CAGGCTACCA**ATGGT**CTACAAGACTCTCTTCGCTCTTTGCATCTTAAGTGCAGGATGGAGGGTA
CAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCACCGACC
ACCATCTGGACTAGCTCTCCACAAACACTGATGCAGACACTGCCTCCCCATCCAACGGCACT
CACAACAACCTCGGTGCTCCCAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAAGAACATT
TCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCCAGGTTTGAATTGGGAAGGCACAAACACA
GACCCCTCACCTTCTGGGTCTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACCACGTTGGAG
GAACACAGCTCGGGCACTCCTGAAGCAGGCGTGGCAGCTACACTGTCGCAGTCCGCTGCTGAG
CCTCCACACTCATCTCCCCCAAGCTCCAGCCTCATCACCTCATCCCTATCAACCTCACCA
CCTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACCAGCACCCAACCC
ACTGGAGCTCCAACCTGCACCAGAGTCCCCGACAGAGGAGTCCAGCTCTGACCAGCACACCCACT
TCACATGCCACAGCTGAGCCAGTGCCCCAGGAGAAAACACCCCCAACAACTGTGTGAGGCAAA
GTGATGTGTGAGCTCATAGACATGGAGACCACCACCTTTCCAGGGTGATCATGCAGGAA
GTAGAACATGCATTAAGTTCAGGCAGCATCGCCGCCATTACCGTGACAGTCATTGCCGTGGTG
CTGCTGGTGTGGAGTTGCAGCCTACCTAAAAATCAGGCATTCTCCTATGGAAGACTTTTG
GACGACCATGACTACGGGTCTGGGGAACTACAACAACCTCTGTACGATGACTCC**TAACA**A
TGGAATATGGCCTGGGATGAGGATTAAGTCTTTATTTATAAGTGCTTATCCAGTAGAATT
AATAAGTACCTGATGCGCATTTGAACGACAATCTTAAGCCCTGTTTTGTTGGTATGGTTGTTTT
TGTTTTCTCTCCCTCTCCTCTGGCTGCTACAACCTCCCTTTCTGGTACAAGAAGAACCATTCT
TTAAAGGTGAGTGGAGGCTGATTTGCAGCTGAAGTGGGCCAGCCTTGACCAGCCAGGCCAGA
CCACCATGGTGAAGGCTTCTTTCCCCACTGCAGGACCCACTTTGAGAAGGATCGAGGAGGAGG
ATTTGGGTTGTTTTGTTAGGGGTTACTTTAGGGGAACATTTCAATTTGTGTTATTTCTTAAAC
TTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGAAAGGAAATGAGCTCTACGAGGATTT
CACCTTGATGGGAGAGAGCAGGGTTTTCTCAGATTCTTTTAAATCTCTATTTATCTGGTTG
TTTCTGACAGGATGCTGCCTGCTTGGCTCTACGAGCTGGAAAGCAGCTTCTTAGCTGCCTAAT
TAATGAAAGATGAAAATAGGAAGTGCCCTGGAGGGGGCCAGCAGGTACGGGGCAGAATCTCT
CAGGTTGCTGTGGGATCTCAGTGTGCCCCTACCTGTTCTCTCCCTCCAGGCCACCTGTCTCTGT
AAAGGATGTCTGCTCTGTTCAAAAGGCAGCTGGGATCCCAGCCCACAAGTGATCAGCAGAGTT
GCATTTCCAAAGAAAAAGGCTATGAGATGAGCTGAGTTATAGAGAGAAAGGGAGAGGCATGTA
CGGTGTGGGGAAGTGGAAGAGAAGCTGGCGGGGGAGAAGGAGGCTAACCTGCACTGAGTACTT
CATTAGGACAAGTGAGAATCAGCTATTGATAATGGCCAGAGATATCCACAGCTTGGAGGAGCC
CAGAGACTGTTTGCTTTATACCCACACAGCAACTGGTCCACTGCTTTACTGTCTGTTGGATAA
TGGCTGTAAATGTTTAAAAAC

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FIGURE 152

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHNN
SVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEEHS
SGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSLSTSPPEVFSASVTTNHSSTVTSTQPTGA
PTAPESPTEESSSDHTPTSHATAEPVPQEKTPPTTVSGKVMCELIDMETTTTFPRVIMQVEH
ALSSGSIAAITVTVIAVLLVFGVAAYLKIRHSSYGRLLDDHDYGSWGNYNPNPLYDDS

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 258-278

N-glycosylation sites.

amino acids 58-61, 62-65, 80-83, 176-179

Casein kinase II phosphorylation sites.

amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-144, 164-167, 191-194, 195-198, 200-203

Tyrosine kinase phosphorylation site.

amino acids 289-296

N-myristoylation sites.

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

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FIGURE 153

[illegible]

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FIGURE 154

MLVHCVGLLLTGALLGLTLGAGALLASEPIYQPPSAWVPAGGLVGLALLGALLTLRWPRPFTV
LGTTLGSAVLVACVDYFLEGLALGSWLGQRLQTLPALPSLC

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 38-55, 60-78

N-myristoylation sites.

amino acids 7-13, 12-18, 16-22, 22-28, 41-47, 50-56, 84-90, 88-94

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 67-78

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FIGURE 155

TGCAATTAAAGGAGTCGGGTCTCTAACTGTTGATCTGTTTTTTTCCCTTCTGAGCAATGGAGC
TTACCATCTTTATCCTGAGACTGGCCATTTACATCCTGACATTTCCCTTGTACCTGCTGAACT
TTCTGGGCTTGTGGAGCTGGATATGCAAAAAATGGTTCCCCTACTTCTTGGTGAGGTTCACTG
TGATATACAACGAACAGATGGCAAGCAAGAAGCGGGAGCTCTTCAGTAACCTGCAGGAGTTTG
CGGGCCCCCTCCGGGAAACTCTCCCTGCTGGAAGTGGGCTGTGGCACGGGGGCCAACTTCAAGT
TCTACCCACCTGGGTGCAGGGTGACCTGTATTGACCCCAACCCCAACTTTGAGAAGTTTTTGA
TCAAGAGCATTGCAGAGAACCGACACCTGCAGTTTGAGCGCTTTGTGGTAGCTGCCGGGGAGA
ACATGCACCAGGTGGCTGATGGCTCTGTGGATGTGGTGGTCTGCACCCTGGTGCTGTGCTCTG
TGAAGAACCAGGAGCGGATTCTCCGCGAGGTGTGCAGAGTGCTGAGACCGGGAGGGGCTTTCT
ATTTTCATGGAGCATGTGGCAGCTGAGTGTTCGACTTGGAATTACTTCTGGCAACAAGTCCTGG
ATCCTGCCTGGCACCTTCTGTTTGATGGGTGCAACCTGACCAGAGAGAGCTGGAAGGCCCTGG
AGCGGGCCAGCTTCTCTAAGCTGAAGCTGCAGCACATCCAGGCCCCACTGTCCTGGGAGTTGG
TGCGCCCTCATATCTATGGATATGCTGTGAAATAGTGTGAGCTGGCAGTTAAGAGCTGAATGG
CTCAAAGAATTTAAAGCTTCAGTTTTACATTTAAATGCTAAGTGGGAGAAGAGAAACCTTTT
TTTTGGGGGGCGGTTTTTTTTGGTTTTGTGTTGGTTTTTTTTTTTTTTTTTTTGGCAGGAGAATCTC
TTGAACCCAGAAGGCGAAGGTTGCAGTGAACCGAGATCATGCCATTGTACTCTAGCCTGGGTG
ACAAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAGAAGTAGAGACAGGGAGAC
GGGGTCTCACTGTGTTGCCTAGGCCGGTCTTGAACCTCCTGGGCTCAAGTGATTCTCCACCTT
GACCTCCTAAATTGTTGGGATTACAGGTGTGAGACAGTGCACCTGGCCGAAATAGCTCAAGTT
TCTGAAAAACAAATCTGAATCTATTTGTTATTCTTAGCGTCACTGGTCTGGCTTTCAGAATTA
ACATACAAGGTTGCCACACCTAGTTCTGCCCAGCTTTATGTCTTTTATTCCAGTATTCCACCA
AAGTTTGTTCCTGCATTCCAGTTCTCAAGTCTTAAGATAAAGATTGTAAGTGTGACAGTTTAG
TATATCCATAAACTATTTGAGGTGGTTAAGGTTCTTGGGTTCAATTTTCTTAATACTTTGCT
GAATATTGTAGATTGTAGGCAATGAAAAAGTCTACTAAATTAGGAAAACCTTGAATAATTAGG
TATCCTAGGTAAGAGCCCCCTAAACATCAAGCAATCTGTGAGTCTGTAAAGAAATAAATATTTT
TTGGATTATTCTTATCTAATTCCACCCCTGTTGGAAGATGATTTCTTTGTTCTTTGCAACTAT
GGAAGCTGTGAAAATCATCACAAGTGCCTCTGAAAGCGAGTGTAGGTTGGTTAGAGGGTTTA
ATATTTTCTGCAATGGTTTGTAGGAATTTTAATAAATGTAGTATATTTTCTGAGATGATTTTG
TAAAAGTACTATTTTAAATATCAAATCAACCAATAAATTCACATTTGTGTTAGGAACAAAA

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FIGURE 156

MELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRFTVIYNEQMASKKRELFNLQ
EFAGPSGKLSLLEVGCCTGANFKFYPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAA
GENMHQVADGSVDVVVCTLVLCVKNQERILREVCRLRPGGAFYFMEHVAAECSTWNYFWQQ
VLDPAWHLLFDGCNLTRESWKALERASFSLKLQHIQAPLSWELVRPHIYGYAVK

Signal peptide:

amino acids 1-29

N-glycosylation site.

amino acids 203-207

N-myristoylation sites.

amino acids 78-84, 80-86, 91-97, 201-207

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FIGURE 157

CCGCTGAGATGTACGAACTTCCGGTTCTCCGGGCAGCTGCCACTGCTGTAGCTTCTGCCACCT
GCCACGACCGGGCCTCTCCCTGGCGTTTGGTCACCTCTGCTTCATTCTCCACCGCGCCTATGG
TCCCTCTTGAGCCAGCGTGGCGGGCCTGGCGGCTCCCGGGTGGTGAGAGAGCGGTCCGGGAA
CGATGAAGGCCTCGCAGTGCTGCTGTCTCAGCCACCTCTTGGCTTCCGTCCTCCTCCTGC
TGTTGCTGCCTGAACTAAGCGGGCCCCCTGGCAGTCCTGCTGCAGGCAGCCGAGGCCGCGCCAG
GTCTTGGGCCTCCTGACCCTAGACCACGGACATTACCGCCGCTGCCACCGGGCCCTACCCCTG
CCCAGCAGCCGGGCGGTGGTCTGGCTGAAGCTGCGGGGCCGCGGGGCTCCGAGGGAGGCAATG
GCAGCAACCCTGTGGCCGGGCTTGAGACGGACGATCACGGAGGGAAGGCCGGGGAAGGCTCGG
TGGGTGGCGGCCTTGCTGTGAGCCCCAACCTGGCGACAAGCCCATGACCCAGCGGGCCCTGA
CCGTGTTGATGGTGGTGAGCGGCGCGGTGCTGGTGTACTTCGTGGTCAGGACGGTCAGGATGA
GAAGAAGAAACCGAAAGACTAGGAGATATGGAGTTTTGGACACTAACATAGAAAATATGGAAT
TGACACCTTTAGAACAGGATGATGAGGATGATGACAACACGTTGTTTGATGCCAATCATCCTC
GAAGATTAAGAATGTGCCTTTTGATGAAAGAACTTTATCTTTCTACAATGAAGAGTGGAATTC
TATGTTTAAGGAATAAGAAGCCACTATATCAATGTTGGGGGGGTATTTAAGTTACATATATTT
TAACAACCTTTAATTTGCTGTTGCAATAAATACCGTATCCTTTTATTATATCTTTATATGTAT
AGAAGTACTCTATTAATGGGCTCAGAGATGTTGGGGATAAAGTATACTGTAATAATTTATCTG
TTTGAAAATTACTATAAAACGGTGTTTTCTGGTCGGTTTTTGTTCCTGCTTACCATATGATT
GTAAATTGTTTTATGTATTAATCAGTTAATGCTAATTATTTTGCTGATGTCATATGTTAAAG
AGCTATAAATTCCAACAACCAACTGGTGTGTAAAAATAATTTAAATTTCCCTTTACTGAAAGG
TATTTCCCATTTTTGTGGGGAAAAGAAGCCAAATTTATTACTTTGTGTTGGGGTTTTTAAAT
ATTAAGAAATGTCTAAGTTATTGTTTGCAAAACAATAAATATGATTTTAAATTCTCTTAAAA
AAAAA

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FIGURE 158

MKASQCCCCLSHLLASVLLLLLLPELSGPLAVLLQAAEAAPGLGPPDPRPRTLPLPPGPTPA
QQPGRGLAEAAGPRGSEGGNGSNPVAGLETDDHGGKAGEGSVGGGLAVSPNPGDKPMTQRALT
VLMVVSGAVLVYFVVVRTVRMRRNRKTRRYGVLDNIENMELTPLEQDDEDDNTLFDANHPRR

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 124-140

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 69-75, 78-84, 81-87, 97-103, 103-109, 106-112,
157-160

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FIGURE 159

GCTGCAGGCGGGCGACGGCTACACCA**ATG**GGCCGGCTGCTGCGGGCCGCCGGCTGCCGCCGCTG
CTTTTCGCCGCTGCTGCTTCTGCTGGTTGGGGGAGCGTTCCTGGGTGCCTGTGTGGCTGGGTCT
GATGAGCCTGGCCCAGAGGGCCTCACCTCCACCTCCCTGCTAGACCTCCTGCTGCCACTGGC
TTGGAGCCACTGGACTCAGAGGAGCCTAGTGAGACCATGGGCCTGGGAGCTGGGCTGGGAGCC
TCTGGCTCAGGCTTCCCCAGCGAAGAGAATGAAGAGTCTCGGATTCTGCAGCCACCACAGTAC
TTCTGGGAAGAGGAGGAAGAGCTGAATGACTCAAGTCTGGACCTGGGACCCACTGCAGATTAT
GTTTTTCTGACTTAACTGAGAAGGCAGGTTCATTGAAGACACTAGCCAGGCTCAAGAGCTG
CCAAACCTCCCCTCTCCCTTGCCCAAGATGAATCTGGTTGAGCCTCCCTGGCATATGCCTCCC
AGAGAGGAGGAAGAAGAGGAAGAGGAAGAGGAGGAGAGGGAGAAGGAAGAGGTAGAGAAACAA
GAGGAGGAGGAAGAGGAGGAGCTGCTCCCTGTGAATGGATCCCAAGAAGAAGCCAAGCCTCAG
GTCCGTGACTTTTCTCTCACCAGCAGCAGCCAGACCCAGGGGCCACCAAAAGCAGGCATGAA
GACTCCGGGGACCAGGCCTCATCAGGTGTGGAGGTGGAGAGCAGCATGGGGCCCAGCTTGCTG
CTGCCTTCAGTCACCCCAACTACAGTGAATCCGGGGGACCAGGACTCCACCAGCCAAGAGGCA
GAGGCCACAGTGCTGCCAGCTGCAGGGCTTGGGGTAGAGTTCGAGGCTCCTCAGGAAGCAAGC
GAGGAAGCCACTGCAGGAGCAGCTGGTTTGTCTGGCCAGCAGGAGGTGCCGGCCTTGCCCT
TCATTCCCTCAAACCACAGCTCCCAGTGGGGCCGAGCACCCAGATGAAGATCCCCTTGCTCT
AGAACCTCAGCCTCTTCCCCACTGGCCCTGGAGACATGGAACCTGACACCTTCCTCTGCTACC
TTGGGACAAGAAGATCTCAACCAGCAGCTCCTAGAAGGGCAGGCAGCTGAAGCTCAATCCAGG
ATACCCTGGGATTCTACGCAGGTGATCTGCAAGGACTGGAGCAATCTGGCTGGGAAAACTAC
ATCATTCTGAACATGACAGAGAACATAGACTGTGAGGTGTTCCGGCAGCACCGGGGGCCACAG
CTCCTGGCCCTGGTGGAAGAGGTGCTGCCCCGCCATGGCAGTGGCCACCATGGGGCCTGGCAC
ATCTCTCTGAGCAAGCCCAGCGAGAAGGAGCAGCACCTTCTCATGACACTGGTGGGCGAGCAG
GGGGTGGTGCCCACTCAAGATGTCCTTTCCATGCTGGGTGACATCCGCAGGAGCCTGGAGGAG
ATTGGCATCCAGAACTATTCCACAACCAGCAGCTGCCAGGCGCGGGCCAGCCAGGTGCGCAGC
GACTACGGCACGCTCTTCGTGGTGCTGGTGGTCATTGGGGCCATCTGCATCATCATCATTGCG
CTTGGCCTGCTCTACAACTGCTGGCAGCGCCGGCTGCCCAAGCTCAAGCACGTGTGCGACGGC
GAGGAGCTGCGCTTCGTGGAGAACGGCTGCCACGACAACCCACGCTGGACGTGGCCAGCGAC
AGCCAGTCGGAGATGCAGGAGAAGCACCCAGCCTGAACGGCGGGGGGCCCTCAACGGCCCCG
GGGAGCTGGGGGGCGCTCATGGGGGGCAAGCGGGACCCCGAGGACTCGGACGTGTTGAGGAG
GACACGCACCTG**TGA**GCGCAGCCGAGGCGCAGGCCGAGTGGGCCGCCAGGACCAAGCGAGGTG
GACCCCGAAACGGACGGCCCCGAGCCCCGACCCCGCGCCTACCCGGGGCGCCCCCGCGG
CCTGGCCCTCGGCGCGGGCTCCTTCCCGCTTCCCCGACTTCACACGGCGGCTTCGGACCAAC
TCCCTCACTCCCGCCCCGAGGGGCAGGCCTCAAAGCCCCGCTTGGCCCCGCTTCCCGCCCCTG
AACCCCGCCCCCGCGGGCGGGCGGGCGCTTCTGCGCCCCGGGACTCAATTAAACCCGCC
GGAGACCACGCCGGGCCAGCAAAA

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FIGURE 160

MGRLLRARLPPLLSPLLLLLLVGGAFLGACVAGSDEPGPEGLTSTSLDLLLPTGLEPLDSEE
PSETMGLGAGLGASGSGFPSEENEESRILQPPQYFWEEEEELNDSSLDLGPTADYVFPDLTEK
AGSIEDTSQAQELPNLPSPLPKMNLVEPPWHMPPREEEEEEEEEEREKEEVEKQEEEEEEEL
LPVNGSQEEAKPQVRDFSLTSSSQTPGATKSRHEDSGDQASSGVEVESSMGPSLLLPSVTPTT
VTPGDQDSTSQAEEATVLPAAAGLGVEFEAPQEASEEATAGAAGLSGQHEEVPALPSFPQTAP
SGAEHPDEDPLGSRTSASSPLAPGDMELTPSSATLGQEDLNQQLLEGQAAEAQSRIPWDSTQV
ICKDWSNLAGKNYIILNMTENIDCEVFRQHRGPQLLALVEEVLPRHGSGHHGAWHISLSKPSE
KEQHLLMTLVGEQGVVPTQDVLSMLGDIRRSLEEIGIQNYSTTSSCQARASQVRSYGTLFVV
LVVIGAICIIIIALGLLYNCWQRRPKLKHVSHGEELRFVENGCHDNPTLDVASDSQSEMQEK
HPSLNGGGALNGPGSWGALMGGKRDPESDVFEEDTHL

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 499-521

N-glycosylation sites.

amino acids 106-110, 193-197, 395-399, 480-484

Glycosaminoglycan attachment site.

amino acids 77-81

N-myristoylation sites.amino acids 24-30, 28-34, 41-47, 69-75, 71-77, 73-79, 75-81,
216-222, 327-333, 455-461, 519-525, 574-580, 581-587, 584-590**Amidation site.**

amino acids 588-592

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FIGURE 161

CCAGGGCGGAGCGCAGCTGCGCCGGGCTTGGGCGCCTGGGGCCGCGCTCCCCACCGTCGTTT
TCCCCACCGAGGCCGAGGCGTCCCGGAGTCA**ATG**GCCGGCCTGAACTGCGGGGTCTCTATCGCA
CTGCTAGGGGTTCTGCTGCTGGGTGCGGCGCGCCTGCCGCGCGGGGCAGAAGCTTTTGAGATT
GCTCTGCCACGAGAAAGCAACATTACAGTTCTCATAAAGCTGGGGACCCCGACTCTGCTGGCA
AAACCCTGTTACATCGTCATTTCTAAAAGACATATAACCATGTTGTCCATCAAGTCTGGAGAA
AGAATAGTCTTTACCTTTAGCTGCCAGAGTCCTGAGAATCACTTTGTCATAGAGATCCAGAAA
AATATTGACTGTATGTCAGGCCCATGTCCTTTTGGGGAGGTTTCTGCTTCTAGCCCTCGACATCG
TTGTTGCCTACCCCTCAACAGAACTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCGGTTTA
GAGCTGCAGTTTTCATCCCTCGCCTGAGGCAGATCGGTCCGGGTGAGAGCTGCCAGACGGA
GTCCTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGC
AATGGCACTGTGTCCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGG
TTCCACCCCAGAAATGTCTCCGGCTTCTGAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGC
ATCATCGAGTCTGTGTTTGAGGGTGAAGGCTCAGCAACCCTGATGTCTGCCAACTACCCAGAA
GGCTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTTCGTTTCTGCACACCTGCGGGGCCAGC
GTCTCCTTCCCTCAACTTCAACCTCTCCAACCTGTGAGAGGAAGGAGGAGCGGGTTGAATACTAC
ATCCCGGGCTCCACCACCAACCCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGGGAACATG
GCGGGGAACCTTCAACCTCTCTCTGCAAGGCTGTGACCAAGATGCCCAAAGTCCAGGGATCCTC
CGGCTGCAGTTCCAAGTTTGGTCCAACATCCACAAAATGAAAGCAGTGAG**TGA**GCCCCACTT
TCCTTTTCTTCTCCTCCTCCAGCACCTTCGTTGTTTCTGGGTAGTCTGCCTGGGTGAGGCTCC
CTTCTGTTTCTCATCTGTGGCTTCTGAAACACTTAGACTCTGGACCCAGCAAGAGTTTTCAGG
AAGTGGGTTGCTAGGCAGTTAGACAGGCTTGTGGTGAACACCCGGTATGTAGTTCCATTTCA
GCACAATAAAAAGAAATCTTGCAATCAAGATGCTAAATTGTTTTTAACGAAAA

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FIGURE 162

MAGLNCGVSIALLGVLLLGAARLPRGAFAFEIALPRESNITVLIKLGTPPTLLAKPCYIVISKR
HITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLPPTLNRTFI
WDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQ
EGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDELMTW
QFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQG
CDQDAQSPGILRLQFQVLVQHPQNESSE

Signal peptide:

amino acids 1-29

N-glycosylation sites.amino acids 39-43, 122-126, 180-184, 205-209, 213-217, 270-274,
310-314, 339-343**Tyrosine kinase phosphorylation site.**

amino acids 276-284

N-myristoylation sites.

amino acids 3-9, 7-13, 158-164, 175-181, 191-197, 303-309

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FIGURE 163

CAACCACACACCTGGGGAATTGCTGGCCTGACTTCTGACCCCTGACTCCTCATACCCTTCCTC
CAGAGCATGACATTTGACCACCAACTGAAACCTGACCTCTGACCCAGACCACTGGCCCTTCC
CCCGCCCTGTGGTGACTTCATAAAGTTACTAGCTTCTCCCCTGGCCTTGAGACCCACACGAT
GGCCCTGCTGGCTCTGGCCAGTGCCGTCCCCCTCTGCCCTGCTGGCCCTGGCTGTCTTCAGGGT
GCCCCCTGGGCCTGTCTCCTCTGCTTCACAACCTACTCTGAGCGCCTCCGCATCTGCCAGAT
GTTTGTGGGATGCGGAGCCCCAAGCTTGAAGAGTGTGAGGAGGCCTTCACGGCCGCCTTCCA
GGGCCTCTCTGACACCGAAATCAGTGAGGAGACCATCCACACTTCATCAGTGTCTTGGGGAAG
GTGCAGAGGGAGGGCAGGAGAGGCCAGAGGGTCAGGCTGAGGGACAGACAGAGAGAAACAGT
CAGAGGAGAAAGGCTCAAAGACCATGAGAACAACAGAGACTTAGGGACAGAGAGACACAGACA
GGGGAAGACAGCAGGGCAAAGACTCAGAGAGGGGAGGATGGAGAGTCAGAGAGGGGAAGATGG
AGACTCAGAGAGAGGGGAGGATGGAGACTCAGAGAGAGAGGAAGATGGAGACTCAGAGGGAAA
GATGGAGACTCAGGAGTATGGAGAGTCAGAGAGGGGAGGATGGACACTCAGGGGAGGATGGAG
AGTCAGGAGGATGGAGACTCATAGAAAGGGGAGGATGGAGAGTCAGGAGAGGTTGGAGACTGG
AGAGGGGAATAGAGACCCAGAAAGGGGAGGATGGAGACTCAGAGGGGTGGAAGATGGAGACTCAA
AGAGGATGGAAACCCAGAGAGAGGAGGACAGAGATGAGGCGCAGAGACTAGGGGAAGCAGGATAG
CGACTGGTCGGGGGCAGAGACTCAGGGAGGATAGAGACTCACAGAGAGGTGAGGATAGAGACT
TGGGAGGGACTCAGGAAGCATAGCGACTGTGGGGCAAAGAGTCAGAGAGGGGAGGATACAGAC
TTGGGAGGGCAGAGACTCAGAAACAGAATGTTTCGATTAGGGACATGGTGTTCGGGGAGCTG
CCTCCCCCAGCCCTGCTCCCTCCCTCACCGCCAGACTATGATGAGAGAAGCCACCTGCATGA
CACCTTCACCCAGATGACCCATGCCCTGCAGGAGCTGGCTGCTGCCAGGGATCCTTTGAGGT
TGCCTTCCCTGATGCTGCAGAGAAAATGAAGAAGGTCATTACACAGCTTAAAGAAGCCAGGC
TTGCATCCCTCCCTGCGGTCTCCAGGAGTTCGCCCCGCGTTTCCTCTGCAGCGGGTGCTACTC
TAGGGTCTGCGACCTCCCGCTGGACTGCCCAGTTCAGGATGTGACAGTGAATCGGGGCGACCA
GGCTATGTTTTCTTGATCGTAAACTTCCAGCTGCCAAAGGAGGAGATCACCTATTCCTGGAA
GTTTCGAGGAGGAGGTCTCCGACTCAGGACTTGTCTTATTTCCGAGATATGCCGCGGGCCGA
AGGATACCTGGCGCGGATCCGGCCGGCTCAGCTCACGCACCGCGGGACGTTCTCCTGCGTGAT
CAAGCAAGACCAGCGCCCCCTGGCCCCGCTCTACTTCTTTCTTAACGTCCTCGGGGCCCTCGC
ATCAGCGAGTGCGACAGTGTGGCGTGGTGAGTTCTGGGGACTCCGGAGCCCCAGCATCTAGC
TCCCCGCTGTCTCAGATCCCACCGAGAAGTCTGGGTCCCAGCAACCTCCAACCCAGGAGGAT
GTTCTTTTCATGGTACTGCAGTGGCAACTAACAAAGGTATCTTTCTCCTCCTTCCCTATCCTATT
TCCATCCTGAAAATAAAGAATATATTTCAACTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 164

MALLALASAVPSALLALAVFRVPAWACLLCFTTYSERLRICQMFVGMRS PKLEECEEAF TAAF
QGLSDTEISEETIHTSSVSWGRRCRGRAGEAQRVRLRDRQRETVRGERLKD HENN RDLGTERHR
QGKTAGQRLREGRMESQRGEDGDSERGEDGDSEREEDGDSE GKMETQEYGESERGGWTLRGGW
RVRRMETHRKGRMESQERLETGEGIETQKGEDGDSEGGRWRLKEDGNPERGGQR

Signal peptide:

amino acids 1-26

N-myristoylation site.

amino acids 65-71

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FIGURE 166

MELSDVTLIEGVGNEVMVVAGVVVLILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGH
VDHLVAGQGNPEPTELPHPSEGNDKAEAEAGEGRGDSTGEAGAGGGVEPSLEHLLDIQGLPKR
QAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLNDTEELAVARPEDTVGALKSKYFPGQES
QMKLIYQGRLQLQDPARTLRSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVGS
LMVPVFVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLVFGMYGR

Signal peptide:

amino acids 1-36

Transmembrane domains:

amino acids 246-267, 275-301

N-glycosylation sites.

amino acids 162-166, 211-215

N-myristoylation sites.

amino acids 48-54, 105-111, 109-115, 129-135, 177-183, 247-253

Cell attachment sequence.

amino acids 97-100

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FIGURE 167

GGCGGCTGTGTGTCGCCGGAGCCGAAGCGCGCAGGCCCGTCCCGGTGGCCGGGGAGCGGGCGGGTGGGGGCGCCA
TGTGGTTTCATGTACCTGCTGAGCTGGCTGTGCTCTTTCATCCAGGTGGCCTTCATCACGCTGGCTGTGCGGGCTG
GACTCTATTACCTGGCAGAACTGATAGAAGAATACACAGTGGCCACCAGCAGGATCATAAAATACATGATCTGGT
TCTCCACCGCTGTACTGATTGGCCTCTACGTCTTTGAGCGCTTCCCCACCAGCATGATTGGAGTGGGCCTATTCA
CCAACCTCGTCTACTTTGGCCTCCTCCAGACCTTCCCCCTTCATCATGCTGACCTCGCCTAACTTCATCCTGTGCT
GTGGACTAGTGGTGGTGAATCATTACCTAGCATTTAGTTTTTGCAGAAGAATATTATCCCTTCTCAGAGGTCC
TGGCCTATTTCACTTTCTGCCTGTGGATAATTCGGTTTGGCTTTTGTGTCACTTTTCGGCCGGGGAGAACGTCC
TGCCCTCTACCATGCAGCCAGGAGATGATGTCGTCTCCAATTATTTACCAAAGGCAAGCGGGGCAAACGCTTAG
GGATCCTGGTTGTCTTCTCCTTCATCAAAGAGGCCATTCTACCCAGTCGTCAGAAGATATACTGACCCCCATGCA
GGCAGGATGTGGGGGGCAAGATCAGGAGAGTCAGGCCCTGGGCCTCTATGCCAGGTGGGGACCAGAAGTCGGGA
AGGCACCTACCACCTGCCCTGGCTTCTTCCCCCTCAACTCTGGAGCCCCATCCCCACCCTCCTTGGGGGGCTCAG
CTTGGCTCAGATCTGATGCTCAAGAGGCTGTAACCTCAGAGGGCACCAAGGAGGGTGGCAGAGCCTGCTTAGCC
AGGAGGCCGAGGTCCCTCAGTCCTCCCCTGTCCCTTCCAAGTGGGTGAGGAGTTCTGGCCCCGCTGGGGCAGG
CAGGGCAGGGTCTGTGAAGCTTAAGAGCAGATGGTGACAAGTTCTCTGGGCAGGTGGCCATGGGGAGGGGCCATG
GCTTGGCATGTCCAACAGAAATAGTTTTTGTGCTGTTGAACGGTGATTTCTGTCCAAGTGCAGATTTCCGTTTGAAT
AAAGCTTCGCTTCTAGGTGGCACTGTTTGCCTTAATACCCTGACAGTTCATCTTCTTCTTCTCCTGCTAACCTTC
TGCTCTGGACTGGACTCACTTTTCTGCTCCAGGGACTCCTTTTCTGGGTTTGGGTCTTGGCCTTCCCAAGGGACT
GTTCTTGTGGCCCTTAATGGGAAGGGGGCAGGGGTGAGGAGCTGAGCCTGCTCAAGGAGTGGGAAGTGGGGCTAT
AGGCAGCCTCTCTGATGCACTCTCTTCCATCTCTTCCCCAAGGCTCCGTGACTGTCAAACCTGGGAGTAGGAGAG
GGGACAATTTAGGACTGGGCTAGATTTTCAGAAGAATCTACAATATCCTATTTATAAATCTTCTCTGGGAAA
AGGAGTGGTTTCTGGCTGAATACTATCTTAGGCTCAAGGAGAAACAAAATAAAATTAGCTTCCAGGCAGCCTGT
TTTTAAAGAAATGGGACTAATGGGAGAAGCTTTTGTCACTCTAAGAGCATCCAAGCCCTGGCCCCGTCTGTGCAC
TCTTGGCTCCTGGGGAGATATATCTGCCTTCTAAGAAGGCAGGCCAGGTCTTGGGCACAGACCTGCATTTGTGA
CCTTGCACCTCAACTATAGTGCCTTGCAAGTGCTCAACAGTACATATTGGAATGAAGTCCCTATGAGAGCCATTT
CTGGCCATGTTCTATACCTCAAAGTGAGGCTGGCAGGTACAGAGATGAAGTGTACACATGTGATACATTTAAGCC
ACTGGAAAAACCCCTGTGCTTGAATAATTTCTCTATATCATGCCTGGAGTTCATCATAGCCCTTCATTTCTCT
TGGCTTTAGCATTTACCTTCTCTTAAGAATACCAGCTTTCCCCTTTCCCTGAGAGGAAGAGCACATGTTGGTCTC
CTCTTAGTGTGAACGAGATTGCCAGGCCCTTTTCTCCTATGCACACCAGGATAGACAAGGCAGGGGATACTGGCA
GCCTGCATCATCTCCCATTGGGCTGACAGCTGGCCCTACTTTTCTCCTCTGCTGCTTGGTCCCTCACCTTGAT
GATGTGGCTTCGCCCCCTCCACTCTACTGCCAGTGTCTCCCAGGGGTTGCTAAATCCAGCAGACCCCTTTCTCTG
TCTTACTAGATCTGGGCAGCATTTGACATGGCTGATCACCCCTTGCTTCTTGGATGGCACTTCCCTGGCACCTCT
GTGGCTAGTTGTCTTACCTCCCTGGCTGTTCTTTTCCAGGCTTCCGTGCAGGCTTCTCCACTTGCCCATGCACAGT
AGGGTCTTTCAGGGTCTGCTGTGGGCTCCCTAGGGAAGCCCATCCATCTGGATGGTTTCAAGGATGGTGAGGAA
TTTAGAGTTGACCTCCAGCCCCAACATCCTTCTGATCACCTGAACCACAGTTTGTGCTGCTCTAGGTGCACAG
ACAATTCAGGTCCATGGCCAGATGGTACTTGCTGTCTTCTGCAAACCTGCCCTTCTGGGTACTTCCCTTGACC
CCGAGATCACTCAGGAGCCAGACAGGAACTTATTCTATTCTGTTTTCTCTTTCTGCCCCACCACATCCAATCTC
TCAAAACGGTCAGGTCTACCTTAACATCTCTTGATTGAGCCACTCCCACTGTCACTCAGCTTTACCTGGATTAT
CGTGACAGCCTCCTACTGCTTCTCTATCATGTGGCCAGAGCTATCTTCTTAAATGCATTGCATAGTTGATCAAG
TCACTCTCTGGCCTAAAACCTTCTTGGCTCCCTGCTGCCCTCAGGATAAAGTCTGGACCCCTCAGCATGGCTTG
TGAGACTCATGGTGTCTTGTCCCTGCTCACCTCTCTGGTCTCATCACTTGCCTTCTTGCACTTGGGTCCCAGC
CTCCTGTATCCAGAGATGCAGTGGCTCTCCATTGCCACTCTGATTCCCTCCTTTCTTTTGGTCCACAGAGAAAGGT
ACTTTCTCTGTCAAATCTCAACTTAGACTTGACTTCTCCAAAGGAGCTTTGGCTATACTCTCTCTCTCCCGACCCC
CACCTGGCATACTACACAGATCACTTGGGCTCACTTGCTGCCTAATGGTCATCTCCCCAGTAGACTGTAAGC
TCCTTGAGGGCAAGGATTGTGTTGGAATTTTGTATTAAAGTGCCTGGCTTGGTGCCTGGCACCTAGAAAGCAC
TCAATAAATGTTTGTAAATGAA

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FIGURE 168

MWFMYLLSWLSLFIQVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIGLYVFE
RFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCGLVVVNHYLAFQFFAEYYPFSEVL
AYFTFCLWIIIPFAFFVSLSAGENVLPSTMQPGDDVVSNYFTKGKRGKRLGILVVFSFIKEAIL
PSRQKIY

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 126-146

Casein kinase II phosphorylation site.

amino acids 145-148

N-myristoylation sites.

amino acids 73-78, 82-87

Amidation sites.

amino acids 168-171, 171-174

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 91-101

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FIGURE 169

CAAAGCCCTACCCTCACCATTACCAGGTCCCTGTGGGAAGAGCAGCGTGGAGGTGGGCTGAGG
TTAGAAGGTGCAGAGCGTGGGAAGAAGATTGTGAGCTGAGTATTGGACATCTGTTCTTGAATAG
TCCCTGGGCCTGCCATAGGAAAGGAAGTTCTCCAGGGTTACAGTTCTTATCCGCGTGAATACA
CATGGCTCTGTTACGAAAAATTAATCAGGTGCTGCTGTTCTTCTGATCGTGACCCTCTGTGT
GATTCTGTATAAGAAAGTTCATAAGGGGACTGTGCCAAGAATGACGCAGATGATGAATCCGA
GACTCCTGAAGAACTGGAAGAAGAGATTCCGTGTGGTGATTTGTGCTGCAGCAGGGAGGATGGG
TGCCACTATGGCTGCCATCAATAGCATCTACAGCAACACTGACGCCAACATCTTGTTCTATGT
AGTGGGACTCCGGAATACTCTGACTCGAATACGAAAATGGATTGAACATTCCAACTGAGAGA
AATAAACTTTAAAATCGTGGAATTCAACCCGATGGTCCCTCAAAGGGAAGATCAGACCAGACTC
ATCGAGGCCTGAATTGCTCCAGCCTCTGAACCTTGTTCGATTTTATCTCCCTCTACTTATCCA
CCAACACGAGAAAGTCATCTATTTGGACGATGATGTAATTGTACAAGGTGATATCCAAGAACT
GTATGACACCACCTTGCCCTGGGCCACGCGGCGGCTTTCTCAGATGACTGCGATTTGCCCTC
TGCTCAGGACATAAACAGACTCGTGGGACTTCAGAACACATATATGGGCTATCTGGACTACCG
GAAGAAGGCCATCAAGGACCTTGGCATCAGCCCCAGCACCTGCTCTTTCAATCCTGGTGTGAT
TGTTGCCAACATGACAGAATGGAAGCACCAGCGCATCACCAAGCAATTGGAGAAATGGATGCA
AAAGAATGTGGAGGAAAACCTCTATAGCAGCTCCCTGGGAGGAGGGGTGGCCACCTCCCCAAT
GCTGATTGTGTTTCATGGGAAATATTCCACAATTAACCCCTGTGGCACATAAGGCACCTGGG
CTGGAATCCAGATGCCAGATATTCGGAGCATTTTCTGCAGGAAGCTAAATTACTCCACTGGAA
TGGAAGACATAAACCTTGGGACTTCCCTAGTGTTTACAACGACTTATGGGAAAGCTGGTTTGT
TCCTGACCTGCAGGGATATTTAAACTCAATCACCATAGCTGTGATATAACTCTACCCTTAAAT
ATTCCTGTATAGAAATGTGGAATTGTCCCTTTGTAGCCAACCTATAACATTGTTCTTTATGAA
TATTACCTTTGATACATATGATCCACAATATAAAAACCAAAACTACTGTGTGCAAATTATAC
CTTGACCATATAGGCATTGATTAACCTTCTTTAAGTACATGTGATAACTATGGAAATCAAGAT
TATGTGACTGAAAAACATAAAGGAAGAGACCCATCTAGATAACAGCAATCAACCTGCTTAATT
CTGAATGACAATTATATCCACAAATTTTTAAACTTCTACATGTATTTTTTACATGAAGATCT
CCTTAACAGGTTGCCAACCTTTTCTTTTATAAACTATTACATTTAAATATGGACGTCTGAA
AAATAAAATATTCATCATTTTTTAAAA

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FIGURE 170

MALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESETPEELEEIPVVICAAAGRMG
ATMAAINSIYSNTDANILFYVVGLRNTLTRIRKWIEHSLREINFKIVEFNPMVLKGKIRPDS
SRPELLQPLNFVRFYLPLLIHQHEKVIYLDLDDVIVQGDIQELYDTTLALGHAAAFSDDCDLPS
AQDINRLVGLQNTYMGYLDYRKKAIKDLGISPSTCSFNPGVIVANMTEWKHQIRITKQLEKWMQ
KNVEENLYSSSLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFLQEAKLLHWN
GRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 234-238

Tyrosine kinase phosphorylation site.

amino acids 253-261

N-myristoylation sites.amino acids 63-69, 86-92, 198-204, 218-224, 229-235, 265-271,
266-272

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FIGURE 171

GCCAGAGGCTGCAGCTGGAGCCCAGAGCCCAAGATGGAGCCCCAGCTGGGGCCTGAGGCTGCC
GCCCTCCGCCCTGGCTGGCTGGCCCTGCTGCTGTGGGTCTCAGCCCTGAGCTGTTCTTTCTCC
TTGCCAGCTTCTTCCCTTTCTTCTCTGGTGCCCCAAGTCAGAACCAGCTACAATTTTGGAAGG
ACTTTCCTCGGTCTTGATAAATGCAATGCCTGCATCGGGACATCTATTTGCAAGAAGTTCTTT
AAAGAAGAAATAAGATCTGACAACTGGCTGGCTTCCCACCTTGGACTGCCTCCCGATTCCCTG
CTTTCTTATCCTGCAAATTACTCAGATGATTCCAAAATCTGGCGCCCTGTGGAGATCTTTAGA
CTGGTCAGCAAATATCAAACGAGATCTCAGACAGGAGAATCTGTGCCTCTGCATCAGCCCCA
AAGACCTGCAGCATTGAGCGTGTCTGCGGAAAACAGAGAGGTTCCAGAAATGGCTGCAGGCC
AAGCGCCTCACGCCGGACCTGGTGCAGGACTGTCACCAGGGCCAGAGAGAACTAAAGTTCCTG
TGTATGCTGAGATTAACACCAGTGAAAAAGCCTGGCATGGAGCCCAGCACTGAGAACTTCCAGA
AAGTGTTAGCCTTCTCCCAACTGTGTTATACCAACCACATTTTCAAATAGTAATCATTAAAGA
GGCTTCTGCATCAA

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FIGURE 172

MEPQLGPEAAALRPGWLALLLWVSALSCSFSLPASSLSSLVPQVRTSYNFGRTFLGLDKCNAC
IGTSICKKFFKEEIRSDNWLASHLGLPPDSLLSYPANYSDDSKIWRPVEIFRLVSKYQNEISD
RRICASASAPKTCSIERVLRKTERFQWLQAKRLTPDLVQDCHQGQRELKFLCMLR

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 100-103

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 158-161

N-myristoylation sites.

amino acids 56-61, 65-70

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 18-28

Prenyl group binding site (CAAX box).

amino acids 179-182

Leucine zipper pattern.

amino acids 5-26

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FIGURE 173

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTTTGAAGGTCCTAGCCACCTGGGCTGGCTC
ACGCGCACGACTAGCCGCTCCCATACAGCACGCCCGGACTCTGTCTGCTGCTTAAGGCCACTCC
TATTCTACGGCTGACCCCTGGTGGTCACGTGGATCTGTTTCGCCACGCAAGTCTGGGTCTTCG
GCGATTGACCGGGGTCCTTGCTGTTTCGGGAGCCTCTCCTAAGCTGCCTGTTTCGCGCGAGAGTT
TGGAGGGGCGGGTTTGGGGTCGGTGTCTGATTGGGGCTCGCACCGCAGCACGCTGGAGTCCCG
CTTAGGTACCAGTTAGCGTCAGGGGAGCTGGGTTCAGGCGGTTCGCCGGGACACCCCGTGTGTGG
CAGGCGGCGAAGCGCTCTGGAGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTC
GGGAGCCACTGGGGCCAAAGTGAGAGTCCAGCGGTCTTCAGCGCTTGGGCCACGGCGGGCGGC
CCTGGGAGCAGAGGTGGAGCGACCCATTACGCTAAAGATGAAAGGCTGGGGTTGGCTGGCCC
TGCTTCTGGGGGCCCTGCTGGGAACCGCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG
CATGCAGGGCTCTGGTGGATGAACTAGAAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCA
TTCAGATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATG
CCCGCTCAGAGGCCCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATG
GGGAACAGATTGATCCTTCCACCCATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAG
AATCCAGTGAAGTGGACCTACAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCCTCAAGT
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGG
CTGACAATGTTAAAGACAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACA
TATCGCATGATGAGCTATGAACCACTGGAGCAGCCCACACTGGCTTGATGGATCACCCCCAGG
AGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAATTAAGTAAAAATA
TGAAACCAAAAAGT

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FIGURE 174

MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINPDGS
QSVVEVPYARSEAHLTELEEICDRMKEYGEQIDPSTHRKNYVRVVGVRNGESSELDLQGIRID
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTDLCDHALHISHDEL

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 12-18, 16-22, 29-35

Endoplasmic reticulum targeting sequence.

amino acids 179-184

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FIGURE 175

CGCAGCGCGGCAGTCCTGATGGGCCCGGCATGGGTTACCGCTGCTGCCCCTGCTGTCGCTCCTG
GTCGGCGCGTGGCTCAAGCTAGGAAATGGACAGGCTACTAGCATGGTCCAAGTGCAGGGTGGG
AGATTCCCTGATGGGAACAAATTCTCCAGACAGCAGAGATGGTGAAGGGCCTGTGCGGGAGGGC
ACAGTGAAACCCTTTGCCATCGACATATTTCTGTACCAACAAAGATTTTCAGGGATTTTGTC
AGGGAGAAAAAGTATCGGACAGAAGCTGAGATGTTTGGATGGAGCTTTGTCTTTGAGGACTTT
GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA
GTGGAAAAGGCATTTTGGAGGCAGCCTGCAGGTCCTGGCTCTGGCATCCGAGAGAGACTGGAG
CACCCAGTGTTACACGTGAGCTGGAATGACGCCCGTGCCTACTGTGCTTGGCGGGGAAAACGA
CTGCCCACGGAGGAAGAGTGGGAGTTTGCCGCCCGAGGGGGCTTGAAGGGTCAAGTTTACCCA
TGGGGGAACTGGTTCCAGCCAAACCGCACCAACCTGTGGCAGGGAAAGTTCCCCAAGGGAGAC
AAAGCTGAGGATGGCTTCCATGGAGTCTCCCCAGTGAATGCTTTCCCCGCCCAGAACAACCTAC
GGGCTCTATGACCTCCTGGGGAACGTGTGGGAGTGGACAGCATACCGTACCAGGCTGCTGAG
CAGGACATGCGCGTCTCCGGGGGGCATCCTGGATCGACACAGCTGATGGCTCTGCCAATCAC
CGGGCCCCGGGTACACCAGGATGGGCAACACTCCAGATTCAGCCTCAGACAACCTCGGTTTC
CGCTGTGCTGCAGACGCAGGCCGGCCGCCAGGGGAGCTGTAAGCAGCCGGGTGGTGACAAGGA
GAAAAGCCTTCTAGGGTCACTGTCAATCCCTGGCCATGTTGCAAACAGCGCAATTCCAAGCTC
GAGAGCTTCAGCCTCAGGAAAGAACTTCCCCTTCCCTGTCTCCCATCCCTCTGTGGCAGGCGC
CTCTACCCAGGGCAGGAGAGGACTCAGCCTCCTGTGTTTTGGAGAAGGGGGCCCAATGTGTGTT
GACGATGGCTGGGGGCCAGGTGTTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAAA
CACACAAACAGTTGGAACAGAGCACTCTGAAAGGCCATTTTTTAAGCATTTTAAAATCTATTC
TCTCCCCCTTTCTCCCTGGATGATTCAGGAAGCTGACATTGTTTCTCAAGGCAGAATTTTCC
TGGTTCTGTTTTCTCAGCCAGTTGCTGTGGAAGGAGAATGCTTTCTTTGTGGCCTCATCTGTG
GTTTCGTGTCCCTCTGAAGGAACTAGTTTCCACTGTGTAACAGGCAGACATGTAAGTATTTA
AAGCACAGTTCAGTCTAAAGGGTCTGGGAGAACCAGATGATGTACTAGGTGAAGCATTGCA
TTGTGGGAATCACAAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTTCCTATTCTTT
TTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGGGTCTTTCTCTGTTGCCCAGGCTAGAGTGCACTG
GTGATCACGGCTCACTCTAGCCTTGAATTCCTGGGCCCCAAGCAATTCTCCACCTCAGCCTCC
TGAGTAGCTGGGACTACAAGTGTGCACCACCATGCCTGGCTAATTTTTTTGAATTTTTGTAGTG
ATGGGATCTCGCTCTGTTGCCCAGGGTGGTCTCGAACTCCTGGCCTCAAGCGATCCTCCCACC
TCGACCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCTCGCCTGGGCCCCCTTCTCCATA
TGCCTCCAAAAACATGTCCCTGGAGAGTAGCCTGCTCCACACTGTCACTGGATGTATGGGG
CCAATAAAATCTCCTGCAATTGTGTATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

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FIGURE 176

MARHGLPLLPLLSLLVGAWLKLGNQGQATSMVQLQGGREFLMGTNSPDSRDGEGPVREATVKPFA
IDIFPVTNKDFRDFVREKKYRTEAMFGWSFVFEDFVSDELNRNKATQPMKSVLWWLPVEKAFW
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ
PNRTNLWQGKFPKGDKAEDGFHGVSPVNAFPAQNNGLYDLLGNVWEWTASPYQAAEQDMRVL
RGASWIDTADGSANHRARVTTRMGNTPDSDNLGFRCAADAGRPPGEL

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 191-195

N-myristoylation sites.

amino acids 23-29, 25-31, 175-181

Amidation site.

amino acids 159-163

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FIGURE 177

GCCTTCTCGCGCCTGACCATGCACCCCTGCATCTTCCTGCTGGGCCACAGGCGAGCGCTTTAT
TTCTGGAGCTGAGGGCTAAACCTTTTTTGACTTTTCTTCTCCTCAACATCTGAATCATGCCAT
GTGCCCAGAGGAGCTGGCTTGCAAACCTTTCCTGGTGGCTCAGCTCCTTAACTTTGGGGCGC
TTTGCTATGGGAGACAGCCTCAGCCAGGCCCGGTTTCGCTTCCCGGACAGGAGGCAAGAGCATT
TTATCAAGGGCCTGCCAGAATACCACGTGGTGGGTCCAGTCCGAGTAGATGCCAGTGGGCATT
TTTTGTCATATGGCTTGCACTATCCCATCACGAGCAGCAGGAGGAAGAGAGATTTGGATGGCT
CAGAGGACTGGGTGTACTACAGAATTTCTCACGAGGAGAAGGACCTGTTTTTTAACTTGACGG
TCAATCAAGGATTTCTTTCCAATAGCTACATCATGGAGAAGAGATATGGGAACCTCTCCCATG
TTAAGATGATGGCTTCCTCTGCCCCCTCTGCCATCTCAGTGGCACGGTTCTACAGCAGGGCA
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTTTCCAACCTACCAC
ATGGAGACTTTTTTCAATTGAACCCGTGAAGAAGCATCCACTGGTTGAGGGAGGGTACCACCCGC
ACATCGTTTACAGGAGGCAGAAAGTTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA
TTGTGACTCACATGTCCTCCTGGGTTGAAGAATCTGTTTTGTTCTTTTGGTAGTTTTATTAA
ACATGACCTATTCTTACTCAAGTCTCTTATCTCCTCTGTATTCTTTTTTTTTTAATATCTTCA
TGACATTCAAATCTCTTCTGTATTCTCTTGCCAGAAAGTGTACATTCTTTTTGCTTGATAAA
CCCTTTCACTTGTC

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FIGURE 178

MPCAQRSWLANLSVVAQLLNFGALCYGRQPQGPVRFPPDRRQEHFIKGLPEYHVVGPPVRVDAS
GHFLSYGLHYPTSSRRKRDLDGSEDWVYYRISHEEKDLFFNLTVNQGFLSNSYIMEKRYGNL
SHVKMMASSAPLCHLSGTVLQQGTRVGTAALSACHGLTGFFQLPHGDFFIEPVKKHPLVEGGY
HPHIVYRRQKVPETKEPTCGLKGIVTHMSSWVEESVLFFW

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 11-15, 105-109, 125-129

N-myristoylation site.

amino acids 149-155

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FIGURE 179

CAGATTTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATACGAATTCCTTTTCT
TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGATATGTGTGGATTACAGTTTTCTCT
GCCTTGCTACGACTGTTTCTGGTTGTTACCTGTTATCTTTTATTATTACTCCACAAAGAAAT
ACTTGGATGTTCTGCTGTTTGTCTGAGCTCTGCACTGGGAGACAAATTAAGTCCGTAACCTTAGG
CCTTTCGAGTATTCCTAAGAATTTTCCTGAAAGTACAGTTTTTCTGTATCTGACTGGGAATAA
TATATCTTATATAAATGAAAGTGAATTAACAGGACTTCATTCTCTTGTAGCATTGTATTTGGA
TAATTCTAACATTCTGTATGTATATCCAAAAGCCTTTGTTCAATTGAGGCATCTATATTTTCT
ATTTCTAAATAATAATTTTCATCAAACGCTTAGATCCTGGAATATTTAAGGGACTTTTAAATCT
TCGTAATTTATATTTACAGTATAATCAGGTATCTTTTGTTCCGAGAGGAGTATTTAATGATCT
AGTTTCAGTTCAGTACTTAAATCTACAAAGGAATCGCCTCACTGTCCTTGGGAGTGGTACCTT
TGTTGGTATGGTTGCTCTTCGGATACTTGATTTATCAAACAATAACATTTTGAGGATATCAGA
ATCAGGCTTTCAACATCTTGAAAACCTTGCTTGTTTGATTTAGGAAGTAATAATTTAACAAA
AGTACCATCAAATGCCTTTGAAGTACTTAAAAGTCTTAGAAGACTTTCTTTGTCTCATAATCC
TATTGAAGCAATACAGCCCTTTGCATTTAAAGGACTTGCCAATCTGGAATACCTCCTCCTGAA
AAATTCAGAATTAGGAATGTTACTAGGGATGGGTTTAGTGGAATTAATAATCTTAAACATTT
GATCTTAAGTCATAATGATTTAGAGAATTTAAATTCTGACACATTCAGTTTGTTAAAGAATTT
AATTTACCTTAAGTTAGATAGAAACAGAATAATTAGCATTGATAATGATACATTTGAAAATAT
GGGAGCATCTTTGAAGATCCTTAATCTGTCAATTAATAATCTTACAGCCTTGCATCCAAGGGT
CCTTAAGCCGTTGTCTTCATTGATTCATCTTCAGGCAAATCTAATCCTTGGGAATGTAAGT
CAAATTTTGGGCCTTCGAGACTGGCTAGCATCTTCAGCCATTACTCTAAACATCTATTGTCA
GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATATTAACATTACAAATTGTGTTACATC
TTCAATAAATGTATCCAGAGCTTGGGCTGTTGTAAAATCTCCTCATATTCATCACAAGACTAC
TGCGCTAATGATGGCCTGGCATAAAGTAACCACAAATGGCAGTCCTCTGGAAAATACTGAGAC
TGAGAACATTACTTTCTGGGAACGAATTCCTACTTCACCTGCTGGTAGATTTTTTCAAGAGAA
TGCCTTTGGTAATCCATTAGAGACTACAGCAGTGTTACCTGTGCAAATACAATTAAGTCTC
TGTTACCTTGAATTTGGAAAAAACAGTGCTCTACCGAATGATGCTGCTTCAATGTCAGGGAA
AACATCTCTAATTTGTACACAAGAAGTTGAGAAGTTGAATGAGGCTTTTGACATTTTGCTAGC
TTTTTTCATCTTAGCTTGTTGTTTAAATCATTTTTTTGATCTACAAAGTTGTTTCAAGTTTAAACA
AAAATAAGGCATCAGAAAATCAAGGGAAAATAGACTTGAATACTACAGCTTTTATCAGTC
AGCAAGGTATAATGTAAGTGCCTCAATTTGTAACACTTCCCCAAATTCTCTAGAAAGTCTGG
CTTGGAGCAGATTCGACTTCATAACAAATTGTTCTGAAAATGAGGCACAGGTCAATCTTTT
TGAACATTCTGCTTTATAACTCAACTAAATATTGTCTATAAGAACTTCAGTGCCATGGACAT
GATTTAAACTGAAACCTCCTTATATAATTATATACTTTAGTTGGAAATATAATGAATTATATG
AGGTTAGCATTATTAAATATGTTTTTTNTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 180

MCGLQFSLPCLRLFLVVTCTYLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPPESTV
FLYLTGNNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNNFIKRLDPG
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSVQYLNLRNRLTVLGSGTFVGMVALRILDLSN
NNILRISESGFQHLENLACLYLGSNNLTKVPSNAFEVLKSLRRLSLSHNPIEAIQPFQFKGLA
NLEYLLLKNSRIRNVTRDGFSGINNLKHLILSHNDLENLNSDTFSLLKNLIYKLDNRNRIISI
DNDTFENMGASLKILNLSFNNLTALHPRVLKPLSSLIHLQANSNPWECNCKLLGLRDWLASSA
ITLNIYCQNPPSMRGRALRYINITNCVTSSINVSRAWAVVKSPIHHKTTALMMAWHKVTTNG
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTNLNLEKNSALPN
DAASMSGKTSLECTQEVEKLNEAFDILLAFFILACVLIIFLIYKVVQFKQKLKASENSRENRL
EYYSFYQSARYNVTASICNTSPNSLESPLGLEQIRLHKQIVPENEAQVILFEHSAL

Signal peptide:

amino acids 1-41

Transmembrane domain:

amino acids 530-547

N-glycosylation sites.amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,
336-340, 400-404, 410-414, 451-455, 579-583**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

N-myristoylation sites.

amino acids 3-9, 69-75, 126-132, 174-180

ATP/GTP-binding site motif A (P-loop).

amino acids 506-514

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FIGURE 181

GGCCTGGCGCGGCGCTCCGGTAAGGCGTGTGTGCGGCAGGGCGGGGACAGAACCGTCCTCTCG
GGCTCTGGGCGTGTCCGAGACCGCGCTCCCCGCCGAAATCAAGCTCCGAGTCATCCGTGTGGG
GCATTTCGTCCTCCCTGGCACAGTTGGCCTCTTTCCAGAAGCCCGTTTTGTTTGTTTTACGTCT
AAATTCGCGTCGGTTCTTATTTCTCTCCCTGGCAAGGTCTGAAGACGGGTAGGAGAATAACCT
GTGTCAGCGTGTTATGATGCCGTCCCGTACCAACCTGGCTACTGGAATCCCCAGTAGTAAAGT
GAAATATTCAAGGCTCTCCAGCACAGACGATGGCTACATTGACCTTCAGTTTAAGAAAACCCC
TCCTAAGATCCCTTATAAGGCCATCGCACTTGCCACTGTGCTGTTTTTGATTGGCGCCTTTCT
CATTATTATAGGCTCCCTCCTGCTGTCAGGCTACATCAGCAAAGGGGGGCGAGACCGGGCCGT
TCCAGTGCTGATCATTGGCATTCTGGTGTTCCTACCCGGATTTTACCACCTGCGCATCGCTTA
CTATGCATCCAAAGGCTACCGTGGTTACTCCTATGATGACATTCCAGACTTTGATGACTAGCA
CCCACCCCATAGCTGAGGAGGAGTCACAGTGGAAGTGTCCCAGCTTTAAGATATCTAGCAGAA
ACTATAGCTGAGGACTAAGGAATTCTGCAGCTTGAGATGTTTAAGAAAATAATGGCCAGATT
TTTTGGGTCCCTCCCAAAGATGTTAAGTGAACCTACAGTTAGCTAATTAGGACAAGCTCTATT
TTTCATCCCTGGGCCCTGACAAGTTTTTCCACAGGAATATGTATCATGGAAGAATAGAGGTTA
TTCTGTAATGGAAAAGTGTGCTGCCACCACCCTCTGTAGAGCTGAGCATTCTTTTAAATA
GTCTTCATTGCCAATTTGTTCTTGTAGCAAATGGAACAATGTGGTATGGCTAATTTCTTATTA
TTAAGTAGTTTATTTTAAAAATATCTGAGTATATTATCCTGTACACTTATCCCTACCTTCATG
TTCCAGTGGAAGACCTTAGTAAAATCAAAGATCAGTGAGTTCATCTGTAATATTTTTTTTACT
TGCTTTCTTACTGACAGCAACCAGGAATTTTTTTATCCTGCAGAGCAAGTTTTTCAAATGTAA
ATACTTCCTCTGTTTAACAGTCCTTGGACCATTCTGATCCAGTTCACCAGTAGGTTGGACAGC
ATATAATTTGCATCATTTTGTCCCTTGTAATCAAGATGTTCTGCAGATTATTCCTTTAACGG
CCGGACTTTTGGCTGTTTCCTAATGAAACATGTAGTGGTTATTATTTAGAGTTTATAGCCGTA
TTGCTAGCACCTTGTAGTATGTCATCATTCTGCTCATGATTCCAAGGATCAGCCTGGATGCCT
AGAGGACTAGATCACCTTAGTTTGATTCTATTTTTTTAGCTTGCAAAAAGTGACTTATATTCCA
AAGAAATTAAATGTTGAAATCCAAATCCTAGAAATAAATGAGTTTNNNTCCAAAAA
AAA

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FIGURE 182

MMPSTRNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIALATVLFLLIGAFLLIIG
SLLLSGYISKGGADRAVPVLLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

Transmembrane domains:

amino acids 45-66, 79-95

N-myristoylation sites.

amino acids 11-17, 75-81

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FIGURE 183

CTAAAAAATACAAAAATTAGCTGGGCGTGGTGTACGTGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGA
GAATCGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATTAAGTCACTGCACTCCAGCCTGGGTGACAGA
GCAAGACTCTGTATCAAAATAAAATAAAGTACAACCTCTGGATGGGCATGGTGGCTTATGCTGTAAATCCCAG
CACTTTGGGAACCTTGAGGCGGGTAGATTGCTTGAGTCCGGGAGTTTGAGACCAGTCTGGGTAATATGGTAACCT
GTCTACCAAAAAATACAGGTATTAGCCAGTCTCATAACTCGGTCTCAAAATAAATAAATACATACATAGATG
AAAATTTAAAAATAAAGTCCAACCTCAGCGGTTTTCAGCATATTTACAGAGTTGTACAATCTTCACCACTATCTA
ATTTCAGAACATTTTCATCACCCCCAAAAGAAACCTAACCCATTGACTATCTCTCCATTTCTCCCTCTCCCTAG
CCTCTGGCAACCACTAATCTCTTTTTTGTCTCTATAGATTTGCCTATTTTGACAGTTTCATATACAAGGAATCAT
ACCACATGTAGCCTTTTGTGTCCGGCTTCTTTGATTAATAGAATGTTTTCAAGGCTCATCTATGCTGTAGCCTGT
ATCAGCACTTCATTCTTTCTATGGCTGAATAATAGTCCACTGTAGGGATGTGCCATGTTTTTCCACTAGCTGAT
GGACATTTGGGTTGTTTCCACCTTCTGGCTATTATAAATATTGCTGCTATAAATATTCACCTACAAGTTTTTGTG
TGGACATATGTTTTTATTTCTTCTGGTATATCCTTCGGAGTGGAACTGCTGGATCAGGTGGTAACCTTAGGTCTA
ACCTGGCAGTTAAACAGAATCCTATGCTATGCTAGTCCATGAGTTGAAATAAACACTTGACCCATAGTAAGTGC
CAGATCATCTTCATTTTCACAGCAACCAGTAATTTACAGATGAGGAAATGAAGGCTCCAGAGGTGAAGTGGCTT
TTCCCATTTGAGCAGTTCCAAGTCAGACAGTTAAAAAGTGGCAGGACCTGGAAGAGAAGCTAGTTCTTTTACCCT
GGCATTACAGGGCTGCCTCCTGGGCTACGGGGCTGGCATTTAGAATAGAGCTAAGGTCTGCTGCCAAGGCAGGTGC
CCCAGTCTGCCTCCTCTGTGTCTTATTCCACTTTCTCTGCAGCCCTCCAGGGGACCCCTCTCTCAGCCACCCCTC
TCTCTGGTGAATGTACAGTGCTGCCGGAAGATCAAAGATACGGTGCAGAACTGGCTTCGGACCATTAAGGACATT
CACAGCAGTGTATCCCGAGTGGGCAAAGCCATTGACAGGAACCTTCGACTCTGAGATCTGTGGTGTGTGTGTCAGAT
GCGGTGTGGGACGCGCGGGAACAGCAGCAGCAGATCCTGCAGATGGCCATCGTGGAAACCTGTATCAGCAGGGC
ATGCTCAGCGTGGCCGAGGAGCTGTGCCAGGAATCAACGCTGAATGTGGAATTTCAAGCAGCCTTTTCTTA
GAGTTGAATCGAATCCTGGAAGCCCTGCACGAACAAGACCTGGGTCTGCGTTGGAATGGGCCGTCTCCACAGG
CAGCGCTGCTGGAACCTCAACAGCTCCCTGGAGTTCAAGCTGCACCGACTGCACTTCATCCGCTCTTGGCAGGA
GGCCCCGCGAAGCAGCTGGAGGCCCTCAGCTATGCTCGGCACTTCAGCCCTTTGCTCGGCTGCACCAAGCGGGAG
ATCCAGGTGATGATGGGCAGCCTGGTGTACCTGCGGCTGGGCTTGGAGAAGTCACCTACTGCCACCTGCTGGAC
AGCAGCCACTGGGCAGAGATCTGTGAGACCTTTACCCGGGACGCCTGTTCCCTGCTGGGGCTTTCTGTGGAGTCC
CCCCCTTAGCGTCAGCTTTGCCTCTGGCTGTGTGGCGCTGCCTGTGTTGATGAACATCAAGGCTGTGATTGAGCAG
CGGCAGTGCAGTGGGGTCTGGAATCACAGGACGAGTTACCGATTGAGATTGAAGTAGGCATGAAGTGTGGTAC
GCTCATCTGTGGCCATGTTATCTCCCGAGATGCACTCAATAAGCTCATTAAATGGAGGAAACACTCCGTGTTCCGT
TGCCCCATCCTCCGCCAGCAGACGTGAGATTTCAACCCCTCCCATCAAGCTGAAGTGTCCCTACTGTCCCATGGAG
CAGAACC CGGCAGATGGGAAACGCATCATATTCTGATTCTTACCTGGAAGGAATTTTGTGAAAGGGGTTTTTAC
CTGTGAGCCTTGGTCTGTCTCGGTAGGGTGGTCAACTTCAGTGGACTGTGGTGGTTTTCAGAGCGCCTGGCTGAG
GAGTTCCACTGAGGGGAGCACTGGAGCAGCCCTTTGGCAGAGGCTGAGGAGGGAGATGGACCAGCCACGCTGG
CACCTGGCTCCATGGCATAAGGAAAGGGAGATGCTGGCCTCTGTGCTCCTGCTGTCTTTTCTGTTTCTGTTGC
GTTTGACTTAGTAGCAACCGACAGAGTGGCAAGGGATTGGTCTTCAGCAGTAGACATCTTCCACCCCTGCCCT
CAGCCAAGTCTCTTGTGCTGCCATGCCAATGCTATGTCCACCCTTGGCCCTCGGCCCCAAGAGTGTCCAGCGGTGGCC
CACCTCTTCTCCCACTACAGCCTCAACAGTATGTACCATCTCCACTGTAAATAGTCCAGTTAGAACGGAATG
CCGTTGTTTTATAACTTTGAACAAATGTATTTACTGCCCTTCTCAAAA

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FIGURE 184

QCCRKIKDTVQKLASDHKDIHSSVSRVGKAIDRNFSEICGVVSDAVWDAREQQQQIILQMAIV
EHL YQQGMLSVAEELCQESTLNVDLDFKQPFLELNRIEALHEQDLGPALEWAVSHRQRLEL
NSSLEFKLHRLHFIRLLAGGPAKQLEALS YARHFQPFARLHQREIQVMMGSLVYLRLGLEKSP
YCHLLDSSHWAEICETFTRDACSLGLSVESPLSVSFASGCVALPVL MNIAKAVIEQRQCTGVW
N HKDELPIEIELGMKCWYHSVFACPI LRQQTSDSNPPIKLCGHVISRDALNKLINGGKLKCP
YCPMEQNPADGKRIIF

Transmembrane domain:

amino acids 222-241

N-glycosylation site.

amino acids 129-133

Tyrosine kinase phosphorylation site.

amino acids 151-159, 184-193

Amidation site.

amino acids 327-331

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 222-233

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FIGURE 185

GAGCGACGCTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTAAT
CTGCGCAAACCTTTTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCATCAAAGC
TTTGCGCAACGCCAACCTCAGGCGAGATGACTTGTACCGAAGAGATGAGACCATCCAGGTGAA
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTGAC
ATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACAATCAGTTTGGATT
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC
CAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCCTCCAAGGATAAAATCAAG
AACGAACCAAATTAAAATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAA
GATTTATTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGGAATC
TGTCACAAGCTCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGAT
TGCGGATGCTCTGGACAAAAAATTGCAGAATTTGATACAGTGGAAGATCTGCTCAAGTACTT
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGG
CAGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG
TTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGT
GGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGT
CAACTGGAGGTCTGACATGCAATTCAGGGAAAACCGTGAAAAAGTATCATGAGGTATTACA
GTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCA
GTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATTAAGAGAATGT
GCACATCCTTACATTAAGCCTGAGAGAA

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FIGURE 186

MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDDLYRRDETIQVKNGYVQSPRF
PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDISETSTIIRGRWCG
HKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSY
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKV
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFFPRCLLVQRCGNCGCGTVNWRSCTCNSG
KTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHERCDCICSSRPPR

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 270-274

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 262-266

Tyrosine kinase phosphorylation site.

amino acids 256-265

N-myristoylation sites.

amino acids 94-100, 186-192, 297-303, 298-304

TonB-dependent receptor proteins signature 1.

amino acids 1-56

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FIGURE 187

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTG
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCATCCTTTTTTTAGAAACACAAAT
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGGAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA
CCCAGCAAATTTGATTTTGAATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
AAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAG
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT
TTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGAAACGTTACAGTACTCATACACCCC
TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCTCGCT
GTCCAGCTTCGACCAGGATTGAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGAATTCATGGAGGAATGGGGTTATATGTGCAGATGGAAAACTGATGCCAACA
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGAGTGTCTGTGAGAA

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FIGURE 188

MPLPPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHANLILYIGNEFDKRFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGETSLTQQESLS
RTIPDPKTVIEYEDVRTTDICAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP
QLQDLDPQAQHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

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FIGURE 189

ATGTGCTGCTGGCCGCTGCTCCTGCTGTGGGGGCTGCTCCCCGGGACGGCGGGCGGGGGGCTCG
GGCCGAACCTATCCGCACCGGACCCTCCTGGACTCGGAGGGCAAGTACTGGCTGGGCTGGAGC
CAGCGGGGCAGCCAGATCGCCTTCCGCCTCCAGGTGCGCACTGCAGGCTACGTGGGCTTCGGC
TTCTCGCCCCACCGGGGCCATGGCGTCCGCCGACATCGTCGTGGGCGGGGTGGCCCACGGGCGG
CCCTACCTCCAGGATTATTTTACAAATGCAAATAGAGAGTTGAAAAAAGATGCTCAGCAAGAT
TACCATCTAGAATATGCCATGGAAAATAGCACACACACAATAATTGAATTTACCAGAGAGCTG
CATAATGTGACATAAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGGCCTAC
CACCATGAAGATGCAGGAGAAGCTGGTCCCAAGTACCATGACTCCAATAGGGGCACCAAGAGT
TTGCGGTTATTGAATCCTGAGAAAAGTAGTGTGCTATCTACAGCCTTACCATACTTTGATCTG
GTAAATCAGGACGTCCCCATCCCAACAAAGATACAACATATTGGTGCCAAATGTTTAAAGATT
CCTGTGTTCCAAGAAAAGCATCATGTAATAAAGGTTGAGCCAGTGATACAGAGAGGCCATGAG
AGTCTGGTGCACCACATCCTGCTCTATCAGTGCAGCAACAACCTTTAACGACAGCGTTCTGGAG
TCCGGCCACGAGTGCTATCACCCCAACATGCCCGATGCATTCCCTCACCTGTGAAACTGTGATT
TTTGCCTGGGCTATTGGTGGAGAGGGCTTTTCTTATCCACCTCATGTTGGATTATCCCTTGGC
ACTCCATTAGATCCGCATTATGTGCTCCTAGAAGTCCATTATGATAATCCCACTTATGAGGAA
GGCTTAATAGATAATTCTGGACTGAGGTTATTTTACACAATGGATATAAGGAAATATGATGCT
GGGGTGATTGAGGCTGGCCTCTGGGTGAGCCTCTTCCATACCATCCCTCCAGGGATGCCTGAG
TTCCAGTCTGAGGGTCACTGCACTTTGGAGTGCCTGGAAGAGGCTCTGGAAGCCGAAAAGCCA
AGTGGAATTCATGTGTTTGCTGTTCTTCTCCATGCTCACCTGGCTGGCAGAGGCATCAGGCTG
CGTCATTTTCGAAAAGGGAAGGAAATGAAATTACTTGCCTATGATGATGATTTTGACTTCAAT
TTCCAGGAGTTTCAGTATCTAAAGGAAGAACAACAATCTTACCAGGAGATAACCTAATTACT
GAGTGTGCTACAAACAGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAAGCACCAGGAGT
GAAATGTGTCTCTCATACCTTCTTTATTACCCAAGAATTAATCTTACTCGATGTGCAAGTATT
CCAGACATTATGGAACAACCTTCAGTTCATTGGGGTTAAGGAGATCTACAGACCAGTCACGACC
TGGCCTTTCATTATCAAAAAGTCCCAAGCAATATAAAAACCTTTCTTTCATGGATGCTATGAAT
AAGTTTAAATGGACTAAAAAGGAAGGTCTCTCCTTCAACAAGCTGGTCCTCAGCCTGCCAGTG
AATGTGAGATGTTCCAAGACAGACAATGCTGAGTGGTCGATTCAAGGAATGACAGCATTACCT
CCAGATATAGAAAGACCCTATAAAGCAGAACCTTTGGTGTGTGGCACGTCTTCTTCTCTTCC
CTGCACAGAGATTTCTCCATCAACTTGCTTGTTTGCTTCTGCTACTCAGCTGCACGCTGAGC
ACCAAGAGCTTG**TGA**TCAAATTCCTGTTGGACTTGACAATGTTTTCTATGATCTGAACCTGTC
ATTTGAAGTACAGGTAAAGACTGTGTCCACTTTGGGCATGAAGAGTGTGGAGACTTTTCTTC
CCCATTTTCCCTCCCTCCTTTTCCCTTTCCATGTTACATGAGAGACATCAATCAGGTTCTCTT
CTCTTTCTTAGAAATACCTGATGTTATATACATGGTCAATAAAAATAAACTGGCCTGACTT
AAGATAACCATTTTAAAAAATTGGGCTGTCATGTGGGAATAAAAGAATTCTTTCTTCTCTAA
AAAAAAA

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FIGURE 190

MCCWPLLLLWGLLPGTAAGGSGRTYPHRTLLDSEGKYWLGWSQSGSQIAFRLQVRTAGYVGFG
FSPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTIIEFTREL
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGTKSLRLLNPEKTSVLSTALPYFDL
VNQDVPIPNKDTTYWCQMFKIPVFQEKHHVIKVEPVIQRGHESLVHHILLYQCSNNFNDSVLE
SGHECYHPNMPPDAFLTCTETVIFAWAIGGEGFSYPHVGLSLGTPLDPHYVLLEVHYDNPTYEE
GLIDNSGLRRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTLECLEEALEAEKP
SGIHVFAVLLHAHLAARGIRLRHFRKGKEMKLLAYDDDFDNFQEFQYLKEEQTILPGDNLIT
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLIYPRINLTRCASIPDIMEQLQFIGVKEIYRPVTT
WPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVLVSLPVNVRCSTDNAEWSIQGMTALP
PDIERPYPKAEPLVCGTSSSSSLHRDFSINLLVCLLLLSTLSTKSL

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 56-73, 378-393, 583-602

N-glycosylation sites.

amino acids 114-118, 247-251, 476-480, 517-521

N-myristoylation sites.amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,
316-322, 337-343, 342-348, 456-462, 534-540, 582-588**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474

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FIGURE 191

GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTTTGTCTTTATAACAT
TTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAAAATGAAGAAAATATGCAACTGGCTCAGG
CATATCTCAACCAGTTCTACTCTCTTGAAATAGAAGGGAATCATCTTGTTCAAAGCAAGAATA
GGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGACAGTGACTGGAA
AACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCC
AGTATGGCTACACCCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAATAAACTATA
CTCCGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTTAGAAGTGTGGAGCA
AAGTCACTCCACTAAAATTACCAAGATTTCAAAGGGGATTGCAGACATCATGATTGCCTTTA
GGACTCGAGTCCATGGTCCGTGTCCTCGCTATTTTGATGGTCCCTTGGGAGTGCTTGGCCATG
CCTTTCTCCTGGTCCGGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAAAGTGGACCA
AGGATGGAGCAGGATTCAACTTGTTTCTGTGGCTGCTCATGAATTTGGTCATGCACTGGGGC
TCTCTCACTCCAATGATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTGGATCCCAGAA
AATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG
TACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCTGTGACCCTGACTTGACTTTTGACG
CTATCACAACCTTCCGCAGAGAAGTAATGTTCTTTAAAGGCAGGCACCTATGGAGGATCTATT
ATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTCTGGCCATCTCTGCCAGCTGATC
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAAGTCTGGA
TGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAG
GACGTGTGAAGAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAACCTACTTCTTTG
TGGGCATTTGGTGCTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGA
GAGTGGTAAACACTTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAGGAT
TCTTCTTTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAAAGAATATTACCC
GAATCATGAGAACTAATACTTGGTTTCAATGCAAAGAACCAAGAACTCCTCATTTGGTTTTG
ATATCAACAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCT
TGTTTATTTTTTGGTATTGTTTCAATTTGCTGAAAAACACTTCTATTTATCAATTAAATTCATAGAC
CTAAAATAAACCTCAACAGGTCTTTTAATATAAATTCTGCTTCAAATAGATAAAACCATTCT
TTAACAAC

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FIGURE 192

MKRLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLLDDKI
REMQAFFGLTVTGKLDSENTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTIRIINYTPDMARAA
VDEAIQEGLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHAFPPGPGGL
GGDTHFDEDENWTKDGAGFNLFVAAHEFGHALGLSHSNDQTALMFPNYVSLDPRKYPLSQDD
INGIQSIYGGLPKVPAKPKEPTIPHACDPDLTFDAITTFRREVMFFKGRHLWRIYYDITDVEF
ELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDA
AVCDKTTRKTYFFVGIWCWRFDEMTQTMKGFPQRVVKHFPGISIRVDAAFQYKGFFFFSRGS
KQFEYNIKTKNITRIMRTNTWFQCKEPPKNSSFGFDINKEKAHSGGIKILYHKSLSLFIFGIVH
LLKNTSIYQ

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

N-myristoylation site.

amino acids 71-77, 205-211, 223-229

Hemopexin domain signature.

amino acids 171-202, 207-238, 318-334

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 213-223

Matrixins cysteine switch.

amino acids 89-97, 207-238

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FIGURE 193

CACAATCAGGTCCCATTCTATAGATGGGGAAACTGAGGCTTGAGGTCACATAGGCGTCGTTCA
AGGCTGGTATACCTGCACCCTCTCCCATGTGAACAACATGGTTCTGGGTAATGGGGGCTGTCA
TCCAGTCTCCTCCCTGCCCCTGCTGGTGCACCTTCCTGCCTCTGCTGGTGCACCTTCTGCCCCCT
ACTGGTATATTTGCTGCCTCTGCTGGGGCGCTTCCTGCCTCGGCTGGTGTATCTCCTGCCCCCT
GCTGGTGCACCTTCTGCCCCCGCTGATGCACCTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCT
GCTGGCACACTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCTGCTGGCGCACTTTCCTGCCCC
TGCTGGTGTATTTCTGCCCCTGCTGGTGTACTTCCTTCCCCTGCTGGTGCACCTTCCTGCCTC
TGCTGGCGCACTTCTTGCTCTCCAGGCCCTACCTTAGCCTCTCCCTCTTATATATGGAAGTCT
TCCCAGTTCACCTGACACTGGTAACAGGGACTCTGCTCTTGGTGTGCTGTCTGCCCTGGGGAT
GGGCATCTGTGTCTTCCTTTACTACTGCTGGCTCAGGACCCAGAGCTTTGAAGCATGTCCAGA
TGCAGGTCCGGGCACCAGAGTCTAAGGAGCCCCTACACCCACCAGGATTTTCCAATAAAGAGA
TGTTACCA

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FIGURE 194

MVLGNGGCHPVSSLPLL VHFLPLL VHFLPLL VYLLPLL GRFLPRL VYLLPLL VHFLPPL MHFL
PLL VHFLALL AHFLPLL VHFLALL AHFPAPAGVFPAPAGVLPSPAGALPASAGALLASPGPT

Signal peptide:

amino acids 1-39

N-myristoylation sites.

amino acids 4-10, 109-115, 116-122

Leucine zipper pattern.

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,
65-87, 66-88

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FIGURE 195

[illegible]

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FIGURE 196

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDERRYLN
AKKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLRCTLVYCTDLPPTSIIITFHNEARST
LLRTIRSVLNRTPTHLIREIILVDDFSNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADI
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWS
LHFQWEQLSPEQKARRLDPTPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEISFR
VWMCSSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYYAARPFAL
ERPFGNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQGNIRQRQKCLESQRQNNQET
PNLKLSPCAKVKGEDAKSQVWAFITYTQQILQEELCLSVITLFPVGVVLVLCCKNGDDRQQWTK
TGSHEHIAHLCLDTDMFGDGTENGKEIVVNPCESSLMSQHWDMVSS

Transmembrane domain:

amino acids 475-493

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 2-6

Tyrosine kinase phosphorylation sites.

amino acids 68-75, 401-409

N-myristoylation sites.

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532

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FIGURE 197

GCAGCTCACCTTCGCGAGCCGCGATGGGGGAAGACGACGCCGCTTCGGGCTGGCAGCAGGGGGCTCTCCGACC
CGTGGGCAGACTCAGTGGGAGTGCGACCCCGCACCACGGAGCGCCACATCGCCGTACACAAGCGGCTTGTGCTGG
CCTTCGCTGTGTCCCTCGTGGCATTGCTCGCGGTCACAATGCTCGCTGTGCTGCTCAGCCTGCGCTTCGACGAGT
GCGGGGCGAGTGCCACGCCAGGCGCGGACGGTGGCCCCCTCAGGCTTTCGGGAGCGCGCGGCAACGGGAGCCTCC
CTGGATCGGCCCCGGCGCAACCACCACGACGGCGGGGACTCCTGGCAGCCCCGAGGCGGGTGGGGTGGCCAGTCCGG
GGACCACGTCCGCCCCAGCCGCCGTGGAGGAGGAGCGGGAGCCGTGGGAGCCGTGGACGAGCTGCGCCTGTGCG
GCCACCTGAAGCCGCTGCACTACAATCTGATGCTCACCCTTCATGGAGAATTACCTTCTCCGGGGAGGTCA
ACGTGGAGATCGCGTGCCGGGAACGCCACCCGCTACGTAGTGTGACGCTTCCCGAGTGGCGGTGGAGAAAGTGC
AGCTGGCCGAGGACCGGGCGTTCGGGGCTGTCCCTGTAGCCGTTTCTTCTTACCCGCAAAACCCAGGTCTTAG
TGGTGGTGTGAATAGGACACTGGACGCGCAGAGGAATTACAATCTGAAGATTATCTACAACGCGCTCATCGAGA
ATGAGCTCCTGGGCTTCTTCCGACGCTCCTATGTGCTCCACGGGGAGAGAAGATTCTTGGTGTACTCAGTTTT
CGCTACACATGCCAGAAAGGCATTCTCTTGTGTTTGTATGAGCCAACTCTACAAGGCTACTTTCAAATCAGCATCA
AGCATCAAGCAACCTATTTATCTTATCTAATATGCCAGTGGAACTTCCGTGTTTGGGAAGATGGATGGGTTA
CGGATCACTTTTACAGACCCCTCTCATGTCCACATATTATTTAGCCTGGGCAATTTGCAACTTCACATACAGAG
AACTACCACCAAGAGTGGGGTGTAGTACGATTATATGAAGACCTGATGCTATCAGAAGAGGATCCGGGGACT
ATGCTCTCCATATAACAAAGAGATTAAAGAAATTTATGAAGACTACTTTAAAGTGCCCTATTCTTGCCAAAAC
TAGATCTTTAGCTGTGCTAAGCATCCGTATGCTGCTATGGAGAAGTGGGACTAAGTATTTTGTGGAACAAA
GAATACTGCTGGATCCCAGTGTTCATCTATTTCTTATTTGCTGGATGTCAACATGGTCTTGTTCATGAGATAT
GTCACCAAGTGGTTTGGTGACCTTGTGACGCTGTGTGGTGGGAAGACGTGTGGCTGAAGGAAGGGTTTGTCACT
ACTTTGAATTTGTTGGTACAGACTACCTCTATCTGGCTGGAACATGGAAAAGCAGAGGTTTCTGACCGATGTTT
TGCATGAAGTGATGCTGCTGGACGGTTTGGCCAGTTCCTATCCAGTATCACAGGAAGTGTGACGGCAACAGATA
TTGACAGGGTGTGACTGGATCGCATATAAAAGGGTGTGCTTTAATAAGAATGCTGGCTAATTTTATGGGCC
ATTCAGTTTCCAGAGGGGTTTGAAGATTATTTAAACATTCTAAGTATGGTAATGCAGCCAGAAATGATCTCT
GGAATACATTATCGGAGGCTTTAAAAAGAAATGGGAAATATGTAAATATACAAGAAGTAATGGATCAGTGGACAC
TCCAGATGGGTTATCCTGTTATCACCATCTTGGGAAACACAACAGCAGAAAATAGAATAATAATTACCCAACAGC
ATTTTATCTATGATATCAGTGCTAAACTAAAGCACTTAACTTCAGAATAACAGTTACCTGTGGCAGATTCCAT
TAACTATTGTGGTAGGAAATAGAAGCCATGTGCTTCAGAAGCAATTATTTGGGTGTCTAACAATCAGAGCACC
ACAGAATAACTTATTTGGACAAAGGAAGCTGGCTGTGGGGAACATCAATCAAACTGGCTATTTTAGAGTCAACT
ATGACCTAAGGAAGTGGAGATTATTAATTGATCAATTAATCCGGAATCATGAGGTCTTTCTGTCAAGTACCGAG
CGGGCTTGATCGATGATGCCTTCAGCCTAGCCAGGGCTGGCTATTTGCCTCAGAATATTCTCTGGAGATTATCA
GATACCTGTCTGAGGAGAAGGATTTTCTTCTTGGCATGCTGCCAGCCGAGCTCTTATCCTCTAGATAAATTAC
TGGACCGCATGGAAACTACAACATTTTCAATGAATATATTTTAAAGCAAGTTGCAACAACATATATCAAGCTTG
GGTGGCCGAAAAATAATTTAATGGATCTCTGTTCAGCATCCTACCAACATGAAGAACTACGTAGAGAAGTTA
TAATGCTGGCCTGCAGTTTGGCAACAAGCACTGTCAACAACAGGCATCAACACTTATTTAGATTGGATTCCA
GCAACAGGAACAGAATACCACTAAATGTTAGAGACATCGTATACTGTACAGGAGTGTCACTACTGGATGAGGATG
TCTGGGAATTCATATGGATGAAATTCATTCCACCACAGCAGTCTTCTGAGAAGAAAATATTATTGGAAGCCTTAA
CTTGCAAGTATGACAGGAATTTATTAACAGGCTTCTAAATCTGTCACTGAATCTGAGGTGGTGTGCTGGATCAAG
ATGCAATTGATGTCAATCCATGTAGCTCGAAATCCACATGGTTCGAGACCTTGCCCTGGAAGTTTTTCAGGGATA
AATGGAAGATATTAAATACCAGGTATGGAGAAGCATTGTTATGTATTCCAACTCATCAGTGGTGTACAGAAT
TTCTTAATACTGAAGGTGAAGTCAAGAGCTCAAGAACTCATGAAAACTATGATGGGTAGCTGTGCTTCTT
TCTCAGGAGCTGTGGAAGCTGCGAAGCCAATGTGCGCTGGAAAATGCTTTACCAAGACGAGCTTTTCCAATGGT
TAGGAAAAGCTCTAAGACACTAAATATATGTATCTTATAAACAAACAATTCAACTCAGAAGTTTATGAGAAGACAC
GCTTTTTGTGGAATGAGGAAATGTACTACCTAGAAAATGGCCAGATTTTCAGTGTTAACGTGTGGGAGGAATTT
TTTTTTTTAGTTTTTATTTTTTGGTTTTGGGGGATATTTTTTATTTGTTTCATTCTGTTCTGTTCTCTAC
TGGGTGTTCTCTCTAAAGAACTCTTGCAAGTGAACTAGCCATGATTGCTTCAGCTGTACATTCTTGCTGTA
CAGGACCAATATGATAGTGATGCTGTTGATGTTACAGTCAATTTGGAAGAAACATATTCAGAATATCTGTGCAT
GGATATATTGCTGCTGCTGTTCAGCATGCTTATTTCAAACGTCCAGTGTGTGTGTAATATGTGTACACC
TAGGATGGGCATTATGCAAAAGCACAAAGATTATATGACAACTCAGTATTGCAATGAAAGAAAACTAAAAACA
GAAATGATATTCTCAATTTTGGGCAATGTGAGAGGTAAAATAGCCCTTGACATGATGAACATCACTTATTTAGC
ACTTGGATTGTCTGGCAATGATTACTGTGTTGCTAACTCATTTTCTTTGAGTTAAAGCTGTGTATACATTTAAA
AGGCATATAGATAGTGTATGCATATGTATGTACATAGGGAAGCCCCATATGTATATAGTATGTTGTACTATGC
ACATGTACAAAGAATGTCTTCAGATCAAAGAAAATTTATCTCTTTTATAAAGTAAAGACAGTTGCAAAAGGCT
TCAAGGAATTTATCTCAACATTATCTTCTATGTCCTAAGTAACTTCTCAACTGTTATGAATTTTTCATCTAC
TTCTGAACAGTGGTCTATTCTGCTACATGAAGATGAATACAAACAAAATTTTTGTATAAAGTCCCAAAAAAAA
AAAAA

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FIGURE 198

MGEDDAALRAGSRGLSDPWADSVGVRPRTTERHIAVHKRLVLAFAVSLVALLAVTMLAVLLSL
 RFDECGASATPGADGGPSGFPERGGNGSLPGSARRNHHAGGDSWQPEAGGVASPGTTSAQPPS
 EEEREPEWEPWTQLRLSGHLKPLHYNLMLTAFMENFTFSGEVNVEIACRNATRYVVLHASRVAV
 EKVQLAEDRAFGAVPVAGFFLYPQTQVLVVVLNRTLDAQRNYNLKIIYNALIENELLGFFRSS
 YVLHGERRFLGVTQFSPTHARKAFPCFDEPIYKATFKISIKHQATYLSLSNMPVETSVFEEDG
 WVTDFHSQTPLMSTYYLAWAICNFTYRETTTKSGVVVRLYARPD AIRRGSGDYALHITKRLIE
 FYEDYFKVPYSLPKDLLAVPKHPYAAMENWGLSIFVEQRILLDPSVSSISYLLDVTMVIVHE
 ICHQWFGDLVTPVWVEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLTDVLHEVMLLDGLAS
 SHPVSQEV LQATDIDRVFDWIAYKKGAALIRMLANFMGHSVFQRLQDYLTIHKYGNAARNDL
 WNTLSEALKRNGKYVNIQEVMDQWTLQMGYPVITILGNTTAENRIIITQQHFIYDISAKTKAL
 KLQNNSYLWQIPLTIVVGNRSHVSSEAIWVSNKSEHHRITYLDKGSWLLGNINQTYFRVNY
 DLNRWRLLDQLIRNHEVLSVSNRAGLIDDAFSLARAGYLPQNIPLEIIRYLSEEKDFLPWA
 ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNNFNGLVQASYQHEELRREVIM
 LACSFNGKHCHQQASTLISDWISSNRNRIPLNVRDIVYCTGVSLLEDVWEFIWMKFHSTTAV
 SEKKILLEALTCSDDRNLLNRLNLSLNSEVVLDQDAIDVIIHVARNPHGRDLAWKFFRDKWK
 IILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAAASFRAVETVEANVRWKM
 LYQDELFWLGKALRH

Transmembrane domain:

amino acids 44-63

N-glycosylation sites.amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,
634-638, 649-653, 663-667, 684-688, 800-804, 906-910**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 362-366

Tyrosine kinase phosphorylation site.

amino acids 520-528

N-myristoylation sites.amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,
825-831, 987-993**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 437-447

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FIGURE 199

GCGCCCGGCGCAGCTCGGCCAGAGCGACCGCGGGGCTGAGCGCGCTCCGCCAGGGGGCTCCGGAAGCTGCCCC
GGCCCGGGGCTCCTCCCTCGCTCCCGCTTCCCCTTTCTCGCTACCGCCGCCCTCCTTCCCCAGCTCCCTCGCC
GTCCGCCCCCCCCACAGCCAGCGGCTCCGCGCCCCCTGCAGCCACGATGCCCCGCGGCCGCGCCGCGCGGG
ACTCCGCGGGATCTCGCTGTTCTCGCTCTGCTCCTGGGGAGCCCGCGGCAGCGCTGGAGCGAGATGCTCTTCC
CGAGGGAGATGCTAGCCCTTTGGGTCTTACCTCCTGCCCTCAGGAGCCCCGGAGAGAGGAGCTCCTGGCAAAGA
GCACCTGAAGAGAGAGTGGTAACAGCGCCCCCAGTTCTCAGAGTCGGCGGAAGTGTGGGCGAGCTGGTGCT
GGATGGGACCGCACCTCTGCACATCAGGACATCCAGCCCTGTACCGCTGCTTCCAGAGGAGGCCCGCCCCAA
GCACGCTTGCCCCCAAGAAGAACTGCCTTCGCTCAAGCAGGTGAACTCTGCCAGGAAGCAGCTGAGGCCAA
GGCCACCTCCGCGAGCCTGTCCAAAGGGCAGGGTCCCAGCCAGCGTCCCAGGGCCTAGATCTCCTCTCCTCCTC
CACGGAGAAGCCTGGCCACCGGGGACCCGGACCCATCGTGGCCTCCGAGGAGGCATCAGAAGTGCCCCCTTG
GCTGGATCGAAAGGAGAGTGGGTCCCTACAACACCCGCACCCCTGCAAATCTCCCCCTTCACTTCGCAGCCCTA
TGTGGCCACACACTCCCCAGAGGCCAGAACCCGGGGAGCCTGGGCCTGACATGGCCAGGAGGCCCCCCAGGA
GGACACCAGCCCCATGGCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGA
GACCACTACCTCCACCATTATCACCACCACGGTCATCACCACCGAGCAAGCACCAGCTCTCTGCAGTGTGAGCTT
CTCCAACTCCTGAGGGGTACATTGACTCCAGCGACTACCCACTGCTGCCCTCAACAATTTCTGGAGTGCACATA
CAACGTGACAGTCTACACTGGCTATGGGGTGGAGCTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTGT
CTCCATCCGCGGGGTGGACGGCCCTACCTGACCGTCTGGCCAAACCAGACACTCCTGGTGGAGGGGCAGGTAAT
CCGAAGCCCCACCAACACCATCTCCGTCTACTTCCGGACCTTCCAGGACGACGGCCTTGGGACCTTCCAGCTTCA
CTACCAGGCCTTCATGCTGAGCTGCAACTTTCCCCCGCGGCCTGACTCTGGGGATGTACGGTGATGGACCTGCA
CTCAGTGGGGTGGCCCACTTTCACTGCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCATCAA
TGCCTCCAAGCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGGCAGTGCACAATGCCAC
CATCGGCCGCGTCTCTCCCCAAGTTACCTGAAAACACAAATGGGAGCCAATTCTGCATCTGGACGATTGAAGC
TCCAGAGGGCCAGAAGCTGCACCTGCACTTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTACAG
CGGGCAGACCAACAAGTCAGCTCTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCTTTGAGGGCCTGCTGAG
CGAAGGCAACACCATCCGCATCGAGTTCAGTCCGACCGAGCCCGGGCGCCTCCACCTTCAACATCCGATTGGA
AGCGTTTGAGAAAGGCCACTGCTATGAGCCCTACATCCAGAATGGGAACTTCACTACATCCGACCCGACCTATAA
CATTGGGACTATAGTGGAGTTCACCTGCGACCCCGGCCACTCCCTGGAGCAGGGCCCCGGCCATCATCGAATGCAT
CAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGTGGGGAGCTCTCTGCTGT
GGCTGGGGTGGTATTGTCCCCAACTGGCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGT
GGGAGAAGAGAAACGGATCTTCTTAGATATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGA
TGGCGACGAGGTGATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCTCCAC
GCCAGACTTAACCATCCAGTTCATTCCGAGCCCTGCTGGCCTCATCTTTGGAAAGGGCCAGGGATTTATCATGAA
CTACATAGAGGTATCAAGGAATGACTCCTGCTCGGATTTACCCGAGATCCAGAATGGCTGGAAAACCACTTCTCA
CACGGAGTTGGTGGGGGAGCCAGAATCACCTACCAGTGTGACCCCGGCTATGACATCGTGGGGAGTGACACCT
CACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCCATTTTGTGAGAAAATTATGTACTGCACCGACCCCGG
AGAGGTGGATCACTCGACCCGCTTAATTTCCGATCCTGTGCTGCTGGTGGGGACCACCATCCAATACACCTGCAA
CCCCGTTTTTGTGCTTGAAGGGAGTTCTCTTCTGACCTGTACAGCCGTGAAACAGGGACTCCCATCTGGACGTC
TCGCCTGCCCCACTGCGTTTTCGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCTGAAAATGGATACCAAT
CCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTCATGTGCTACGAAGGCTTTGAGCTCATGGGTGA
AGTGACCATCCGCTGCATCCTGGGACAGCCATCCCACTGGAACGGGCCCCCTGCCCGTGTGTAAAGTTAATCAAGA
CAGTTTTGAACATGCTTTAGAAGCAGAAGCGGCAGCAGAGACGTCGCTGGAAGGGGGGAACATGGCCCTGGCTAT
CTTCATCCCGGTCTCATCATCTCCTTACTGCTGGGAGGAGCCTACATTTACATCACAAGATGTCGCTACTATTC
CAACCTCCGCTGCCTCTGATGTACTCCACCCCTACAGCCAGATCACCGTGGAAACCGAGTTTGACAACCCCAT
TTACGAGACAGGGGAAACAGAGAGTATGAGGTTTCTATCTAAAGAGAGCTACACTTGAGAAGGGGACTTGTGAA
CTCAACCACAATCTCCTCGAGACATTATCCAGAGACCATGTGGCACTTGATTGAAACCCAGAAATGTCGACTGT
CTTTTGTAGACTCTTTATCAAAGTTTACTGTTTTCTTCCCTGTATTATTATATTTAAAGTGAAAAAAA
AAAAAAA

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FIGURE 200

MPAARPPAAGLRGISLFLALLLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKEHPE
ERVVTAPPSSSSQSAEVLGELVLDGTAPSAHHDIPALSPLLPEEARPKHALPPKKKLPSLKQVN
SARKQLRPKATSAATVQRAGSQPASQGLDLLSSSTEKPGPPGDPDPDIVASEEASEVPLWLDRK
ESAVPTTPAPLQISPFTSQPYVAHTLPQRPEPGEPPGDMAQEAPQEDTSPMALMDKGENELTG
SASEESQETTTSTIITTTVITTEQAPALCSVSFSNPEGYIDSSDYPLLPLNNFLECTYNVTYV
TGYGVELQVKS VNLS DGELLSIRGVDGPTLTVLANQTLLEGGVQVIRSPTNTISVYFRTFQDDG
LGT FQLHYQAFMLSCNFPRRPDSGDVTVM DLHSGGVAHFHCHLGYELQGAKMLTCINASKPHW
SSQEPICSAPCGGAVHNATIGRVLSPSYPENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKD
RMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASFNIRFEAFEKGHC
YEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPATIECINVRDPYWNDTEPLCRAMCGG
ELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEKRIFLDIQFLNLSNSDILTIYDGDEVMPHI
LGQYLGNSGPQKLYSSTPDLTIQFHS DPAGLIFGKGQGFIMNYIEVSRNDSCSDLPEIQNGWK
TTSHTELVRGARITYQCDPGYDIVGSDTLTCQWDLWS SDPPFCEKIMYCTDPGEVDHSTRLI
SDPVLLVGTTIQYTCNPGFVLEGSSLLTCYSRETGTPIWTSRLPHCVSEESLACDNPGLPENG
YQILYKRLLYPGESLTFMCYEGFELMGEVTIRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA
AAETSLEGGNMALAI FIPVLIISLLLGAYIYITRCRYYSNLRPLMYSHPYSQITVETEFDN
PIYETGETREYEVS I

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 893-915

N-glycosylation sites.amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,
514-518, 576-580, 618-622, 674-678, 742-746**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 188-192

N-myristoylation sites.amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,
629-635, 695-701, 723-729, 766-772, 877-883, 953-959**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 383-394

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FIGURE 201

GATGGCTACGGCAGGGGGTGGCTCTGGGGCTGACCCGGAAGTCGGGGTCTCCTTCGCCTTCT
GTCTTTCTGCGTCCTACTAGCAGGTTTGTGTCAGGGGAACTCAGTGGAGAGGAAGATATATAT
CCCCTTAAATAAAACAGCTCCCTGTGTTGCGCTGCTCAACGCCACTCATCAGATTGGCTGCCA
GTCTTCAATTAGTGGAGACACAGGGGTTATCCACGTAGTAGAGAAAGAGGAGGACCTACAGTG
GGTATTGACTGATGGCCCCAACCCCTTACATGGTTCTGCTGGAGAGCAAGCATTTTACCAG
GGATTTAATGGAGAAGCTGAAAGGGGAGAACCAGCCGAATTGCTGGTCTTGCAGTGTCCTTGAC
CAAGCCCAGTCTGCTCAGGCTTCTCTCCTAGTGTACAGTGCCCAAATGATGGGTTTGGTGT
TTACTCCAATTCTATGGGCCAGAGTTTGCTCACTGCAGAGAAATACAGTGGAATTTCGCTGGG
CAATGGTTTGGCTTATGAAGACTTTAGTTTCCCCATCTTTCTTGAAGATGAAAATGAAAC
CAAAGTCATCAAGCAGTGCTATCAAGATCACAACTGAGTCAGAATGGCTCAGCACCAACCTT
CCCCTATGTGCCATGCAGCTCTTTTACACATGCATGCTGTCATCAGCACTGCCACCTGCAT
GCGGCGCAGCTCCATCCAAAGCACCTTCAGCATCAACCCAGAAATCGTCTGTGACCCCTGTCT
TGATTACAATGTGTGGAGCATGCTAAAGCCTATAAATACTGGGACATTAAAGCCTGACGA
CAGGGTTGTGGTTGCTGCCACCCGGCTGGATAGTCGTTTCTTTTCTGGAATGTGGCCCCAGG
GGCTGAAAGCGCAGTGGCTTCTTTGTACCCAGCTGGCTGCTGCTGAAGCTTTGCAAAAGGC
ACCTGATGTGACCACCCTGCCCCGCAATGTCATGTTTGTCTTTTCAAGGGGAACTTTTGA
CTACATTGGCAGCTCGAGGATGGTCTACGATATGGAGAAGGGCAAGTTTCCCGTGCAGTTAGA
GAATGTTGACTCATTGTGGAGCTGGGACAGGTGGCCTTAAGAACTTCATTAGAGCTTTGGAT
GCACACAGATCCTGTTTCTCAGAAAAATGAGTCTGTACGGAACCAGGTGGAGGATCTCCTGGC
CACATTGGAGAAGAGTGGTGCTGGTGCTCCCTGCTGTCATCCTCAGGAGGCCAAATCAGTCCCA
GCCTCTCCCACCATCTTCCCTGCAGCGATTTCTTCGAGCTCGAAACATCTCTGGCGTTGTTCT
GGCTGACCACTCTGGTGCCTTCCATAACAAATATTACCAGAGTATTTACGACACTGCTGAGAA
CATTAAATGTGAGCTATCCCGAATGGCTGAGCCCTGAAGAGGACCTGAACTTTGTAACAGACAC
TGCCAAGGCCCTGGCAGATGTGGCCACGGTGTGGGACGTGCTCTGTATGAGCTTGCAGGAGG
AACCAACTTCAGCGACACAGTTTCAAGGCTGATCCCCAAACGGTTACCCGCTGCTCTATGGGTT
CCTGATTAAAGCCAACAACATCATGGTTCCAGTCTATCCTCAGGCAGGACCTAAGGTCCTACTT
GGGTGACGGGCTCTTCAACATTACATCGCTGTCTCCAGCCCCACCAACACCACTTATGTTGT
ACAGTATGCCTTGGCAAATTTGACTGGCACAGTGGTCAACCTCACCCGAGAGCAGTGCCAGGA
TCCAAGTAAAGTCCCAAGTGAACAAGGATCTGTATGAGTACTCATGGGTCCAGGGCCCTTT
GCATTCTAATGAGACGGACCGACTCCCCGGTGTGTGCGTTCTACTGCACGATTAGCCAGGGC
CTTGTCTCCTGCCTTTGAACTGAGTCAGTGGAGCTCTACTGAATACTCTACATGGACTGAGAG
CCGCTGGAAAGATATCCGTGCCCCGATATTTCTCATCGCCAGCAAAGAGCTTGAGTTGATCAC
CCTGACAGTGGGCTTCGGCATCCTCATCTTCTCCCTCATCGTCACCTACTGCATCAATGCCAA
AGCTGATGTCCTTTTCATTGCTCCCCGGGAGCCAGGAGCTGTGTCATACTGAGGAGGACCCCCA
GCTTTTCTTGCCAGNTCAGCAGTTTCACTTCCCTAGAGCATCTGTCCCACTGGGACACAACCACT
AATTTGTCACTGGAACCTCCCTGGGCCTGTCTCAGATTGGGATTAACATAAAAGAGTGGAAC
ATCCAAAAGAGACAGGGAGAAATAAATAAATTGCCTCCCTTCCCTCCGCTCCCTTTCCCATCA
CCCCTTCCCATTTCCTCTTCTTCTACTCATGCCAGATTTTGGGATTACAAATAGAAGCT
TCTTGCTCCTGTTTAACTCCCTAGTTACCCACCCTAATTTGCCCTTCAGGACCCTTCTACTTT
TTCCTTCCCTGCCCCTGTACCTCTCTGCTCCTCACCCCAACCCCTGTACCCAGCCACCTTCCCT
GACTGGGAAGGACATAAAAGGTTTAAATGTCAGGGTCAAACCTACATTGAGCCCCCTGAGGACAGG
GGCATCTCTGGGCTGAGCCTACTGTCTCCTTCCCACTGTCCTTTCTCCAGGCCCTCAGATGGC
ACATTAGGGTGGGCGTGCTGCGGGTGGGTATCCACCTCCAGCCACAGTGCTCAGTTGTACT
TTTTATTAAGCTGTAATATCTATTTTTGTTTTTGTCTTTTTCCTTTATTCTTTTGTAAATAT
ATATATAATGAGTTTCATTAAATAGATTATCCC

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FIGURE 202

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQIGCO
SSISGDTGVIHVVEKEEDLQWVLTGDPNPPYMVLLSKHFTRDLMEKCLKGRTSRIAGLAVSLT
KPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLDENET
KVIKQCYQDHNLSQNGSAPTFPLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLS
DYNVWSMLKPINTTGTCLKPDDRVVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKA
PDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFRLARNISGVVL
ADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFVTD TAKALADVATVLGRALYELAGG
TNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSPTNTTYVV
QYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARA
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAK
ADVLFIAPREPGAVSY

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 671-692

N-glycosylation sites.

amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,
573-577, 580-584, 612-616

Glycosaminoglycan attachment site.

amino acids 404-408

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 232-236

N-myristoylation site.

amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582

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FIGURE 203

GCTAGACCGAGCCCTGGGAGGCTACGGGCTCCCCGGAAACCCTGCCAGGGGAGCCGGGTTTT
GAGCTCAGGCGCCTCTAGCGGCGGCCCCAGAAATCTGACTCGCGAGGCCAGAGTTGCAGGGA
CTGAATAGCAAACCTGAGGCTGAGTAGGGAACAGACCATGAGGTCAGTGCAGATCTTCCTCTCC
CAATGCCGTTTGTCTCTTCTACTAGTTCCGACAATGCTCCTTAAGTCTCTTGGCGAAGATGTA
ATTTTTACCCCTGAAGGGGAGTTTGACTCGTATGAAGTCACCATTCCTGAGAAGCTGAGCTTC
CGGGGAGAGGTGCAGGGTGTGGTCAGTCCCGTGTCTTACCTACTGCAGTTAAAAGGCAAGAAG
CACGTCTCCATTTGTGGCCCAAGAGACTTCTGTTGCCCGACATCTGCGCGTTTTCTCCTTC
ACAGAACATGGGGAACCTGCTGGAGGATCATCCTTACATACCAAAGGACTGCAACTACATGGGC
TCCGTGAAAGAGTCTCTGGACTCTAAAGCTACTATAAGCACATGCATGGGGGGTCTCCGAGGT
GTATTTAACATTGATGCCAAACATTACCAAATTGAGCCCTCAAGGCCTCTCCCAGTTTTGAA
CATGTCGTCTATCTCCTGAAGAAAGAGCAGTTTGGGAATCAGGTTTGTGGCTTAAGTGATGAT
GAAATAGAATGGCAGATGGCCCCCTTATGAGAATAAGGCGAGGCTAAGGGACTTTCCTGGATCC
TATAAACACCCAAAGTACTTTGGAATTGATCCTACTCTTTGATCAAAGTAGGTATAGGTTTGTG
AACAACAATCTTTCTCAAGTCATACATGATGCCATTCTTTTACTGGGATTATGGACACCTAC
TTTCAAGATGTTTCGTATGAGGATACACTTAAAGGCTCTTGAAGTATGGACAGATTTTAAACAA
ATACGCGTTGGATATCCAGAGTTAGCTGAAGTTTTAGGCAGATTTGTAATATATAAAAAAGT
GTATTAATGCTCGCCTGTCATCAGATTGGGCACATTTATATCTTCAAAGAAAATATAATGAT
GCTCTTGTCATGGTCGTTTGGAAAAGTGTGTTCTCTAGAATATGCTGGATCAGTGAGTACTTTA
CTAGATACAAATATCCTTGCCCCTGCTACCTGGTCTGCTCATGAGCTGGGTCATGCTGTAGGA
ATGTCACATGATGAACAATACTGCCAATGTAGGGGTAGGCTTAATTGCATCATGGGCTCAGGA
CGCACTGGGTTTAGCAATTGCAGTTATATCTCTTTTTTAAACATATCTCTTCGGGAGCAACA
TGCTAAATAATATCCCAGGACTAGGTTATGTGCTTAAGAGATGTGGAAACAAATTTGTGGAG
GACAATGAGGAATGTGACTGTGGTTCCACAGAGGAGTGTGAGAAAGATCGGTGTTGCCAATCA
AATTGTAAGTTGCAACCAGGTGCCAAGTGTAGCATTGGACTTTGCTGTGATGATTGTGCGGTTT
CGTCCATCTGGATACGTGTGTAGGCAGGAAGGAAATGAATGTGACCTTGCAGAGTACTGCGAC
GGGAATTCAAGTTCTGCCCCAAATGACGTTTATAAGCAGGATGGAACCCCTTGCAAGTATGAA
GGCCGTTGTTTCAGGAAGGGGTGCAGATCCAGATATATGCAGTGCCAAAGCATTTTTGGACCT
GATGCCATGGAGGCTCCTAGTGAGTGCTATGATGCAGTTAACTTAATAGGTGATCAATTTGGT
AACTGTGAGATTACAGGAATTCGAAATTTTAAAAAGTGTGAAAGTGCAAATTCATATGTGGC
AGGCTACAGTGATATAAATGTTGAAACCATCCCTGATTTGCCAGAGCATACGACTATAATTTCT
ACTCATTTACAGGCAGAAAATCTCATGTGCTGGGGCACAGGCTATCATCTATCCATGAAACCC
ATGGGAATACCTGACCTAGGTATGATAAATGATGGCACCTCCTGTGGAGAAGGCCGGGTATGT
TTTAAAAAAATTTGCGTCAATAGCTCAGTCCTGCAGTTTGACTGTTGCCTGAGAAATGCAAT
ACCCGGGGTGTGTTGCAACAACAGAAAAAAGTCCACTGCATGTATGGGTGGGCACCTCCATT
TGTGAGGAAGTGGGGTATGGAGGAAGCATTGACAGTGGGCCTCCAGGACTGCTCAGAGGGGCG
ATTCCTCGTCAATTTGGGTTGTGTCCATCATAATGTTTCGCCTTATTTTATTAATCCTTTCA
GTGGTTTTTGTGTTTTTCCGGCAAGTGATAGGAAACCACTTAAACCCAAACAGGAAAAAATG
CCACTATCCAAAGCAAAAAGTGAACAGGAAGAATCTAAAACAAAAAGTGTACAGGAAGAATCT
AAAACAAAAAGTGGACAGGAAGAATCTGAAGCAAAAAGTGGACAGGAAGAATCTAAAGCAAAA
ACTGGACAGGAAGAATCTAAAGCAAACATTGAAAGTAAACGACCCAAAGCAAAGAGTGTCAAG
AAACAAAAAAGTAAACGGGCAATCCATACTCATTAGTAACACAGGCTCATTATTTAAACCA
GCTAATCATTTATCCAAAGGCTTTCATTCTTCTCCCAATATTTTTTACTTTAATTTTTCCC
ACAAGTTTTGATCAGCAAATAACAGCATTCTTGTTTTGGAAACAAAA

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FIGURE 204

MRSVQIFLSQCRLLLLLVPTMLLKSLGEDVIFHPEGEFDSYEVTIPEKLSFRGEVQGVVSPVS
YLLQLKGKKHVLHLWPKRLLLPRHLRVFSFTEHGELLEDHPYIPKDCNYMGSVKESLDSKATI
STCMGGLRGVFNIDAKHYQIEPLKASPSFEHVYLLKKEQFGNQVCGLSDDDEIEWQMAPYENK
ARLRDFPGSYKHPKYLELILLFDQSRVRFVNNNLSQVIHDAILLTGIMDTYFQDVRMRIHLKA
LEVWTDNFNKIRVGYPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRKYNDALAWSFGKVCSL
EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGLNCIMGSGRTGFSNCSYISF
FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDGSGTEECQKDRCCQSNCKLQPGANCSI
GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGTTPCKYEGRCFRKGCRSRY
MQCQSIFGPDAMEAPSECYDAVNLIQDQFGNCEITGIRNFKKCESANSICGRLQCINVETIPD
LPEHTTIISTHLQAENLMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNCVNSSVLQ
FDCLPEKCNTRGVCNNRNKCHCMYGWAPPFCEEVGYGGSIDSGPPGLLRGAIPSSIWVVSIIIM
FRLILLILSVVFVFRQVIGNHLKPKQEKMPLSKAKTEQEESESKTKTVQEESESKTKTGQEESEAK
TGQEESEKAKTGQEESESKANIESKRPKAKSVKKQKK

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 684-705

N-glycosylation sites.

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

N-myristoylation sites.amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,
472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,
758-764, 767-773**Amidation site.**

amino acids 69-73

Disintegrins proteins

amino acids 429-479

EGF-like domain proteins

amino acids 650-662

Neutral zinc metalloproteases, zinc-binding region proteins

amino acids 335-345

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FIGURE 205

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGGAAGGTTGAATGGGGTAGAAGGCCTG
TTGTGGAGGGAAACCACCCATCCTCCTGCCTCCCACCACCACCATCATCCTGGCTGGACGGAG
AGGGTGACGGGGGCTGGGAAGGGGCAGCTCATGTTTCAGGTTTCCAGGAGGGGCTACCTGTTGA
CTGTCTTTGCAGGAAGAAGAAAACACCTGAGTGACCAGATGTCCCAGCTCCAGGTGCCTTGCC
AGATGGCCAGAACCACACCTCTTGAAGAGTGACAGTGCTGTGGAGCATGGTTTCTGCACACCT
GGAATGACTGGAACCCCAAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA
ACAGAAGGCTGTGGACCACCTGTCGAGATGGAGAAGTCCTTCTGAGGCTATCCAAACACGGAC
CAGGCCATGAGACCCCGATGACCATCCCTGAATTTTTTCGAGAGTCAGTCAACCGATTTGGAA
CTTATCCAGCCCTCCCATCCAAGAATGGCAAAAAGTGGGAATTTCTGAATTTCAACCAGTACT
ATGAGGCTTGTGCGAAGGCTGCAAAATCCTTGATCAAGCTGGGTTTGGAGCGTTTCCACGGAG
TTGGTATCCTGGGGTTTAACTCTGCAGAGTGGTTTATCACTGCTGTTGGTGCCATCCTAGCCG
GGGGTCTTTGTGTTGGTATTATGCCACCAACTCTGCCGAGGCTTGTCAATATGTCATCACTC
ATGCCAAAGTGAACATCTTGCTGGTTGAGAATGATCAACAGTTACAGAAAATCCTTTTCGATTC
CACAGAGCAGCCTAGAGCCCTAAAAGCGATCATCCAGTACAGACTGCCAATGAAGAAGAACA
ACAACCTTGTAATCTTGGGATGATTTTCATGGAACCTTGGCAGAAGTATCCCTGACACCCAACTGG
AGCAGGTCATCGAGAGCCAGAAGGCGAATCAATGCGCAGTGCTCATCTACACTTCAGGGACCA
CAGGCATACCCAAGGGAGTGATGCTCAGTCATGACAACATCACGTGGATTGCAGGAGCAGTGA
CAAAGGACTTTAACTGACAGACAAGCATGAGACGGTGGTTAGCTACCTCCCACTCAGCCATA
TTGCAGCACAGATGATGGACATCTGGGTACCCATAAAGATTGGGGCGCTCACATACTTTGCTC
AAGCAGATGCTCTCAAGGGCACCTTGGTAAGTACTCTAAAGGAGGTAAACCTACTGTCTTCA
TTGGAGTGCCTCAAATTTGGGAGAAGATACATGAGATGGTGAAGAAAAATAGTGCCAAGTCCA
TGGGCTTGAAGAAGAAGGCATTTCGTGTGGGCAAGAAACATTGGCTTCAAGGTCAACTCAAAAA
AGATGTTGGGGAAATATAATACTCCCGTGAGCTACCGCATGGCTAAGACTCTCGTGTTCAGCA
AAGTCAAGACATCCCTTGGCTTGGATCACTGTCACTCTTTTATCAGTGGGACTGCGCCCTCA
ACCAAGAGACTGCCGAGTTCTTTCTAAGCTTGGACATACCTATAGGCGAGTTGTATGGGTTGA
GTGAGAGCTCGGGACCCACACGATATCCAACCAGAATAACTACAGGCTTCTAAGCTGTGGCA
AGATCTTGACTGGGTGTAAGAATATGCTGTTCCAGCAGAACAAGGATGGCATTGGGGAGATCT
GCCTCTGGGGTAGGCACATCTTCATGGGCTATCTGGAAAGTGAGACTGAACTACAGAGGCCA
TCGATGATGAAGGCTGGCTACACTCTGGGGATCTGGGCCAGCTGGACGGTCTGGGTTTCTCT
ATGTCACCGGCCACATCAAAGAAATCCTTATCACTGCTGGTGGTGAAAATGTGCCCCCATTC
CTGTTGAGACCTTGGTTAAGAAGAAGATCCCCATCATCAGTAACGCCATGTTAGTAGGAGATA
AACTGAAGTTTCTGAGCATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATGAGCGGAGAAC
CTCTGGACAAGCTGAACTTCGAGGCCATCAACTTCTGTGCGGGTCTGGGCAGCCAGGCATCCA
CCGTGACTGAGATTGTGAAGCAGCAAGACCCCTGGTCTACAAGGCCATCCAGCAAGGCATCA
ATGCTGTGAACCAGGAAGCCATGAACAATGCACAGAGGATTGAAAAGTGGGTCTCTTGGAGA
AGGACTTTTCCATCTATGGTGGAGAGCTAGGTCCAATGATGAACTTAAGAGACATTTTGTAG
CCCAGAAATACAAAAACAAATTGATCACATGTACCCTGACTGCTTTGATGGAGCTGCTCTC
AGCTGTTCTGATGCCTTCAGCAGGAAGACCTCATTGCAATAAGTGAATGCTGCTCTAGGTAG
AAGCTCTCCCTGCTGTTTTTAAGAAGCCACATTCCTCATTGGTCAGTTTCTTGATTGTTTCGTC
TGTTGGAGAGGTGCTCCCTAGAAGAACCTGCCATACGTTTCAAAGCAATAAAATCACTGTATA
TCTTTCTAAGGACCTTCAAGTCATGACTCCAGGGAAGCCTATTGGGAAGTCTACTAAAACTG
CCTGATTTACAAGAAAGACCTGAACTTGTGGGCTCCCATTTGATTTTTTCTCCTCAGGGGAC
TCAGACATTAGAAAGAAAAAGCCTCACAGATTTGAAGAACTGGACCCCCAAATCAACTCACCT
GCCTGGAAGCAACTGGGAACCCCTTCCAATAAGTCCTGATAATAAGCACTTCAGGGTCCCAA
AAAAAAAAA

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FIGURE 206

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAASLIKGLERFHGVGILGF
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQLOKILSIPQSSLE
PLKAI IQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTSGTTGIPKG
VMLSHDNITWIAGAVTKDFKLTDKHETVVSYP LSHIAAQMMDIWVPIKIGALTYFAQADALK
GTLVSTLKEVKPTVFIGVPQIWEKIHVMVKNSAKSMGLKKKAFVWARNIGFKVNSKKMLGKY
NTPVSYRMAKTLVFSKVKTSGLDHCHSFISGTAPLNQETAEFFLSLDIPIGELYGLSESSGP
HTISNQNNYRLLSCGKILTGCKNMLFQQNKDGIGEICLWGRHIFMGYLESETETTEAIDDEGW
LHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKKKIPIISNAMLVGDKLKFLS
MLLTLKCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEIVKQQDPLVYKAIQQGINAVNQE
AMNNAQRIEKWVILEKDFSIYGGELGPMMLKRHFVAQKYKKQIDHMYH

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 65-86

N-glycosylation site.

amino acids 196-200

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 282-286

Tyrosine kinase phosphorylation sites.

amino acids 547-555, 608-616

N-myristoylation sites.amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,
253-259, 337-343, 371-377, 448-454, 536-542**Amidation site.**

amino acids 24-28

Putative AMP-binding domain signature.

amino acids 177-189

Putative AMP-binding domain proteins.

amino acids 173-190

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FIGURE 207

CCCACGCGTCCGCCCACGCGTCCGCGGACGCGTGGGGCCAGATCGCGGCCGCGCCAGCGCA
CCGTCCGGTCCACCCGCCAGCCCGCACAGCCGCGCCGCCGCGAGCGTTTCGTGAGCGGCGCT
CCGAGGATCAGGAATGGGGCTTCGGGCGCTGGGCGCGCTCCGAACCCGGCGACGTAAGAGCC
TGGGAGCGCCCGAGCCGCCCGGCTGCCCGGAGCCCCATCGCCTAGGACCGGGAGATGCTGGAA
ATGCAACCGCCTGTTCCCCGAGGAGCCGCTGCCCCGGGACCCCCCTGGCACTGTGCGCACCCCT
GGTCAGCAGCCCCCGGAGAAGACGGCGCCCCCAACGCCCCGACCCGCGTGGCCGTGGCAGCGCC
ACGCGAGCCCTCTAGGCGACCGCAGGGCCACAGCAGCTCAGCCGCCGGTGGCCCCCTCGGAAAC
CATGACCCCCGGCGCGGGGCCCATGGAGCCATGGCCTATAGGGTCTTGGCCGCGCGGGGCCAC
CTCAGCCGCGGAGGGCGCGCAGGCTGCTCTTCGCTTCACGCTCTCGCTCTCCTGCACCTTACC
TGTGTTACAGCTTCCTGTGCTGCTGCGACGACCTGGGTGCGAGCCGCTCCTCGGCGCGCCTC
GCTGCCTCCGCGGCCCCAGCGCGGGCGGCCAGAACTTCTCCAGAAGTCCCGCCCCCTGTGATC
CCTCCGGGCCGACGCCCAGCGAGCCGAGCGCTCCAGCGCGCCCGCGCCCGTGGCCGCC
CTCGCTCTCCGGTTCACCACTCCGGCTCACCAAGCTGGGTACCAAGCGGTTGCCCAAG
CCCTCATTTGTGGGCGTGAAGAAGGGGGGCACCCGGGCCGTGCTGGAGTTTATCCGAGTACACC
CGGACGTGCGGGCCTTGGGACGGAACCCCACTTCTTTGACAGGAACCTACGGCCGCGGGCTGG
ATTGGTACAGGAGCCTGATGCCCAGGACCCTCGAGAGCCAGATCACGCTGGAGAAGACGCCCA
GCTACTTTGTCACTCAAGAGGCTCCTCGACGCATCTTCAACATGTCCCGAGACACCAAGCTGA
TCGTGGTTGTGCGGAACCTGTGACCCGTGCCATCTCTGATTACACGCAGACACTCTCCAAGA
AGCCCGACATCCCGACCTTTGAGGGCCTCTCCTTCCGAACCCGACCCCTGGGCCGTGGTGACG
TGTCATGGAACGCCATCCGCATCGGCATGTACGTGCTGCACCTGGAGAGCTGGCTGCAGTACT
TCCCGCTAGCTCAGATTCATTCGTGCTGCGGAGCGACTCATCACTGACCCGGCCGCGGAGAG
TGGGGCGAGTCCAGGACTTCCTGGGCATTAAGAGATTTCATCACGGACAAGCACTTCTATTTC
ACAAGACCAAAGGATTCCCTTGCTTGAAAAAACAGAATCGAGCCTCCTGCCTCGATGCTTGG
GCAAATCAAAGGGGAGAACTCATGTACAGATTGATCCTGAAGTGATAGACCAGCTCCGAGAAT
TTTATAGACCGTATAATATCAAATTTTATGAAACCGTTGGGCAGGACTTCAGGTGGGAATAAG
CCCACGAAAGGAAAGGGCTCTCAAGGGCTCTTCTGCTCATCTCTTCCGTGAGATTTGCTCCCA
GACCCTCTGATCTCCCTCCAACAAACCCCTGGCTCCAGCCCCCTTCCCAACTTGAGTTGCATC
ATCTTGGAACCAGGAAGCCAGCTAAAGCCAAGAGACCAGAGAGTCCCTGCCACTAGTTTTCA
TCAGTCTGTTCAAGCAAAGTTGATCTGCTCCTGGCACGTCCAGTAAATTCAGAATCATTCTC
CTTTCTGCCATAAAGGGCCTTGGAGAATTGCTTTAAGAAGAGTGAATGTTCCAATGATGATA
GATATTATAAGCGATGATGGTTCTGTTGCTATGAACACAGCAGTCGGTCCCTGTCAATTGTCCA
CCCAGGAGTGGCCTTGTTAATTCCAAGTGGCATGTATCTTCCCTCTGAGCTTCATTTCTTCAA
GATGCTCTGGGTGGTGGGATGGGAGACCATCCTCAGCCCTCCTCAGACCTTATCAATTCATTG
AGAGATTGCAAAGCTGAAAGCACCTCCGGCCACTCCTGGGAGACAGACCCTTTGGTGATGAAA
TAAACCAGTGACTTCAGAGCCTATGGTCTCAACTGTGCTTGAAAAACACTGTCTCTGAAAAA
ACTTTGTGATTCTCCCTGCTCCCTGTGGACAAAAGCACATAATTCTGCTGTTACGGGTACTTT
GCTCATACGAGCTTTCATGTTGAGCATGCAATGGAATCATGCTTGTCCATGTGAAATAAATAT
GGCTCTCTCGTGTCTTAATGCTGGGCTTTTCTCTGTAAGCTGGTTCTGCAGCACAAATTCATT
AATTAAACTTCTCCAGTGCAAGAAGGCAGCTGGTGCTGGGGGTGGTCTGGGGGGTCAGGGAG
GAGGGCAAGGACTACATGGGGCAGAGGCAAGGCGGTGGTGGAGATGAGGAAAGAAGTTCTTCT
TGGCAGAAGCTGGGGCAGAAAGATCACATGAGATCTGTGGGGACACCCCTCTATCTGAAACATA
AGTCTGTGTTCAATTCTCTGCTTAGAAATTTTAGATCTGAAGTGCTACACTGAAGGTCCGAAGG
TTGATGGGGCATCAGATATCTTTTTGGTTGGCCAGCATGATATTTTGAATAAAGTGTCAACAG
TTAGAAACTGGGAGCATTCATATGTAAAAAATATGGATTTTCAGCTTCTTCTTAAAAA
AAAAA
AAAAA

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FIGURE 208

MAYRVLGRAGPPQPRRARRLLFAFTLSLSCTYLCYSFLCCDDLGRSRLLGAPRCLRGPSAGG
QKLLQKSRPCDPSGPTPSEPSAPSAPAAVPAPRLSGSNHSGSPKLGTKRLPQALIVGVKKGG
TRAVLEFIRVHPDVRLGTEPHFFDRNYGRGLDWYRSLMPRTLESQITLEKTPSYFVTQEAPR
RIFNMSRDTKLIVVVRNPVTRAISDYTQTL SKKPDIPTFEGLSFRNRTLGLVDVSWNAIRIGM
YVLHLESWLQYFPLAQIHVSGERLITDPAGEMGRVQDFLG IKR FITDKH FYFNKTKGF PCLK
KTESSLLPRCLGKSKGRTHVQIDPEVIDQLREFYRPNYIKFYETVGQDFRWE

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 102-106, 193-197, 235-239, 306-310

Tyrosine kinase phosphorylation site.

amino acids 296-305

N-myristoylation sites.

amino acids 51-57, 100-106, 121-127, 125-131

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 20-31

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FIGURE 209

CTTTCCTTATCTGTGTGTA CTCTTATCTCACTGTTCTATTTTTTCTCCTCATTATATTA ACT
CTTTCCTTACCTTTTTTCTGAACTTCTAGGCCTTCTCTTTCCAGAACTGGTGGAAGACAAATG
AAACGGCCAAAGATGGTAAGAAACAAGCCGCATTTCTCCTTGGGGAGACTGATAATTTAAAGG
TTTGTTGTGTGTCAGAAACATTCCCAGCTTCATCACCAACCCTTTCTTCCACCTCTGCCCCACTG
GAGACCACTTACATCCCGAAGCGGACGCGGCAGCTGAAGTCAGGAAACCATGCATCACATTAG
CAGGAGCCAACTGCAGACTTTAAACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGT
CCAGACAAGCCGGGGCAGCTCATAAACTGGTTTCATCTGCTCCCTGTGCGTCCCGCGGGTGCGT
AAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGGAGAAACCTTCTGCTGGGCACTGCGTGTGCC
ATCTACTTGGGCTTCCTGGTGAGCCAGGTGGGGAGGGCCTCTCTCCAGCATGGACAGGCGGCT
GAGAAGGGGGCCACATCGCAGCCGCGACACCGCCGAGCCATCCTTCCCTGAGATACCCCTGGAT
GGTACCCTGGCCCCCTCCAGAGTCCCAGGGCAATGGGTCCACTCTGCAGCCCAATGTGGTGTAC
ATTACCCTACGCTCCAAGCGCAGCAAGCCGGCCAATATCCGTGGCACCCTGAAGCCCAAGCGC
AGGAAAAAGCATGCAGTGGCATCGGCTGCCCCAGGGCAGGAGGCTTTGGTCGGACCATCCCTT
CAGCCGCAGGAAGCGGCAAGGGAAGCTGATGCTGTAGCACCTGGGTACGCTCAGGGAGCAAAC
CTGGTTAAGATTGGAGAGCGACCCTGGAGGTTGGTGCGGGGTCCGGGAGTGCGAGCCGGGGGC
CCAGACTTCCTGCAGCCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAGCGCCCCC
TCCTGGCTGAGCAAAGATGACATCCGAAGAATGCGACTCTTGCGGACAGCGCAGTGGCAGGG
CTCCGGCCTGTGTCTCTAGGAGCGGAGCCCGTTTGCTGGTGCTGGAGGGGGGCGCACCTGGC
GCTGTGCTCCGCTGTGGCCCTAGCCCCCTGTGGGCTTCTCAAGCAGCCCTTGACATGAGTGAG
GTGTTTGCTTCCACCTAGACAGGATCCTGGGGCTCAACAGGACCCTGCCGTCTGTGAGCAGG
AAAGCAGAGTTCATCCAAGATGGCCGCCCATGCCCATCATTCTTTGGGATGCATCTTTATCT
TCAGCAAGTAATGACACCCATTCTTCTGTTAAGCTCACCTGGGGAACCTTATCAGCAGTTGCTG
AAACAGAAATGCTGGCAGAATGGCCGAGTACCCAAGCCTGAATCAGGTTGTACTGAAATACAT
CATCATGAGTGGTCCAAGATGGCACTCTTTGATTTTTTGTACAGATTTATAATCGCTTAGAT
ACAAATTGCTGTGGATTGAGACCTCGCAAGGAAGATGCCTGTGTACAGAATGGATTGAGGCCA
AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAAGCATGACCCAAGG
CATTTGGTTTTTATAGACAACAAGGGTTTTCTTTGACAGGAGTGAAGATAACTTAACTTCAA
TTGTTAGAAGGCATCAAAGAGTTTCCAGCTTCTGCAGTTTCTGTTTTGAAGAGCCAGCACTTA
CGGCAGAACTTCTTCACTCTCTGTTTCTGATAAAGTGTATTGGGAAAGTCAAGGAGGTAGA
CAAGGAATTGAAAAGCTTATCGATGTAATAGAACACAGAGCCAAAATTCTTATCACCTATATC
AATGCACACGGGGTCAAAGTATTACCTATGAATGAATGACAAAAGAATCTTCTGGCTAGGGTG
TTAGATATATTTATGCATTTTTTGGTTTTTGTAAATCAAGCACATCAACCTCAAGCCCGTT
TAGCAATGAGGCAGTGTAGATGAATACGTAAAATAAATGACTTTAACCAAGTAGCTATAAAGG
GACTTAGCACTGTATGCATACTTAAAAAGGTTTTGAAAAACAACTACTTGAGAAATATTTGT
TTATATTTTTCTCTAACATCATGCTATGTGTGCTGCTGAACATCTGACAACAGAAATTTTCACT
TATTATTCTAGCTAAGTTTTGAAAACATTTGTGCTGCTGTTTAAATAGAAAACCTGCAAACCAGA
GATACTGACTCCATTAATAAACCATATTTTGTGCCGTTTTGACTGTTCTGACCAAATACTAAT
GGGAACAATTCTTGACGTTTTTCTGTTGCTGATTGTTAACATAGAGCAGTCTCTACACTACCC
TGAGGCAACTCTACATTGGAACACTGAGGCTTACAGCCTGCAAGAGCATCAGAGCTGACCATA
CATTTAAACAGAAATGCTGGTTTTATTTGCAAAATCACCAGTATATTTTCTATTGTGTCTATAA
AAAATCAGTCATTTAAGTACAAGAATCATATTTTCCATTCCTTTTTAGAAATTTATTTTGTG
TCCCTATGGAAATCATTACATCTGACAATTTATATGTTAAAGAGTTTTACTCTCTCTATTTT
GGTCCAATTTGTATCTAGTGGCTGAGAAATTAATAATTCTAAAGTATGAAGTTACCTATCTG
AAAATGTACTTACAGAGTATCATTTTAAATGGATGTCTCTTTAAAAATTTTGTACTTTTAC
CAACAATGTAATATAATTTATGTATATTTTATTAATAATAGTGAATTCCTTAAATTTGTCT
ATGTACTTATATTTAATTTGATTTAATGGTTACTGCCCAGATATTGAGAAATGGTTCAAATAT
TGAGTGTGTTTCAATAA

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FIGURE 210

MTC PDKPGQLINWFICSLCVPRVRKLWSSRRPRTTRNLLLGTACAIYLGFLVSQVGRASLQHG
QAAEKGP HRSRDTAEP SFPEIPLDGT LAPPESQGN GSTLQPNVVYITLRSKR SKPANIRGTVK
PKRRKKH AVASAAPGQEALVGPSLQPQEAAREADAVAPGYAQGANLVKIGERP WRLVVRGPGVR
AGGPDFLQ PSSRESNIRIYSESAPSWLSKDDIRMRLLADSAVAGLRPVSSRSGARLLVLEGG
APGAVLR CGPSPCGLLKQPLDMSEVFAFHLDRI LGLNRTLPSVSRKAEFIQDGRPCPIILWDA
SLSSASNDTHSSVKLTWGTYQQLLKQKCWQNGRV PKPESGCTEIH HHEWSKMALFDLLQIYN
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAA LAHIIQRKHDPRHLVFIDNKGFFDRSEDNL
NFKLLEGIKEFPASAVSVLKSQHLRQKLLQSLFLDKVYWESQGG RQGIEKLIDVIEHRAKILI
TYINAHGVKVLPMNE

Transmembrane domain:

amino acids 40-56

N-glycosylation sites.

amino acids 98-102, 289-293, 322-326

N-myristoylation sites.amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,
287-293, 484-490

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FIGURE 211

GTGGGGTGGTGAGCGCAGCGCCGAGGATGAGGAGGTGCAACAGCGGCTCCGGGGCCGCCGCCGCTCGCTGCTGCTGC
TGCTGCTGTGGCTGCTCGCGGTTCCCGGCGCTAACGCGGCCCGCGGTGCGGCGCTCTATTGCGCTTCCGACCCGC
TGACGCTGCTGCAGGCGGACACGGTGCGCGGCGCGGTGCTGGGCTCCCGCAGCGCCTGGGCCGTGGAGTTCTTCG
CCTCTGGTGCGGCCACTGCATCGCCTTCGCCCCGACGTGGAAGGCGCTGGCCGAAGACGTCAAAGCCTGGAGGC
CGGCCCTGTATCTCGCCGCCCTGGACTGTGCTGAGGAGACCAACAGTGCAGTCTGCAGAGACTTCAACATCCCTG
GCTTCCCGACTGTGAGGTTCTTCAAGGCCTTTACCAAGAACGGCTCGGGAGCAGTATTTCCAGTGGCTGGTGCTG
ACGTGCAGACGCTGCGGGAGAGGCTCATTGACGCCCTGGAGTCCCATCATGACACGTGGCCCCCAGCCTGTCCCC
CACTGGAGCCTGCCAAGCTGGAGGAGATTGATGGATTCTTTCGAGAAATAACGAAGAGTACCTGGCTCTGATCT
TTGAAAAGGGAGGCTCCTACCTGGGTAGAGAGGTGGCTCTGGACCTGTCCAGCACAAAGGCGTGGCGGTGCGCA
GGGTGCTGAACACAGAGGCCAATGTGGTGAGAAAGTTTGGTGTCAACGACTTCCCCCTCTTGCTACCTGCTGTTCC
GGAATGGCTCTGTCTCCCGAGTCCCGGTGCTCATGGAATCCAGGTCTTCTATACCGCTTACCTGCAGAGACTCT
CTGGGCTCACCAGGGAGGCTGCCAGACCACAGTTGCACCAACCACTGCTAACAGATAGCTCCCACTGTTTGA
AATTGGCAGATCGCTCCAAGATCTACATGGCTGACCTGGAATCTGCACTGCACTACATCCTGCGGATAGAAGTGG
GCAGTTCCCGGTCTTGGAAAGGGCAGCGCCTGGTGGCCCTGAAAAAGTTTGTGGCAGTGTGGCCAAGTATTTCC
CTGGCCGGCCCTTAGTCCAGAATCTTCTGCACTCCGTGAATGAATGGCTCAAGAGGCAGAAAGAAATAAAATTC
CCTACAGTTTCTTTAAACTGCCCTGGACGACAGGAAAGAGGGTGCCGTCTTTCGAAGAAGGTGAAGTGGATTG
GCTGCCAGGGAGTGAGCCGATTTCCGGGCTTTCCCTGCTCCCTGTGGGTCTCTTCCACTTCTTGAGTCTG
AGGCAGCTCGGCAAAATGTAGACCACTCACAGGAAGCAGCCAAGGCCAAGGAGGTCTCCAGCCATCCGAGGCT
ACGTGCACTACTTCTTCCGCTGCCGAGACTGCGCTAGCCACTTCGAGCAGATGGCTGCTGCCTCCATGCACCGGG
TGGGGAGTCCCAACGCCGCTGTCTCTGGCTCTGGTCTAGCCACAACAGGGTCAATGCTCGCCTTGCAAGTGCC
CCAGCGAGGACCCCAAGTTCCCAAGGTGCAGTGGCCACCCCGTGAACCTTGTCTGCTGCCACATGAACGCC
TGGATGTGCCCGTGTGGGACGTGGAAGCCACCCTCAACTTCTCAAGGCCCACTTCTCCCAAGCAACATCATCC
TGGACTTCCCTGCAGCTGGGTGAGTGCCTGGGAGGGATGTGCAGAAATGTGGCAGCCGCCCCAGAGCTGGCGATGG
GAGCCCTGGAGCTGGAAGCCGGAATCAACTCTGGACCCTGGGAAGCCTGAGATGATGAAGTCCCCACAAACA
CCACCCACATGTGCCGGCTGAGGGACCTGAGGCAAGTCGACCCCGAAGCTGCACCCTGGCCTCAGAGCTGCAC
CAGGCCAGGAGCTCCTGAGCACATGGCAGAGCTTCAGAGGAATGAGCAGGAGCAGCCGCTTGGGCAGTGGCACT
TGAGCAAGCGAGACACAGGGGCTGCATTGCTGGCTGAGTCCAGGGCTGAGAAGAACCCTCTGGGGCCCTTTGG
AGGTGAGGCGCTGGGCCGAGCTCCAAGCAGCTGGTGCACATCCCTGAGGGCCAGCTGGAGGCCCCAGCTGGAC
GGGGCCGAGGCAAGTGGCTGCAGGTGCTGGGAGGGGCTTCTCTTACCTGGACATCAGCCTCTGTGTGGGGCTCT
ATTCCCTGTCTTATGGGCTGCTGGCCATGTACACCTACTTCCAGGCCAAGATAAGGGCCCTGAAGGGCCATG
CTGGCCACCCTGCAGCTGGAACCACTGGGGAGGAGGCGGGAGAGGGAGCTGCCATCTCTAGGCACCTCAAGCCC
CCTGACCCCATTCCTTCCCTCCCAACCCCTTGCTCCTTGTCTGGCCTAGAAGTGTGGGAAATTGAGGAAACGAG
TTGCTCCAGTGAAGCTTCTTGGGGTTGCTAGGACAGAGAGCTCCTTTGACACAAAAGACAGGAGCAGGGTCCAGG
TTCCCTGCTGTGCAGGAGGGCAGCCCCGGGCACTGGGCATAGGGCAGCTCAGTCCCTGGCCTCTTAGCACCAC
ATTCTGTTTTTTCAGCTTATTTGAAGTCTGCTCATTTCTCACTGGAGCCTCAGTCTCTCTGCTTGGTCTTGGC
CCTCAACTGGGGCAAGTGAAGCCAGAGGAGGTCCCCAGCTGGGTGGGCTGGAATGGAAGTCTCACTAGCTGC
TGGGGCTCCGCCACCCTGCTCCCTTCCGGACAATGAAGAAGCCTTTCACCCCTGGGAGGAAGGACCACCCCGG
CCCTCTATGCCTGGCCAGCCTCCAGCTCCTCAGACCTCCTGGGTGGGGTTTGGCTTCAGGGTGGGGTTTGAAGC
TTCTGGAAGTCGTGCTGGTCTCCAGGTGAGGCAAGCCATGGTTGCTGGGCTGTAGGGTGAGTGGCTTGCTTGGT
GGGACCTGACGAGTTGGTGGCATGGGAAGGATGTGGGTCTTAGTGCCTTGGCCTGGCTTAGCTGCAGGAGAAGA
TGGCTGCTTTCACTTCCCCCATTGAGCTCTGCTCCCTCTGAGCCTGGTCTTTTGTCTTTTATTTTGGTCTC
CAAGATGAATGCTCATCTTTGGAGGGTGCCAGGTAGAAGCTAGGGAGGGGAGTGTCTTCTCTCCAGGTTTCAC
CTTCAGTGTGCAGAAGTTAGAAGGGTCTGGCGGGGCGAGTGCCTTACACATGCTTGATTCCACGCTACCCCT
GCCTTGGGAGGTGTGTGAATAAATTATTTTGTAAAGGCA

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FIGURE 212

MRRCSGSGPPPSLLLLLLWLLAVPGANAAPRSALYSPSDPLTLLQADTVRGAVLGSRSAWAV
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDENIPGFPTVRFFKA
FTKNGSGAVFPVAGADVQTLRERLIDALESHHDTWPPACPPLEPAKLEEIDGFFARNNEEYLA
LIFEKGSYLGREVALDLSQHKGVAVRRVLNTEANVVRKFGVTDFPSCYLLFRNGSVSRVPVL
MESRSFYTAYLQRLSGLTREAAQTTVAPTANKIAPTVMWKLADRSKIYMADLESALHYILRIE
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPLVQNFLHSVNEWLKRQKRNKIPYSFFKTALDDR
KEGAVLAKKVNWIGCQGSEPHFRGFPCSLWVLFHFLTQVQAAQNVVDHSQEAAKAKEVLPAIRG
YVHYFFGCRDCASHFEQMAAASMRVGGSPNAAVLWLWSSSHNRVNARLAGAPSEDPOQFPKVQWP
PRELCSACHNERLDVPVWDVEATLNLKAFHSPSNIILDFFAAGSAARRDVQNVAAAPELAMG
ALELESRNSTLDPGKPEMMKSPTNTTPHVPAGPEASRPPKLHPGLRAAPGQEPPEHMAELQR
NEQEQPLGQWHLKRDGTGAALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGRG
RGQWLQVLGGGFSYLDISLCVGLYSLSFMGLLAMYTYFQAKIRALKGHAGHPAA

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 705-728

N-glycosylation sites.

amino acids 130-134, 243-247, 575-579

Glycosaminoglycan attachment site.

amino acids 6-10

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 644-648

N-myristoylation sites.amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,
468-474, 684-690, 702-708**Cytochrome c family heme-binding site signature.**

amino acids 509-515

Thioredoxin family proteins

amino acids 62-78

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FIGURE 213

GCACGAGGCCGACTTCCAGACCATCTACAACTGCACGGCCTGGAACAGCTTCGGCTCCGACAC
TGAGATCATCCGGCTCAAGGAGCAAGGTTCTGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGA
GTCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCCT
TATGGCAACCATCGTGGCGTTCTGCTGTGCCCCTTCCCAGAGAAATCTCAAAGGTGTTGTGTC
AGCCAAAATGATATCCGAGTGGAAATTGTCCACAAGGAACCAGCCTCTGGTCGGGAGGGTGA
GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGGTGAATTCCAGCAAGACTCAGTCCT
GAAACAGCTGGAGGTCCTCAAAGAAGAGGAGAAAGAGTTTCAGAACCTGAAGGACCCACCAA
TGGCTACTACAGCGTCAACACCTTCAAAGAGCACCCTCAACCCCGACCATCTCCCTCTCCAG
CTGCCAGCCCGACCTGCGTCCTGCGGGTAAGCAGCGTGTGCCACAGGCATGTCCTTCACCAA
CATCTACAGCACCCTGAGCGGCCAGGGCCGCTCTACGACTACGGGCAGCGGTTTGTGCTGGG
CATGGGCAGCTCGTCCATCGAGCTTTGTGAGCGGGAGTTCAGAGAGGCTCCCTCAGCGACAG
CAGTCCTTCCTGGACACGCAGTGTGACAGCAGCGTCAGCAGCAGCGGCAAGCAGGATGGCTA
TGTGCAGTTCGACAAGGCCAGCAAGGCTTCTGCTTCCTCCTCCCACCACTCCCAGTCCTCGTC
CCAGAACTCTGACCCCAGTCGACCCCTGCAGCGGCGGATGCAGACTCACGTCTTAAGGATCACA
CACCGCGGGTGGGGACGGGCCAGGGAAGAGGTCAGGGCACGTTCTGGTTGTCCAGGGACGAGG
GGTACTTTGCAGAGGACACCAGAATTGGCCACTTCCAGGACAGCCTCCCAGCGCCTCTGCCAC
TGCCTTCCTTCGAAGCTCTGATCAAGCACAATCTGGGTCCCCAGGTGCTGTGTGCCAGAGGT
GGGCGGGTGGGGAGACAGACAGAGGCTGCGGCTGAGTGCCTGTGCTTAGTGCTGGACACCCG
TGTCCCCGGCCCTTTCCTGGAGGCCCTCTACCACCTGCTCTGCCCACAGGCACAAGTGGCAG
CTATAACTCTGCTTTCATGAACTGCGGTCCACTCTCTGGTCTCTCTGTGGGCTCTACCCCTC
ACTGACCACAAGCTCTACCTACCCCTGTGCCTGTGCTCCCATACAGCCCTGGGGAGAAGGGGA
TGACGTCTTCCCAGCACTGAGCTGCCCCAGAAACCCCGGCTCCCCACTGCTGCTCATAGCCCA
TACCCTGGAGGCTGACAAGCCAGAAATGGCCTTGGCTAAAGGAGCCTCTCTCTCACCAGGCTG
GCCGGGAGCCACCCCAATTTGTTTTGGTGTGTTTGTGTCCATACTCTTGCACTTCTGTCTTG
GACTTGATGCCGCTGAACTCTGCGGTGGGACCGGTCCCGTCAGAGCCTGGTGTACTGGGGGA
GGGAGGGAGGAGGGAGCCTGTGCTGACGGAGCACCTCGCCGGGTGTGCCCCCTCCTGGGCTGTG
TGACCCAGCCTCCCCACCCACCTCCTGCTTTGTGTACTCCTCCCCTCCCCCTCAGCACAATC
GGAGTTCATATAAGAAGTGCGGGAGCTTCTCTGGTCAGGGTTCTCTGAACACTTATGGAGAGA
GTGCTTCCTGGGAAGTGTGGCGTTTGAAGGGGCTGGAGGGCAGGTCTTTAAGATGGCGAGACT
GCCCTTCTCAGCTGATAAACACAAGAACGGCGATCCTGTCTTCAGTAAGGCTCCACGAGAAGA
GAGGAAGTATATCTACACCTCAACCCTCCTAGTCACCACCTGAAATAAATGTTAGGGAAAAAAA

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FIGURE 214

MAVIIGVAVGAGVAFLVLMATIVAFCCARSQRNLKGVVSAKNDIRVEIVHKEPASGREGEEHS
TIKQLMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYYSVNTFKEHHSTPTISLSSCQP
DLRPAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFQRGSLSDSSSF
LDTQCDSSVSSSGKQDGYVQFDKASKASASSSHHSQSSSQNSDPSRPLQRRMQTHV

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 150-154

N-myristoylation sites.

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 114-125

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FIGURE 215

CAGCCTTCCTCCCCAGCCTGAGTGA CTACTCTATTCCCTTGGTCCCTGCTATTGTCGGGGACG
ATTGCAATGGGCTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTGATTGGGGCTGGCG
CCTGCTATTGCATTTATAGACTGACTAGGGGAAGAAAACAGAACAAAGGAAAAAATGGCTGAGG
GTGGATCTGGGGATGTGGATGATGCTGGGGACTGTTCTGGGGCCAGGTATAATGACTGGTCTG
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTTGGGCTCGGATTG
GGACTGAAGCTGGAACCAGAGCTAGGGCCAGGGCAAGGGCCAGGGCTACCCGGGCACGTCGGG
CTGTCCAGAAACGGGCTTCCCCCAATTCAGATGATACCGTTTTGTCCCCTCAAGAGCTACAAA
AGGTTCTTTGCTTGTTGAGATGTCTGAAAAGCCTTATATTCTTGAAGCAGCTTTAATTGCTC
TGGGTAACAATGCTGCTTATGCATTTAACAGAGATATTATTCGTGATCTGGGTGGTCTCCCAA
TTGTCGCAAAGATTCTCAATACTCGGGATCCCATAGTTAAGGAAAAGGCTTTAATTGTCCTGA
ATAACTTGAGTGTGAATGCTGAAAATCAGCGCAGGCTTAAAGTATACATGAATCAAGTGTGTG
ATGACACAATCACTTCTCGCTTGAACCTCATCTGTGCAGCTTGCTGGACTGAGATTGCTTACAA
ATATGACTGTTACTAATGAGTATCAGCACATGCTTGCTAATTCCATTTCTGACTTTTTTCGTT
TATTTTCAGCGGGAAATGAAGAAACCAAACCTTCAGGTTCTGAAACTCCTTTTGAATTTGGCTG
AAAATCCAGCCATGACTAGGGAACTGCTCAGGGCCCAAGTACCATCTTCACTGGGCTCCCTCT
TTAATAAGAAGGAGAACAAAGAAGTTATTCTTAAACTTCTGGTCATATTTGAGAACATAAATG
ATAATTTCAAATGGGAAGAAAATGAACCTACTCAGAATCAATTGCGTGAAGGTTCACTTTTTT
TCTTTTTTAAAAGAATTTCAAGTGTGTGCTGATAAGGTTCTGGGAATAGAAAGTCACCATGATT
TTTTGGTGAAAGTAAAAGTTGGAAAATTCATGGCCAACTTGCTGAACATATGTTCCCAAAGA
GCCAGGAATTAACACCTTGATTTTGTAAATTTAGAAGCAACACACATTGTAAACTATTCAATTTT
TCCACCTTGTTTATATGGTAAAGGAATCCTTTCAGCTGCCAGTTTTGAATAATGAATATCATA
TTGTATCATCAATGCTGATATTTAACTGAGTTGGTCTTTAGGTTTAAAGATGGATAAATGAATA
TCACTACTTGTTCTGAAAACATGTTTGTTGCTTTTTATCTCGCTGCCTAGATTGAAATATTTT
GCTATTTCTTCTGCATAAGTGACAGTGAACCAATTCATCATGAGTAAGCTCCCTTCTGTCATT
TTCATTGATTTAATTTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAAGA

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FIGURE 216

MGYARKVGWVTAGLVIGAGACYCIYRLTRGRKQNKEMAEGGSGDVDDAGDCSGARYNDWSDD
DDDSNESKSIVWYPPWARIGTEAGTRARARARARATRRARRAVQKRASPNSDDTVLSPQELQKV
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKALIVLNN
LSVNAENQRRLLKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRLF
SAGNEETKLQVLKLLLNLAE NPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDN
FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPSQE

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 68-72, 189-193, 217-221, 230-234

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-111

N-myristoylation sites.amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,
290-296**Amidation site.**

amino acids 29-33

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FIGURE 218

MAIAQLATEYVFSDFLLKEPTEPKFKGLRLELAVDKMVTCTIAVGLPLLLISLAFQAQEISIGTQ
ISCFSPSSFSWRQA AFVDSYCWA AVQQKNSLQSESGNLPLWLHKFFPYILLFFAILLYLPPLF
WRFAAAPHICSDLKFIMEELDKVYNRAIKAAKSARDLDMRDGACSVPGVTENLGQSLWEVSES
HFKYPIVEQYLKTKKNSNNLI IKYISCRLLTLIIILLACIYLGYYFSLSSLSDEFVCSIKSGI
LRNDSTVPDQFQCKLIAVGIFQLLSVINLVVYVLLAPVVVYTLFVPFRQKTDVLKVYEILPTF
DVLHFKSEGYNDLSLYNLFLEENISEVKS YKCLKVLENIKSSGQGIDPMLLLTNLGMIMKMDVV
DGKTPMSAEMREEQGNQTAE LQGMNIDSETKANNGEKNARQRLDSSC

Transmembrane domains:

amino acids 37-55, 108-126, 216-232, 273-290

N-glycosylation sites.

amino acids 255-259, 338-342, 394-398

Glycosaminoglycan attachment site.

amino acids 357-361

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 203-207

N-myristoylation sites.

amino acids 61-67, 174-180, 251-257, 393-399

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 218-229

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FIGURE 219

CTGTGAGTGACACACGCTGAGTGGGGTGAAGGGAAATGCTGGTGAATTTTCATTTTGAGGTGTG
GGTTGCTGTTAGTCACTCTGTCTCTTGCCATTGCCAAGCACAAGCAATCTTCCTTCACCAAAA
GTTGTTACCCAAGGGGAACATTGTCCCAAGCTGTTGACGCTCTCTATATCAAAGCAGCATGGC
TCAAAGCAACGATTCCAGAAGACCGCATAAAAAATATACGATTATTA AAAAAGAAAACAAAAA
AGCAGTTTATGAAAACTGTCAATTTCAAGAACAGCTTCTGTCCTTCTTCATGGAAGACGTTT
TTGGTCAACTGCAATTGCAAGGCTGCAAGAAAATACGCTTTGTGGAGGACTTTCATAGCCTTA
GGCAGAAATTGAGCCACTGTATTTCTGTGCTTCATCAGCTAGAGAGATGAAATCCATTACCA
GGATGAAAAGAATATTTTATAGGATTGGAAACAAAGGAATCTACAAAGCCATCAGTGAAGTGG
ATATTCTTCTTTCTGGATTAAAAAATTATTGGAAAGCAGTCAGTAAACCAAAGCCAAGTACA
TTGATTTTACAGTTATTTTGAAATACAATAAGAACTGCTAGAAATATGTTTATAACAGTCTAT
TTCTTTTAAAACTTTTTAACATAATACTGACGGCATGTTAGGTGATTCAGAATAGACAAGAA
GGATTTAGTAAATTAACGTTTTGGATATAAGTTGTCACTAATTGTCACATTTTCTGTGTTTTC
AAATAATGTTTCCATTCTGAACATGTTTTGTCAATCACAAGTACATTGTGTCAACTTAATTTA
AAGTATGTAACTGAATTAACCTCGTGTAAATATTTGTGTGTGGAGTGGGATGTGGGGGGTGGAG
GGGGAATGACAGATTTCTGGAATGCAATGTAATGTTACTGAGACTTAAATAGATGTTATGTAT
ATGATTGTCTGTTTAAGTGTGTTGAAAATTGTTAATTATGCCCAGTGTGAACTTAGTACTTAAC
ACATTTTGATTTTAATTAAATAAATTGGGTTTCCTTCTCAAAAAAAAAAAAAAAAAAAAAA
AAAAA

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FIGURE 220

MLVNFILRCGLLLVTLSLAIKHKQSSFTKSCYPRGTL SQAVDALYIKA AWLKATIPEDRIKN
IRLLKKKTKKQFMKNCQFQEQLLSFFMEDVFGQLQLQGCKKIRFVEDFHSLRQKLSHCISCAS
SAREMKSITRMKRIFYRIGNKGIYKAISELDILLSWIKKLESSQ

Signal sequence:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 68-71

N-myristoylation site.

amino acids 148-153

Interleukin-10 proteins.

amino acids 58-94, 74-102, 128-170

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FIGURE 221

GACCACGGCCCTGCGCCCCAGCCAGGCCTGAGGACATGAGGCGGCCGGCGGGTGCCGCTCC
TGCTGCTGCTGTGTTTTGGGTCTCAGAGGGCCAAGGCAGCAACAGCCTGTGGTCGCCCCAGGA
TGCTGAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCA
TCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTGGGTCTTGACGG
CTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCCTGCTGGGGGCAAGGC
AGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGTGAGGCAGGTGGAGAGCAACCCCC
TGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAGTGCCCT
TCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGA
ACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGAAGACCTCCTGCCCGAACCGCGGATCC
TGCAGAAACTCGCTGTGCCCATCATCGACACACCCAAGTGCAACCTGCTCTACAGCAAAGACA
CCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTTCGAGGAGG
GCAAGAAGGATGCCTGCAAGGGCGACTCGGGCGGGCCCCCTGGTGTGCCTCGTGGGTCAAGTCGT
GGCTGCAGGCGGGGGTGATCAGCTGGGGTGAGGGCTGTGCCCCGCCAGAACCGCCCAGGTGTCT
ACATCCGTGTCACCGCCCCACCACAACCTGGATCCATCGGATCATCCCCAACTGCAGTTCCAGC
CAGCGAGGTTGGGCGGCCAGAAGTGAGACCCCCGGGGCCAGGAGCCCCCTTGAGCAGAGCTCTG
CACCAGCCTGCCCCGCCACACCATCCTGCTGGTCCCTCCCAGCGCTGCTGTTGCACCTGTGAG
CCCCACCAGACTCATTTGTAAATAGCGCTCCTTCCTCCCCTCTCAAATACCCTTATTTTATTT
ATGTTTCTCCAATAAAAACCCAGCCTGTGTGCCAGCTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 222

MRRPAAVPLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGS
LIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVA
LVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTP
KCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEG
CARQNRPGVIYIRVTAHHNWIHRIIPKLQFQPARLGGQK

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 55-58, 79-82

Casein kinase II phosphorylation sites.

amino acids 121-124, 165-168, 167-170, 248-251

Tyrosine kinase phosphorylation sites.

amino acids 78-86, 197-203

N-myristoylation sites.

amino acids 16-21, 37-42, 56-61, 62-67, 118-123

Amidation site.

amino acids 219-222

Serine proteases, trypsin family, histidine active site.

amino acids 71-76

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FIGURE 223

CAAGATGTGGACAGCTCTTGTGCTCATTGATTTTCTCCTTGTCTTATCTGAAAGCCATGC
GGCATCCAACGATCCACGCAACTTTGTCCCTAACAAATGTGGAAGGGATTAGTCAAGAGGAA
TGCATCTGTGGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGCAGCTTCTCC
TGTCACATTGACCAAAGGGACTTCGGCAGCCCACCTCAACTCTATGGAAGTCACAACAGAGGA
CACAAGCAGGACAGATGTGAGTGAACCAGCAACTTCAGGAGTTGCAGCTGATGGTGTGACCTC
CATTGCTCCACGGCTGTGGCCTCCAGTACGACTGCGGCCTCCATTACGACTGCGGCCTCCAG
TATGACTGTGGCCTCCAGTGCTCCACGACTGCAGCCTCCAGTACAACCTGTGGCCTCCATTGC
TCCCACGACTGCAGCCTCCAGTATGACTGCGGCCTCCAGCACTCCCATGACACTTGCAGCTCCC
CGCGCCACGTCCACTTCCACAGGGCGGACCCCGTCCACTACCGCCACTGGGCATCCATCTCT
CAGCACAGCCCTCGCACAAAGTGCCAAAGAGCAGCGCGTTGCCAAGAACAGCAACCCTGGCCAC
ATTGGCCACACGTGCTCAGACTGTAGCGACCACAGCAAACACAAGCAGCCCCATGAGCACTCG
TCCAAGTCCTTCCAAGCACATGCCCAGTGACACCGCGGCAAGCCCTGTACCCCTATGCGTCC
CCAAGCACAAGGTCCCATTAGCCAGGTGTCAGTGGACCAGCCTGTGGTTAACACAACAAATAA
ATCCACACCCATGCCCTCAAACACAACCCCAAGAGCCCGCCCCACCCCCACAGTGGTGACCAC
CACCAAGGCACAAGCCAGGGAGCCAACTGCCAGCCCAGTGCCAGTACCTCACACCAGCCCAAT
CCCTGAGATGGAGGCCATGTCCCCACGACACAGCCAAGCCCCATGCCATATACCCAGAGGGC
CGCTGGGCCAGGCACATCCCAGGCACCGGAGCAGGTAGAGACTGAAGCCACACCAGGTACTGA
TTCCACTGGGCCAACACCCAGGAGCTCAGGGGGCACTAAGATGCCAGCCACGGACTCGTGCCA
GCCCAGCACCCAAGGCCAGTACATGGTGGTCACCACTGAGCCCCTCACCCAGGCCTGTGGTAGA
CAAACTCTCCTTCTGGTGGTGTGTTACTCGGGGTGACCCTTTTCATCACAGTCTTGGTTTT
GTTTGGCCTGCAGGCCTATGAGAGCTACAAGAAGAAGGACTACACCCAGGTGGACTACTTAAT
CAACGGGATGTATGCGGACTCAGAAATGTGAGGGGGGGCGGGGGCCTGGCGGGAGGCCTGGCCC
CTTCCTCGTCCTTTCTTTTGCCCTTGAGACCAAACCAAGTGCTTCCAAATTCTTTTGGTGCA
ATTGAGGAGATATGCCAGATGCTTAAACACATTTAATTGCTGTCAGATTAATTCCATGATCAC
TAAAGAGTTGCTGCTTTTTTTCATATTTATTTTGTAAATGATTCTGTGCCAGGAGCAGCTGG
GGGTTCCACCTCAGGGTGGGGCGGGCAGGACCCCGTCTCCCCAGGTGTCGGAGCCTGACCTGA
ATTAAAGTACTGACTGCTCGCCA

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FIGURE 224

MWTALVLIWIFSLSLSESHAASNDPRNFVPNKMWGLVKRNASVETVDNKTSSEDTVMAAASP
TLTKGTSAAHLNSMEVTTEDTSRTDVSEPATSGVAADGVTSIAPTAVASSTTAASITTAASSM
TVASSAPTTAASSTTVASIAPTTAASSMTAASSTPMTLALPAPTSTSTGRTPSTTATGHPSLS
TALAQVPKSSALPRTATLATLATRAQTVATTANTSSPMSTRPSPSKHMPSDTAASPVPMPRPQ
AQGPISQVSVDQPVVNTTNKSTPMPSNTTPEPAPTPTVVTTTKAQAREPTASPVVPHTSPIP
EMEAMSPPTQSPMPYTQRAAGPGTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQP
STQGQYMVVTTEPLTQAVVDKTL LLLVLLLVLTFLITVLVLFALQAYESYKKKDYTQVDYLIN
GMYADSEM

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 396-420

N-glycosylation sites.

amino acids 41-44, 49-52, 222-225, 268-271, 271-274

Casein kinase II phosphorylation sites.

amino acids 14-17, 51-54, 80-83, 85-88, 280-283, 434-437

N-myristoylation sites.

amino acids 68-73, 354-359

Aldo/keto reductase family putative active site signature.

amino acids 195-210

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FIGURE 225

GGAAGGCGCTCAAGGTGCGCGGCCCGGGGCGCGCTACTGGGGGCGCCCTCCGCGGTGGGCAGC
GCGCCAGGGATCGGCCTGGGCAGCCGCGGGGCGCGCGAAGGCTGCGCTTTCCCTACGGCCCCC
CTCGCTTCCTCCGGCACGGCGGCAACGGAGATTTCTCTCGGGGAACTACGCGGATCCTTTT
CGGGGATCCTCGCCCCGCCAGTTCTCGCCCCCTCCCTTTGCTGGGGCGCCTGGGCTGGC
CCGCGCAGGGGAGGAGGCTCTGGCAGCCTGGGCAGGAGGCGGGGGGGCCGCGGAGCCGCT
GGCCATCGATTCTCCCCGCCATGTGACGCCGTCTTAGCCCTGCGACCCCCAGCGGTCCCGG
GCCTGCGCCTCCGCCCCGCCGCGCAGCGCACGATGCTTCTGCCGGGACGCGCACGCCAACCGC
CGACGCCCCAGCCCGTGCAGCATCCCGGCCTCCGCCGGCAGGTAGAGCCGCCGGGGCAGCTCC
TGCGCCTCTTCTACTGCACTGTCCTGGTCTGCTCCAAAGAGATCTCAGCGCTACCGACTTCT
CTGGTTACCTAACCAAACCTCCTGCAAACACACCACCTATGCCTGTGATGGGGACTATTTGA
ATCTACAGTGCCCTCGGCATTCTACGATAAGTGTCCAATCGGCATTTTATGGGCAAGATTACC
AAATGTGTAGTTCCCGAAGCCTGCCTCCAGAGGGAAGACAGCTTAACCTGTGTGGCAGCCA
CCACCTTCCAGAAGGTGCTGGACGAATGCCAGAACAGCGGGCCTGCCACCTCCTGGTCAATA
GCCGTGTTTTTGGACCTGACCTTTGTCCAGGAAGCAGTAAATACCTCCTGGTCTCCTTTAAAT
GCCAACCTAATGAATTAAAAACAAAACCGTGTGTGAAGACCAGGAGCTGAACTGCACTGCC
ATGAATCCAAGTTCCTCAACATCTACTCTGCGACCTACGGCAGGAGGACCCAGGAAAGGGACA
TCTGCTCCTCCAAGGCAGAGCGGCTCCCCCCTTTCGATTGCTTGTCTTACTCAGCTTTGCAAG
TCCTATCCCGAAGGTGCTATGGGAAGCAGAGATGCAAAATCATCGTCAACAATCACCATTTTG
GAAGCCCCTGTTTGCCAGGCGTGAAAAATACCTCACTGTGACCTACGCATGTGTTCCCAAGA
ACATACTCACAGCGATTGATCCAGCCATTGCTAATCTAAACCTTCTTTGAAGCAGAAAGATG
GTGAATATGGTATAAACTTCGACCCAAGCGGATCGAAGGTTCTGAGGAAAGATGGAATTCTTG
TTAGCAACTCTCTGGCAGCCTTTGCTTACATTAGAGCCCACCCAGAGAGAGCTGCCCTGCTGT
TCGTGTCCAGTGTCTGCATCGGCCTGGCCCTCACACTGTGCGCCCTGGTCATCAGAGAGTCCT
GTGCCAAGGACTTCCGCGACTTGCACTGGGGAGGGAGCAGCTGGTGCCAGGAAGTGACAAGG
TCGAGGAGGACAGCGAGGATGAAGAAGAGGAGGAGGACCCCTCTGAGTCTGATTTCCAGGGG
AACTGTGGGGTTCTGTAGGACTTCATATCCTATATACAGTTCCATAGAAGCTGCAGAGCTCG
CAGAAAGGATTGAGCGCAGGGAGCAAATCATTCAGGAAATATGGATGAACAGTGGTTTGGACA
CCTCGCTCCCAAGAAACATGGGCCAGTTCTACTGAAAACACATGCATCTTGATGCGATCGCA
CTTTCTGAAGAAGGAAGGATCCCAAATGCCCCCTCAGTTCTGGTTCACCTGTACCTTCTATGA
AGGAGAATTCGTATGTCATTCAACACTCGTGAGGCCAGGAAGCTATTAAAGGGATGTTTCAA
GCTGTTTCTAGCACATTCCAAAATAAATGAGGAGGGAGGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 226

MLLPGRARQPPTPQPVQHPGLRRQVEPPGQLLRLFYCTVLVCSKEISALTDGSGYLTKLLQNH
TTYACDGDYLNLCQPRHSTISVQSAFYQGQDYQMCSSQKPASQREDSLTCVAATTFQKVLDECQ
NQRACHLLVNSRVFGPDLCPGSSKYLVSFKCQPNELKNKTVCEDQELKLHCHEKFLNIYSA
TYGRRTQERDICSSKAERLPPFDCLSYALQVLSRRCYGKQRCKIIVNNHHFGSPCLPGVKKY
LTVTYACVPKNILTAIDPAIANLKPSLKQKDGEYGINFDPGSGKVLKDGILVSNLAAAFAYI
RAHPERAALLFVSSVCIGLALTLCALVIRESCAKDFRDLQLGREQLVPGSDKVEEDSEDEEEE
EDPSESDFPGELSGFCRTSYPIYSSIEAAELAERIERREQIIQEIWMNSGLDTS LPRNMGQFY

Transmembrane domains:

amino acids 32-49, 322-343

N-glycosylation sites.

amino acids 62-66, 165-169

Tyrosine kinase phosphorylation site.

amino acids 280-287

N-myristoylation site.

amino acids 302-308, 333-339, 428-434

Amidation site.

amino acids 191-195

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FIGURE 227

GGCACGAGGTGGAAGGGCTTTTACAAACAGATTGCTGGCCCCACCCCCAGAATTTCTCATCA
GGAGTGGGCAAGACCAATCATTTGCATTTCTGACAAGTTCCCAGGAGCTGCAGCTGCTGGCCC
TGGAACCACACTTTGAGAACCACTGCTTTAGACCAAACACCAAAGGAAGATGCAGCCACCCCTC
CTTTACATGTACAAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCTGAGCTCCACCTG
CAGCAGCCGAGATTCCCGACTCGCTCCACCATTGGGGGCTAGGAGTGAAGCGTGTCAACCATGG
TCAGCTCATGGCCAGCCAGGAAAGCCTCTCTGCTGTGCGTCTGTGCAGTTCTTGTTCTTCCCT
GGAGGACTCTTGGATCGCCTGTGATCTTGGCCAGGAGACCAGGTGCCTGGGTCCCTTCCTGGA
AGGGGACAAGTTACACACCCCAGCCCCATTTTCCCACCAACTTCTACATGCCTTGGGAGAACC
TTCTACATGTTGGCTGCCCCCTTCCCCTATTTTCAGCAGTGCCCAGTCCTGCTTATAAACCTGA
GGCCTGCTCCCCATACCTTCCCTGTGCAAGTGCCAGCCGTTATTCCAGGCAGCCCAATGTTGT
TGAGGCCAGATGGATTCTGGAAGCAGCTGGCCCCATGGATGTGAGTCATCACAGTATTCTAGA
AACAGAGAAGAGGTCTTAACCTAATGCGCATAGAGAAATTGTTCTCATTGTAAACATACCCCT
GTCCTTAGCTGATCTAGGTGGAAGCCCAGCTTCATGTGCTAGGGGGCATGATAATGATAATAA
AGGAATTGTATCTAGGACTAA

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FIGURE 228

MVSSWPARKASLLCVC AVLVL PWRTL GSPVILARRPGAWVPSWKGT SYTPQPHFPTNFYMPWE
NLLHVGCPLPLFQQCPVLLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFLEAAGPWM

Signal peptide:

amino acids 1-27

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 8-12

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FIGURE 229

GGGAAGGGATGCAAGGAAGCCCTCCGGCGCTGCGCTCCGAGGCGGGAGACAGCGTCCCGCTGA
AAATGTGTGTCTGACATGCAAGCTCAGTGGGGCAGAGACCCGTGGATTGCTGTGCCCTGCCCT
CCGGACCTGGATC**ATGA**AGGTGTTGGGAAGAAGCTTCTTCTGGGTGCTGTTTCCCGTCCCTTCC
CTGGGCGGTGCAGGCTGTGGAGCACGAGGAGGTGGCGCAGCGTGTGATCAAACCTGCACCGCGG
GCGAGGGGTGGCTGCCATGCAGAGCCGGCAGTGGGTCCGGGACAGCTGCAGGAAGCTCTCAGG
GCTTCTCCGCCAGAAGAATGCAGTCTGAACAACTGAAAACCTGCAATTGGAGCAGTGGAGAA
AGACGTGGGCCTGTCCGATGAAGAGAACTGTTTCAGGTGCACACGTTTGAAATTTTCCAGAA
AGAGCTGAATGAAAGTGAATTTCCGTTTTCCAAGCTGTCTACGGACTGCAGAGAGCCCTGCA
GGGGGATTACAAAGATGTCGTGAACATGAAGGAGAGCAGCCGGCAGCGCCTGGAGGCCCTGAG
AGAGGCTGCAATAAAGGAAGAAACAGAATATATGGAACCTTCTGGCAGCAGAAAAACATCAAGT
TGAAGCCCTTAAAAATATGCAACATCAAAACCAAGTTTATCCATGCTTGACGAGATTCTTGA
AGATGTAAGAAAGGCAGCGGATCGTCTGGAGGAAGAGATAGAGGAACATGCTTTTGACGACAA
TAAATCAGTCAAGGGGGTCAATTTTGAGGCAGTTCTGAGGGTGGAGGAAGAAGAGGCCAATTC
TAAGCAAAATATAACAAAACGAGAAGTGGAGGATGACTTGGGTCTTAGCATGCTGATTGACTC
CCAGAACAACCAGTATATTTTGACCAAGCCCAGAGATTCAACCATCCCACGTGCAGATCACCA
CTTTATAAAGGACATTGTTACCATAGGAATGCTGTCTTGCCTTGTGGCTGGCTATGTACAGC
CATAGGATTGCCTACAATGTTTGGTTATATTATTTGTGGTGTACTTCTGGGACCTTCAGGACT
AAATAGTATTAAAGTCTATTGTGCAAGTGGAGACATTAGGAGAATTTGGGGTGTTTTTTACTCT
TTTTCTTGTTGGCTTAGAATTTTCTCCAGAAAAGCTAAGAAAGGTGTGGAAGATTTCCCTTACA
AGGGCCGTGTTACATGACACTGTTAATGATTGCATTTGGCTTGCTGTGGGGCATCTCTTGCG
GATCAAACCCACGCAGAGCGTCTTCAATTTCCACGTGTCTGTCTTGTCAAGCACACCCCTCGT
GTCCAGGTTCCCTCATGGGCAGTGTCTCGGGGTGACAAAGAAGGCGACATTGACTACAGCACCGT
GCTCCTCGGCATGCTGGTGACGCAGGACGTGCAGCTCGGGCTCTTCATGGCCGTATGCCGAC
TCTCATACAGGCGGGCGCCAGTGCATCTTCTAGCATTGTCTGTGGAAGTTCTCCGAATCCTGGT
TTTGATTGGTCAGATTCTTTTTTCACTAGCGGCGGTTTTTCTTTTTATGTCTTGTTATAAAGAA
GTATCTCATTGGACCCTATTATCGGAAGCTGCACATGGAAAGCAAGGGGAACAAAGAAATCCT
GATCTTGGGAATATCTGCCTTTATCTTCTTAATGTTAACGGTCACGGAGCTGCTGGACGTCTC
CATGGAGCTGGGCTGTTTCCCTGGCTGGAGCGCTCGTCTCCTCTCAGGGCCCCGTGGTCACCGA
GGAGATCGCCACCTCCATCGAACCCATCCGCGACTTCCCTGGCCATCGTTTTCTTCGCCTCCAT
AGGGCTCCACGTGTTCCCCACGTTTGTGGCGTACGAGCTCACGGTGCTGGTGTTCCCTCACCTT
GTCAGTGGTGGTGATGAAGTTTCTCCTGGCGCGCTGGTCCCTGTCTCTCATTCTGCCGAGGAG
CAGCCAGTACATCAAGTGGATCGTCTCTGCGGGGCTTGCCCAGGTGAGCGAGTTTTCCCTTTGT
CCTGGGGAGCCGGGCGGAAGAGCGGGCGTCATCTCTCGGGAGGTGTACCTCCTTATACTGAG
TGTGACCACGCTCAGCCTCTTGCTCGCCCCGGTGCTGTGGAGAGCTGCAATCACGAGGTGTGT
GCCCAGACCGGAGAGACGGTCCAGCCTC**TGAT**GGCTCGGAGATGATGGACCGTGGAAGGGAAG
CGTCTGTGGGGAGTGAGCGCTTAGATGGCCAGCAGCTGCTCCTTCTGGGAAGCTCGCACCTTG
GCAACAGAACAGCCCTCTAGCAGAGCGTCAGTGCAGTCGTGTTATCCCGGCTTTTACAGAATA
TTCTTGTCCTATTTTAGAATTTTCCGGAGTAGTTTATTTGCAGTCTGTTGATTATGTGCAGTA
GACCCGGGACACTGCGTTTTACCGATCACCTTGAATGTGGTGCCTGGATGTGCCTTTTTTTTT
TTTCCCTGAAATTATTATTAATTTTCTATTGTGAGTTCATCAGTTCATAGTTTTTTTAGTAAA
GAAGCAAAATTAAAAGGCTTTTAAAAATGTACAACCTTCAGAATTATAATCTGTTAGTCAAATA
TTTGTTATTAAACATTTCTGTAATATGAAGTTGTAATCCTGGCCGTGAGCTTGAAGCTTACT
TTTGATTCTTAAAGCCTATGTTTTCTAAAATGAGACAAATACGGATGTCTATTTGCCTTTTTAT
TGTAACTTTTAAATGAAATAATTTTCATGTCAATTTCTATTAGATATATCACTTAAATATTTG
GTTTTAAATCACAAGAATATGTATTCTTTAATAAAGATAATTTATGATCATGGTAAAAA

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FIGURE 230

MKVLGRSFFWVLPVLPWAVQAVEHEEVAQRVIKLRGRGVAAMQSRQWVRDSCRKLSGLLRQ
KNAVLNKLKTAIGAVEKDVGLSDEEKLQVHTFEIFQKELNESENSVFQAVYGLQRALQGDYK
DVVNMKESSRQRLEALREAAIKEETEYMELLAAEKHQVEALKNMQHQNQSLSMLDEILEDVRK
AADRLEEEIEEHAFDDNKSVMGVNFEAVLRVEEEEEANSKQNTKREVEDDLGLSMLIDSQNNQ
YILTKPRDSTIPRADHHFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSTGLNSIK
SIVQVETLGEFGVFFTLFLVGLFEFSPEKLRKVKISLQGPCYMTLLMIAFGLLWGHLLRIKPT
QSVFISTCLSLSSSTPLVSRFLMGSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPPTLIQA
GASASSSIVVEVLRLILVLIGQILFSLAAVFLLCVKKYLLIGPYRKLHMESSKGNKEILILGI
SAFIFLMLTVTELLDVSMELGCFLAGALVSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHV
FPTFVAYELTVLVFLTLVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQVSEFSFVLGSR
ARRAGVISREVYLLILSVTTLSLLLAPVLWRAAITRCVPRPERRSSL

Signal peptide:

amino acids 1-22

Transmembrane domains:amino acids 282-304, 322-337, 354-370, 379-395, 445-474, 501-520,
576-598, 641-660**N-glycosylation sites.**

amino acids 104-108, 174-178, 206-210, 230-234

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 55-59, 673-677

Tyrosine kinase phosphorylation site.

amino acids 407-414

N-myristoylation sites.amino acids 116-122, 327-333, 366-372, 401-407, 419-425, 429-435,
442-448, 525-531, 530-536**Cell attachment sequence.**

amino acids 404-407

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FIGURE 231

GAGAAAAACAACAGGAAGCAGCTTACAACTCGGTGAACAACTGAGGGAACCAAACCAGAGAC
GCGCTGAACAGAGAGAATCAGGCTCAAAGCAAGTGGAAGTGGGCAGAGATTCCACCAGGACTG
GTGCAAGGCGCAGAGCCAGCCAGATTTGAGAAGAAGGCAAAAAGATGCTGGGGAGCAGAGCTG
TAATGCTGCTGTTGCTGCTGCCCTGGACAGCTCAGGGCAGAGCTGTGCCTGGGGGCAGCAGCC
CTGCCTGGACTCAGTGCCAGCAGCTTTCACAGAAGCTCTGCACACTGGCCTGGAGTGCACATC
CACTAGTGGGACACATGGATCTAAGAGAAGAGGGAGATGAAGAGACTACAAATGATGTTCCCC
ATATCCAGTGTGGAGATGGCTGTGACCCCCAAGGACTCAGGGACAACAGTCAGTTCTGCTTGC
AAAGGATCCACCAGGGTCTGATTTTTTATGAGAAGCTGCTAGGATCGGATATTTTCACAGGGG
AGCCTTCTCTGCTCCCTGATAGCCCTGTGGGCCAGCTTCATGCCTCCCTACTGGGCCTCAGCC
AACTCCTGCAGCCTGAGGGTCACCACTGGGAGACTCAGCAGATTCCAAGCCTCAGTCCCAGCC
AGCCATGGCAGCGTCTCCTTCTCCGCTTCAAATCCTTCGCAGCCTCCAGGCCTTTGTGGCTG
TAGCCGCCCCGGTCTTTGCCCATGGAGCAGCAACCCTGAGTCCCTAAAGGCAGCAGCTCAAGG
ATGGCACTCAGATCTCCATGGCCCAGCAAGGCCAAGATAAATCTACCACCCAGGCACCTGTG
AGCCAACAGGTTAATTAGTCCATTAATTTTAGTGGGACCTGCATATGTTGAAAATTACCAATA
CTGACTGACATGTGATGCTGACCTATGATAAGGTTGAGTATTTATTAGATGGGAAGGGAAATT
TGGGGATTATTTATCCTCCTGGGGACAGTTTGGGGAGGATTATTTATTGTATTTATATTGAAT
TATGTACTTTTTTCAATAAAGTCTTATTTTTGTGGCTAAAAAAAAAAAAA

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FIGURE 232

MLGSRAVMLLLLLPWT AQGRAVPGGSSPAWTQCQQLS QKLCTLAWSAHPLVGHMDLREEGDEE
TTNDVPHIQCGDGC DPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTGEPSLLPDSPVGQLHA
SLLGLS QLLQPEGHHWETQQIPSLSPSQPWQRLLLRFKILRSLQAFVAVAAARVFAHGAATLSP

Important features of the protein:

Signal peptide:

amino acids 1-21

Casein kinase II phosphorylation site.

amino acids 64-67

N-myristoylation sites.

amino acids 25-30, 81-86, 122-127

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FIGURE 233

CCCACGCGTCCGGCCCTGTAACCAAGATACTGACTGAACATGGCTGGCGGACTCAGGCTGGGGTCTGCAGTGCAG
CATTAAATGGGCGGCTGACATGAATATGGAGTAGTTTTCTCTAGCAAAGAGTAATGTTGGGCCATGGAGTCAAGGCCA
CCTCCTCTGGGCTCTGCTGTTTCATGCAGTCTTGTGGCCTCAACTGACTGATGGAGCCACTCGAGTCTACTACCT
GGGCATCCGGGATGTGCAGTGGAACTATGCTCCCAAGGGAAGAAATGTCATCACGAACCAGCCTCTGGACAGTGA
CATAGTGGCTTCCAGCTTCTTAAAGTCTGACAAGAACCGGATAGGGGGAACCTACAAGAAGACCATCTATAAAGA
ATACAAGGATGACTCATACACAGATGAAGTGGCCAGCCTGCCTGGTTGGGCTTCCTGGGGCCAGTGTTCAGGC
TGAAGTGGGGGATGTCATTCTTATTCACCTGAAGAATTTTGCCACTCGTCCCTATACCATCCACCCTCATGGTGT
CTTCTACGAGAAGGACTCTGAAGGTTCCCTATACCCAGATGGCTCCTCTGGGCCACTGAAAGCTGATGACTCTGT
TCCCCGGGGGGCAGCCATATCTACAACCTGGACCATTCCAGAAGGCCATGCACCCACCGATGCTGACCCAGCGTG
CCTCACCTGGATCTACCATTCTCATGTAGATGCTCCACGAGACATTGCAACTGGCCTAATTGGGCTCTCATCAC
CTGTAAAAGAGGAGCCCTGGATGGGAACCTCCCCTCCTCAACGCCAGGATGTAGACCATGATTCTTCTCCTCTT
CAGTGTGGTAGATGAGAACCCTCAGCTGGCATCTCAATGAGAACATTGCCACTTACTGCTCAGATCCTGCTTCAGT
GGACAAGAAGATGAGACATTTTCAGGAGAGCAATAGGATGCAATGCAATGAGCTTTGTTTTTGGGAATTTACC
TGAGCTGAACATGTGTGCACAGAAACGCTGTGGCCTGGCACTTGTTCGGCATGGGCAATGAAATGATGTCCACAC
AGCATTTTCCATGGACAGATGCTGACTACCCGTGGACACCACACTGATGTGGCTAACATCTTCCAGCCACCTT
TGTGACTGCTGAGATGGTGGCCTGGGAACCTGGTACCTGGTTAATTAGCTGCCAAGTGAACAGTCACTTTCGAGA
TGGCATGCAGGCACTCTACAAGGTCAAGTCTTGCTCCATGGCCCCCTCTGTGGACCTGCTCAGGCAAGATTCG
ACAGTACTTCATTGAGGCCCATGAGATTCAATGGGACTATGGCCGATGGGGCATGATGGGAGTACTGGGAAGAA
TTTGAGAGAGCCAGGCAGTATCTCAGATAAGTTTTTCCAGAAGAGCTCCAGCCGAATTGGGGGCACTTACTGGAA
AGTGGCATATGAAGCCTTTTCAAGATGAGACATTTCCAAGAGAAGATGCATTTGGAGGAAGATAGGCATCTTGGAA
CCTGGGGCCAGTGATCCGGGCTGAGGTGGGTGACACCATTTCAGGTGGTCTTCTACAACCGTGCCTCCAGCCATT
CAGCATGCAGCCCATGGGGTCTTTTATGAGAAAGACTATGAAGGCACTGTGTACAATGATGGCTCATCTTACCC
TGGCTTGGTTGCCAAGCCCTTTGAGAAAGTAACATACCGCTGGACAGTCCCCCTCATGCCGGTCCCCTGCTCA
GGATCCTGCTTGTCTCACTTGGATGTACTTCTGCTGCAGATCCCATAGAGACACAAATCTGGCCTGGTGGG
CCCCCTGCTGGTGTGCAGGGCTGGTGCCTTGGGTGCAGATGGCAAGCAGAAAGGGTGGATAAAGAATCTTCTCT
TCTCTTCACTGTGTGGATGAGAACAGAGCTGGTACAGCAATGCCAATCAAGCAGCTGCTATGTTGGATTTCCG
ACTGCTTTTCAGAGGATATTGAGGGCTTCCAAGACTCCAATCGGATGCATGCCATTAATGGGTTTCTGTTCTCTAA
CCTGCCCAGGCTGGACATGTGCAAGGGTGACACAGTGGCCTGGCACCTGCTCGGCCTGGGCACAGAGATGATGT
GCATGGAGTCATGTTCCAGGGCAACACTGTGCAGCTTCAAGGCATGAGGAAGGGTGCAGCTATGCTCTTCTCA
TACCTTTGTATGGCCATCATGCAGCCTGACAACTTCCCTAGTGTCTGGCCACCAAGCCACCCCTCGCCAACGCTACCA
AGAAGCAGGGATGAGGGCAATCTATAATGTCTCCCTAGTGTCTGGCCACCAAGCCACCCCTCGCCAACGCTACCA
AGCTGCAAGAATCTACTATATCATGGCAGAAGAAGTAGAGTGGGACTATTGCCCTGACCGGAGCTGGGAACGGGA
ATGGCACAACCAGTCTGAGAAGGACAGTTATGGTTACATTTTCTGAGCAACAAGGATGGGCTCCTGGGTTCGAG
ATACAAGAAAGCTGTATTTCAGGGAATACACTGATGGTACATTTCAGGATCCCTCGGCCAAGGACTGGACCAAGA
ACACTTGGGAATCTTGGGTCCACTTATCAAAGGTGAAGTTGGTGATATCCTGACTGTGGTATTCAAGAATAATGC
CAGCCGCCCCCTACTCTGTGCATGCTCATGGAGTGTGCTACTACTGTCTGGCCACTGGCTGCTGAGCCTGG
TGAGGTGGTCACTTATCAGTGGAAACATCCCAGAGAGGTCTGGCCCTGGGCCAATGACTCTGCTTGTGTTTCTCTG
GATCTATTATTCTGCAGTGGATCCCATCAAGGACATGTATAGTGGCCTGGTGGGGCCCTTGGCTATCTGCCAAA
GGGCATCCTGGAGCCCCATGGAGGACGGAGTGACATGGATCGGGAATTTGCATTGTTGTTCTTGATTTTGTATGA
AAATAAGTCTTGGTATTTGGAGGAAAATGTGGCAACCCATGGGTCCCAGGATCCAGGCAGTATTAACCTACAGGA
TGAAACTTTCTTGGAGAGCAATAAAATGCATGCAATCAATGGGAAACTCTATGCCAACCTTAGGGGTCTTACCAT
GTACCAAGGAGAACGAGTGGCCTGGTACATGCTGGCCATGGGCAAGATGTGGATCTACACACCATCCACTTTCA
TGCAGAGAGCTTCTCTATCGGAATGGCGAGAATACCGGGCAGATGTGGTGGATCTGTTCCAGGGACTTTTGA
GGTTGTGGAGATGGTGGCCAGCAACCTGGGACATGGCTGATGCACTGCCATGTGACTGACCATGTCCATGCTGG
CATGGAGACCCTCTTCACTGTTTTTCTCGAACAGAACCTTAAGCCCTCTCACCCTCATACCAAAGAGACTGA
AAAAGTGCCCCCAGAGACATTGAAGAAGGCAATGTGAAGATGCTGGGCATGCAGATCCCCATAAAGAATGTTGA
GATGCTGGCCTCTGTTTTGGTTGCCATTAGTGTACCCCTTGTCTGCTGTTGTTCTGGCTCTTGGTGGAGTGGTTG
GTACCAACATCGACAGAGAAAGCTACGACGCAATAGGAGGTCCATCCTGGATGACAGCTTCAAGCTTCTGTCTTT
CAACACGTAACATCTGGAGCCTGGAGATATCCTCAGGAAGCACATCTGTAGTGCATCCCAGCAGGCCATGGACT
AGTCACTAACCCACACTCAAGGGGCATGGGTGGTGGAGAAGCAGAAGGAGCAATCAAGCTTATCTGGATATTT
CTTTCTTTATTTATTTTACATGGAAATAATATGATTTTCACTTTTCTTTAGTTTCTTTGCTCTACGTGGGCACCT
GGCACTAAGGAGTACCTTATTATCTACATCGCAAATTTCAACAGCTACATTATATTTCTTCTGACCTTGGGA
AGGTATTGAATTTCTAGAAATGTATCCTTCTCACAAGTAGAGACCAAGAGAAAACTCATTGATTGGGTTTCT
ACTTCTTTCAAGGACTCAGGAAATTTCACTTTGAACTGAGGCCAAGTGAGCTGTTAAGATAACCCACACTTAAC
TAAAGCTAAGAAATATAGGCTTGTGGGAAATTGAAGGTAGGCTGAGTATTGGGAATCCAAATTGAATTTTGATT
CTCCTTGGCAGTGAACACTTTGAAGAAGTGGTCAATGGGTTGTTGCTGCCATGAGCATGTACAACCTCTGGAGC
TAGAAGCTCCTCAGGAAAGCCAGTTCTCCAAGTTCTTAACCTGTGGCACTGAAAGGAATGTTGAGTTACCTCTTC
ATGTTTTAGACAGCAACCCCTATCCATTAAGTACTTGTAGACCAAAAAAAAAAAAAA

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FIGURE 234

MWAMESGHELLWALLFMQSLWPQLTDGATRVYYLGIRDVQWNYAPKGRNVITNQPLDSDIVASS
FLKSDKNRIGGTYKKTIIYKEYKDDSYTDEVAQPAWLGFGLGPVLQAEVGDVILHLKNEFATRPY
TIHPHGVFYEEKDSEGSLYPDGSSGPLKADDSVPPGGSHIYNWTIPEGHAPTDADPACLTWIIYH
SHVDAPRDIATGLIGPLITCKRGALDGNSPQQRQDVHDFFLLFSVVDENLSWHLNENIATYC
SDPASVDKEDETFOESNRMHAINGFVFGNLPPELNMCAQKRVAWHLFGMGNEIDVHTAFFHGM
LTTRGHHTDVANIFPATFVTAEMVPWEPGTWLISCQVNSHFRDGMQALYKVKSCSMAPPVDLL
TGKVRQYFIEAHEIQWDYGPMGHGSGTGKNLREPGSISDKFFQKSSSRIGGTYWKVRYEAFQD
ETFQEKMHLEEDRHLGILGPVIRAEVGDTIQVVFYNRASQPFMSQPHGVFYEEKDYEGTVYNDG
SSYPGLVAKPFEEKVYRWTVPFHAGPTAQDPACLTWMYFSAADPIRDTNSGLVGPLLVCRA
LGADGKQKGVDEKFFLLFTVLNENKSWYSNANQAAAMLDLFRLLSEIDIEGFQDSNRMHAINGFL
FSNLPRLDCKGDTVAWHLGLGTETDVHGVFMFQGNQVQLQGMKGAAMLPHTFVMAIMQPD
NLGTFEIYCQAGSHREAGMRAIYNVSQCPGHQATPRQRYQAARIYYIMAEVEWDYCPDRSWE
REWHNQSEKDSYGYIFLSNKDGLLGSRYKKAUFREYTDGTFRIIPRPTGPEEHLGILGPLIKG
EVGDILTVVFKNNASRPYSVHAHGVLESTTVWPLAAEPGEVVITYQWNIPERSGPGPNDSACVS
WIIYSADVPIKDMYSGLVGPLAICQKGILEPHGGRSDMDREFALLFLIFDENKSWYLEENVAT
HGSQDPGSINLQDETFLSNKMHAINGKLYANLRLTMYQGERVAWYMLAMQDQDVLHTIHFH
AESFLYRNGENYRADVVDLFPGTFEVVMVASNPGTWLMHCHVTDHVVHAGMETLFTVFSRTEH
LSPLTVITKETEKVPPRDIEEGNVKMLGMQIPIKNVEMLASVLVAISVTLLLVVLALGGVVWY
QHRQRKLRNRNRSILDDSFKLLSEFKQ

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 1109-1130

N-glycosylation sites.amino acids 167-171, 239-243, 591-595, 717-721, 761-765, 832-836,
876-880, 934-938**Glycosaminoglycan attachment site.**

amino acids 871-875

Tyrosine kinase phosphorylation sites.

amino acids 82-90, 137-145, 494-502, 513-521

N-myristoylation sites.amino acids 212-218, 313-319, 498-504, 566-572, 672-678, 778-784,
843-849**Multicopper oxidases signature 1.**

amino acids 344-365, 696-717, 1043-1064

Multicopper oxidases signature 2.

amino acids 1048-1060

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FIGURE 235

GGAAAGAGTGCTGGTACTACAACCAGGAAGTGACAGATAATGTGCTTTAAACTACATTAGAAAAGCTTCTCATAG
CAAAACTGAGAGATTGAAGCAGTGATTATTTTACATAGTTGTCATTAAATATTTGGAGCTCTGCTGTGCATAGA
GATGGCAACATACTTAGAATACACAGCTTTCTGGGCCAGAAATTGATCTTCTGACTTTTGAGCCTTATCTGATTA
CTGCTTGGTTTCATCTTTATTTTGTAACTACTCTGTAGGCTGAAAGGGAGAGACTCTCCTTGGTTTGAGAGCC
TGACTAGACAGGAATTCTGGCAACTGCTCCAGCAGAATATGGCACTGAGCTAGGTTTAAATGCTGAGGAGATGG
AAAACCTGTCACTGTGATTGAGGATGTGCAGCCAAGAAGTCCAGGAAGAAGCAGCTTGGATGACTCTGGGGAGA
GAGATGAAAAATTATCCAAGTCAATCAGTTTACCAGTGAATCAATTAGTCGGGTTTCAGAAACAGAGTCATTCTG
ATGGAAATTCATCAAAAGGAGGATTAGGCAAGAGGAGTCCCAAAATGAGAAACAGACCAGGAGAGTCTCTTAC
CAACTTTGGAAAAGAAGTTAACTAGAGTGCCATCAAAGTCACTGGACTTGAATAAAAATGAATATCTTCTCTGG
ACAAAAGCAGCACTTCAGATTCTGTTGATGAAGAAAATGTTCTGAGAAAGATCTTCATGGAAGACTTTTTATCA
ACCGTATTTTTCATATCAGTGCTGACAGAATGTTTGAATTGCTCTTACCAGTTACCGCTTTATGCAGAAATTTG
CCAGTTCTAGAAATATAATAGATGTAGTATCTACCCCTTGGACTGCAGAACTTGGAGGTGATCAGCTGAGAACGA
TGACCTACACTATAGTCCTTAATAGTCCACTTACTGGAAAATGCACTGCTGCCACTGAAAAGCAGACACTGTATA
AAGAAAGTCGGGAAGCAGATTTTATTTGGTAGATTTCAGAAGTACTGACACATGATGTCCCCTACCATGATTACT
TCTATACCGTGAACAGATACTGTATCATCCGATCTTCAAACAGAAATGCAGGCTAAGAGTTTCCACAGATTTGA
AATACAGAAAAACAGCCATGGGGCCTTGTCAAATCTTTAATTGAAAAGAATTCCTGGAGTTCTTTGGAGGACTATT
TCAAACAGCTTGAATCAGATTTGTTAATTGAAGAATCTGTATTAAATCAGGCCATTGAAGACCCCTGGAAAACCTA
CTGGCCTACGAAGGAGAAGGCGAACCTTCAACCGAACAGCAGAAACAGTTCTTAACTTTCTCTCAGCATTCTT
CTGGAGATGTGGGCTTAGGTGCCAAAGGGGATATTACAGGAAAGAAAAGGAAATGGAAAACCTATAACGTCACCT
TTATTGTGGTAATGAGTATTTTGTGTGTTATTAGTTTTGTTGAATGTGACACTGTTTCTGAAGCTGTCAAAGA
TAGAACATGCTGCTCAGTCTTTTACCCTCTCCGCTCCAAGAAGAGAAATCTTTAAATTTAGCCTCTGATATGG
TGTCAGAGCAGAACTATTGAGAAGATAAGATCAGGCCATCGTTTAAAGGGAGTGCTCCGAGACTCCATAG
TGATGCTTGACAGCTGAAGAGCTCACTCATTATGCTTCAGAAAACGTTTGATCTACTAAATAAGAATAAGACTG
GCATGGCTGTGAAAGCTAGTGATCTGAAGGACTAAAACCGCAGAGATACTTGGAACTTAAAGAAAATACCTGGA
AGAAAACCAGACGAATGAAGGATTTTGGCATAGAACATTTCTATGTTTTTTCATTATTGAGATTTCTAATATGAA
CATTCTCTTTCAGTAACATTTATTTGATAATTAGTTTTCTGCTGGCCTTAATAATCCATCCTTTCACTTCTTATAGA
TATTTTTAAGCTGTGAATTTCTTCAGTGAACCATGAAATATATTATAGAACTGAATTTCTCTGATACAAAAGAA
AATGACACACCCCTGAATTGAGTGGTATGGTCTCATTTCTACAGTGAAGTCTGATGCTTTGTTAGCACAGAATCCG
TACATGTCCAATAGGTGCTTTTGTAACTGAGATAAGACCAAGAGGATAAACAGGACAATATAAGAAGAAACCTC
TATGTCATTACTGATTTTAAAGGTTCTGTTTTTCAGGCATATAACATTTCCAGGTTTGTGTACTGTAAAGATTATA
ATGTCCTTCATTTATTTAGCATGCAAATTTAATAGTCAAACTTTTTGAATCTGCATGTTGATGATTATCAGAA
AGGGTCTTCTGCCATGCTGTATCTTTATGAAAGAAATAGTTGTTTTTCTTAAGGTAACATCAGAGGTGGGATT
ATCTTGCCCTCCTCACTTAGAATACCAACAGTCAAAGGAAGAACCATCCTCTGAGTTTTAAAACCAGAAAGGTTA
TGTTAAATCTGGGCATTTAGTGACAGATCAAATGCATACTTGAACCTAAGATTGGCTTCAGCTTAGCAGTCTTTC
ATGGTGGAAGTGACACATCTGGTTGAAAATAATTTGTGTATTTTCAGTAACCATGTATGGCTTCCTTCTTTATGT
ATGTGTGTGACTTGTTTTAAATTGGTAAGTTATAAGCCAGACATAGATTTTAGCTCTTTAATAAAAACCTCAGGGG
CACGTATGTCCAGTACAAGTGACTGACTATCAAGTTTTAACTCAGATGCAAGCTTTGGCTCTTTCATAAAAAG
TTTTTATGCATATGTGTCTCCATACAAGTGGCTCATTAATAAAGAACTTTGTAACTGACTTAAATCAGATAT
TTTTTCAAGAGTTAGGGAAAGTTGAAGTGTCTTACTGTTTTGTCTCTTGAGCCCTTTCTCTGGGGAAAAATACA
TATCCATCTATCTATCTATATATAAACTGTGTATACATTCTTACTGTTTGAACAACTATTGCCTTTAATTAATG
TTTCATTTTTCTCCAGAGTCCCCAAAGCCACATGGCATTATTATAGTCATTTTGAGATGCCTGTAGAGAATGAA
AGTATTGACTCCGTTAGAGGGAAAATGGGTTTCTCTGGGTGAATTTCCAACGAAGCATACCTAGGGGTAACAGTGA
ACCTACCTGGGTTTGTGTTTTGTTTGGTAAGGATTTATGTAGTGTCTGGCTGTAAGCAAGAATGAGTGGATTATAA
ACTTGAAGATTTCTCTGTATAAGTCAAAAAATGATCGACAAACAATATTTTTGTGATGTTTATTTAAACGTTGT
ATTTTATAACATACTTCAAGGAAGAGTATCGAAGTAAGTTGCTTTATAAATTAAGACTAAATTCGTATGGATGCA
GAATTCATTAATAAAATTTGAGCCTGTTACGTAAATTTGAATATTTAATAAAATTGAAAATTTCAAAA

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FIGURE 236

MENLSLSIEDVQPRSPGRSSLDDSGERDEKLSKSI SFTSESISRVS ETE SFDGNSSKGGLGKE
ESQNEKQTKKSLLP TLEKKL TRVPSKSLDLNKNE YLSLDKSSTSDSVDEENVPEKDLHGRLFI
NRIFHISADRMFELLFTSSRFMQKFASSRNIIDV VSTPWT AELGGDQLRTMTYTIVLNSPLTG
KCTAATEKQ TLYKESREARFYLV DSEVLTHDVPYHDYFYTVNRYCIIRSSKQKCRLRVSTD LK
YRKQPWGLVKSLIEKNSWSSLEDYFKQLES DLLIEESVLNQAIEDPGKLTGLRRRRRTFNRTA
ETVPKLSSQHSSGDVGLGAKGDITGKKKEMENYNVT LIVVMSIFVLLLVL LNVT LFLKLSKIE
HAAQSFYRLRLQEEKSLN LASDMVSRAETIQKNKDQA HRLKGVLRDSIVMLEQLKSSLIMLQK
TFDLLNKNKTGM AVES

Transmembrane domain:

amino acids 352-371

N-glycosylation sites.

amino acids 3-7, 54-58, 312-316, 349-353, 367-371, 449-453

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 81-85, 307-311

Tyrosine kinase phosphorylation sites.

amino acids 202-211, 246-254, 341-349

N-myristoylation site.

amino acids 259-265

Amidation site.

amino acids 339-343

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FIGURE 237

CAGGGGCTGGAGGGCAGGGGAGGGGATGATGTCATTCTGCTCGGCGCAATCCTGACCCTGCT
CTGGGCGCCACGGCTCAGGCTGAGGTTCTGCTGCAGCCTGACTTCAATGCTGAAAAGTTCTC
AGGCCTCTGGTACGTGGTCTCCATGGCATCTGACTGCAGGGTCTTCCTGGGCAAGAAGGACCA
CCTGTCCATGTCCACCAGGGCCATCAGGCCCACAGAGGAGGGCGGCCTCCACGTCCACATGGA
GTTCCCGGGGGCGGACGGCTGTAACCAGGTGGATGCCGAGTACCTGAAGGTGGGCTCCGAGGG
ACACTTCAGAGTCCCGGCCTTGGGCTACCTGGACGTGCGCATCGTGGACACAGACTACAGCTC
CTTCGCCGTCTTTACATCTACAAGGAGCTGGAGGGGGCCCTCAGCACCATGGTGCAGCTCTA
CAGCCGGACCCAGGATGTGAGTCCCCAGGCTCTGAAGTCCTTCCAGGACTTCTACCCGACCCT
GGGGCTCCCCAAGGACATGATGGTCATGCTGCCCCAGTCAGATGCATGCAACCCTGAGAGCAA
GGAGGCGCCCTGACACCTCCGGAGCCCCACCCCGCCCTTCCCAGGTGGAGCCAAAGCAGCAG
GCGCCTTTGCCCCTGGAGTCAAGACCCACAGCCCTCGGGGACCACCTGGAGTCTCTCCATCCT
CCACCCCCCGCCTGTGGGATGCCTTGTGGGACGTCTCTTTCTATTCAATAAACAGATGCTGCA
GCCTCA

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FIGURE 238

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMAASDCRVFLGKKDHLMSSTRAI
RPTEEGGLHVHMEFFPGADGCNQVDAEYLLKVGSEGHFRVPALGYLDVRIVDTDYSSFAVLYIYK
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

Signal peptide:

amino acids 1-20

Tyrosine kinase phosphorylation site.

amino acids 110-117

N-myristoylation sites.

amino acids 7-13, 79-85, 130-136

Amidation site.

amino acids 50-54

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FIGURE 239

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCTGCCCCGAGGCGGTTCA
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGGAAGGAGGCGTGGATATGGAGCTGGCTGCT
GCCAAGTCCGGGGCCCCGCGCCGCTGCCTAGCGCGTCCTGGGGACTCTGTGGGGACGCGCCCCG
CGCCGCGGCTCGGGGACCCGTAGAGCCCGCGCTGCGCGCATGGCCCTGCTCTCGCGCCCCG
GCTCACCTCCTGCTCCTCCTCATGGCCGCTGTTGTCAGGTGCCAGGAGCAGGCCAGACCAC
CGACTGGAGAGCCACCCTGAAGACCATCCGGAACGGCGTTTCATAAGATAGACACGTACCTGAA
CGCCGCTTGGACCTCCTGGGAGGCGAGGACGGTCTCTGCCAGTATAAATGCAGTGACGGATC
TAAGCCTTTCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT
TGGTGTTTCATCTTAACATTGGTATCCCTTCCCTGACAAAGTGTTGCAACCAACACGACAGGTG
CTATGAGACCTGTGGCAAAGCAAGAATGACTGTGATGAAGAATTCCAGTATTGCCTCTCCAA
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTTCAGGCATGTGAAACAAC
AGTGGAGCTCTTGTTTGACAGTGTTATACATTTAGGTTGTAAACCATATCTGGACAGCCAACG
AGCCGCATGCAGGTGTCATTATGAAGAAAAAACTGATCTTTTAAAGGAGATGCCGACAGCTAGT
GACAGATGAAGATGGAAGAACATAACCTTTGACAAATAACTAATGTTTTTACAACATAAACT
GTCTTATTTTTGTGAAAGGATTATTTTGAGACCTTAAAATAATTTATATCTTGATGTTAAAC
CTCAAAGCAAAAAAAGTGAGGGAGATAGTGAGGGGAGGGCACGCTTGTCTTCTCAGGTATCTT
CCCCAGCATTGCTCCCTTACTTAGTATGCCAAATGTCTTGACCAATATCAAAAACAAGTGCTT
GTTTAGCGGAGAATTTTGAAAAGAGGAATATATAACTCAATTTTCACAACCACATTTACCAA
AAAAGAGATCAATATAAAATTCATCATAATGTCTGTTCAACATTATCTTATTTGGAAAATGG
GGAAATTATCACTTACAAGTATTTGTTTACTATGAAATTTTAAATACACATTTATGCCTAGAA
GGAACGGACTTTTTTTTTCTATTTTAATTACACATAATATGTAATTAAAGTACAACATAATAT
GTTGTTTCTCTGTAGCCCGTTGAGCATATGAGTAAGTCACATTTCTATTAGGACTACTTACAA
GGACAAGGTTTCCATTTTCCAGTTGTAAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG
CAACCCAGGATAGCTAAGTGTTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTGAGAA
GCATAGCCACTCCATTTTATGAGCTACTCACATGACAAATGTCATCTTTGCTATAACCTTT
GCCAAGTTAGAGAAAAGATGGATTTAATGAGATAAATGAAAAGATATTTAACCTAAAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 240

MALLSRPALTLLLLLMAAVVRCQEQAQTTDWRATLKTIRNGVHKIDTYLNAALDLLGGEDGLC
QYKCSDGSKPFPRYGYKPSPPNGCGSPLEFGVHLNIGIPSLTKCCNQHDRCYETCGKSKNDCDE
EFQYCLSKICRDVQKTLGLTQHVQACETTVELLFDSVIHLGCKPYLDSQRAACRCHYEKTDL

Important features:**Signal peptide:**

amino acids 1-22

N-myristoylation sites:

amino acids 57-63, 93-99

Phospholipase A2 histidine active site:

amino acids 106-114

Neuraxin and MAP1B proteins repeat proteins Block:

amino acids 109-137

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FIGURE 241

GATTCCGAGCGCCTCCACTGCTGGTCCGTTGGCCAGATCAACTCGCCGCGTGGGCCGGCCGTT
CCCTGAGAGTCTGAGCGCTCGCCGCACCCCTTCCGAGCTTCTATTGGCCGTAGCAGACGTCC
GTCTGCCGCTATCTCCGCCCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGGTG
TCCAGGCCATGGGGCAGCCCTGGGCGGCTGGGAGCACGGACGGGGCGCCCGCGCAGCTGCCTC
TCGTGCTCACCGCGCTGTGGGCCGCGGCCGTGGGCCTGGAGCTGGCTTACGTGCTGGTGCTCG
GTCCCGGGCCGCGCCGCTGGGACCCCTGGCCCGGGCCTTGACAGCTGGCGCTGGCCGCCTTCC
AGCTGCTCAACCTGCTGGGCAACGTGGGGCTCTTCTGCGCTCGGATCCCAGCATCCGTGGCG
TGATGCTGGCCGGCCGCGGTCTGGGCCAGGGCTGGGCTTACTGCTACCAATGCCAAAGCCAGG
TGCCGCCACGCAGCGGACACTGCTCTGCCTGCCGCGTCTGCATCCTGCGTCTGGGACCACCACT
GCCGCTGCTGGGCCGCTGCGTGGGCTTCGGCAACTACCGGCCCTTCCTGTGCCTGCTGCTTC
ATGCCGCCGGCGTCTGCTCCACGTCTCTGTGCTGCTGGGCCCTGCACTGTCGGCCCTGCTGC
GAGCCCACACGCCCTCCACATGGCTGCCCTCCTCTGCTTCCCTGGCTCATGTTGCTCACAG
GCAGAGTGTCTCTGGCACAGTTTGCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGCGC
TGCTGTGCGGGGCTGGGCTGCTCTTCCATGGGATGCTGCTGCTGCGGGGCCAGACCACATGGG
AGTGGGCTCGGGGCCAGCACTCCTATGACCTGGGTCCCTGCCACAACCTGCAGGCAGCCCTGG
GGCCCCGCTGGGCCCTCGTCTGGCTCTGGCCCTTCCTGGCCTCCCCATTGCCTGGGGATGGGA
TCACCTTCCAGACCACAGCAGATGTGGGACACACAGCCTCCTTGACTCCAGGAAGAGCCAGAGC
TGTGCAGGGAGGAAGGGGTGAGAGGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT
GGACCTTAACATCTGCATTGGACAACCTCCACCCCTTCCTTGGCCTTGCCCCTGCCCCGCTACA
CTCCTACGTGTCCAGGGCTTGGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG
GGGCTGCTCAGGCCGCCTAGCTGCCCCTTTGCCAGGTTAATAAAGCACTGACTTGTTAA

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FIGURE 242

MGQPWAAGSTDGAPAQLPLVLTALWAAVGLLAYVLVLGPGPPPLGPLARALQLALAAFQLL
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRSGHCSACRVCILRRDHHCRLL
LGRCVGFGNYRPFCLLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLLPWLMLLTGRV
SLAQFALAFVTDTCVAGALLCGAGLLFHGMILLRGQTTWEWARGQHSDYDLGPCHNLQAALGPR
WALVWLWPFLASPLPGDGITFQTTADVGHSTAS

Important features:**Signal peptide:**

amino acids 1-30

Transmembrane domain:

amino acids 51-66, 143-160, 174-191, 198-214

N-myristoylation sites:

amino acids 2-8, 8-14, 30-36, 81-87, 88-94, 90-96, 206-212

Leucine zipper pattern:

amino acids 143-165, 150-172, 157-179, 164-186

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FIGURE 243

CTTGTCTTTGTGTCGGTTGTGATTTTCCTAATCTCTGATTTTCCTTTTCTCTCGGACGCTCTC
CCTCTTCGGACCCATTTTCTCCCGTGCTTCATGCCCTGATAGCCTGGCCCCCTTCCCGGCTTCC
TTCGCTACCGGGGACGCCTCTAGTTTTTCTGAATTTCTGGCTGGCTCCACCCTCCGCGTTTCAT
CTTCTCAAGAGTTCGCCCCCTCTGGGGGCTCCTCTGTGTAATCGTCGCCTTCTCTGGGTATTT
CTGTGAACTCCGTCTCACACCATCCCGCCATCTTCTCTGCCTTGGCCCCCTTTTCTCTGTACAG
CCAGCTCTGTGTCCTTTTCTTCTCCCCCTCTAAAATCGACTCCTCTTCTCCCTGAGAGCCCCA
CCTTTGTGCCCCACTCCTCATTTTCTACGCCTCCCTCTCTCTGCTGGTCTCTCTCTCCCTG
CAAGGTTCCATTCCATCAATTTGTTTGTCTTTTGTAGGGGTGGCATCCCCCTCTGACTACTGCT
CCATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTGAGGATTTCACTTCAATCTTTTCTGGT
TGCGTCTCCACTGTACTCAGCTTGTTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC
GTGTGCTGTCTTCTCTGATTGGCCTAATCTCCCTCACCCCGTGAGATCTGTTGTACGCCTTC
GTTTCTCTTTCTGTGTCCCAGCTTTTCTGCGGGTCTTGGCACCTTTCTTGGCCACAGATTTCT
TGGGTTACAGAGCATGTGTGTCTGAGGCATTGCAGGCAGAAAAGGGTGGCCGACGTGACCTCT
AGCTGGACTGCTGGGCAGGGGAGCTGTCCTAGATAAAATTGGAAAGAAACAGTGACCCAGAGA
CAGGTGGACAAAGAATTCGGGGACTGATGGGAAGTGAAGTGGGATCCAGACTGAAACTGATT
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGGCCATGGGACCCCAGCATTTGAGACT
TGTGCAGCTGTTCTGCCTTCTAGGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTCTTTTGTG
CTATGAAGCAACAGCCTCAAGATTCAGAGCTGTTGCTTTCCATAACTGGAAGTGGCTTCTGAT
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTCAATTGAGACAGG
GACTGCAAGGGGAGTTGTGGGCTTTAAAGGCTGCAGCTCGTCTTCGTCTTACCCTGCGCAAAT
CTCCTACCTTGTTTCCCCACCCGGAGTGTCCATTGCCTCCTACAGTCGCGTCTGCCGGTCTTA
TCTCTGCAACAACCTCACCAATTTGGAGCCTTTTGTGAAACTCAAGGCCAGCACTCCTAAGTC
TATCACATCTGCGTCCTGTAGCTGCCCCGACCTGTGTGGGCGAGCACATGAAGGATTGCCTCCC
AAATTTTGTACCACTAATTCTTGCCCCCTGGCTGCTTCTACGTGTTACAGTTCCACCTTAA
ATTTTCAAGGCAGGGTTTCTCAATACCACCTTCCTCCTCATGGGGTGTGCTCGTGAACATAACCA
GCTTTTAGCAGATTTTTCATCATATTGGGAGCATCAAAGTGAAGTGGTCTCAACATCTTAGA
GAAGTCTCAGATTGTTGGTGCAGCATCCTCCAGGCAAGATCCTGCTTGGGGTGTGCTCTTAGG
CCTCCTGTTTGCCTTCAGGGACTGACCATCTAGCTGCACCCGACAAGCACCCAGACTCTTTCA
CATAACAAATAAAATAGCAGAGTTCCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

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FIGURE 244

MGPQHLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRAVAFHNWKWLLMRNMVCKLQEGCEE
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSTLKFQAGFLNTTFLLM
GCAREHNQLLADFHHIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFAFRD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites:

amino acids 117-121, 183-187

N-myristoylation sites:amino acids 16-22, 25-31, 60-66, 71-77, 81-87, 100-106, 224-230,
235-241, 239-245**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192

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FIGURE 245

GTGGAGTTGGGTGGTGTCTGGGAGCCTCTCCCTGAGGGGCACCGCGTCTTCAGGAGCTGGGCCTCCAGTGCGGGCGC
GATGTCAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGGCCGTGGCGCTGGGCGGCTGCGGGGCTGACCGG
TCCGCTCCATGGTGCCGCCACGACGCCATCGCGGGCAGGAAGGCCAGGGGTGCTGAGTTCTTCACCTCCTTTTAG
ACTGAGATCTGCCAAGTTTTCCGGCATTGCTCTTGAGGATCTCAGAAGGGCTCTTAAGACAAGACTGCAAATGGT
GTGTGATTTGTTCATGAACCGAATGAATCCCAGAACAGTGGTTTCACTCAGCGCAGGCGAATGGCTCTTGGGAT
TGTTATTCTTCTGCTTGTTGATGTGATATGGGTTGCTTCCTCTGAACCTACTTCGTATGTTTTTACCCAGTACAA
CAAACCATTCTTCAGCACCTTTGCAAAAACATCTATGTTTGTTTTGTACCTTTTGGGCTTTATTATTGGAAGCC
ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTTGCAGATGCTGAAGGTTACTTTGC
TGCTTGACACAACAGATACAACCTATGAATAGTTCTTTGAGTGAACCTCTGTATGTGCCTGTGAAATCCATGATCT
TCCAAGTGAAAAACCTGAGAGCACAACATTGATACTGAAAAACCCCCAAAAAGTCTCGTGTGAGGTTTCAGTAA
TATCATGGAGATTTCGACAGCTTCCGTCAAGTCATGCATTGGAAGCAAAGTTGTCTCGCATGTCATATCCTGTGAA
AGAACAAGAATCCATACTGAAAACTGTGGGGAACTTACTGCAACTCAAGTAGCGAAAATTAGCTTTTTTTTTTTG
CTTTGTGTGGTTTTTTGGCAAATTTGTCATATCAAGAAGCACTTTCAGACACACAAGTTGCTATAGTTAATATTTT
ATCTTCAACTTCCGGACTTTTTACCTTAATCCTTGCTGCAGTATTTCCAAGTAACAGTGGAGATAGATTTACCTT
TTCTAAACTATTAGCTGTAATTTTAAGCATTGGAGGCGTTGTACTGGTAAACCTGGCAGGGTCTGAAAAACCTGC
TGGAAGAGACACAGTAGGTTCCATTTGGTCTCTTGCTGGAGCCATGCTCTATGCTGTCTATATTGTTATGATTAA
GAGAAAAGTAGATAGAGAAGACAAGTTGGATATTCCAATGTTCTTTGGTTTTGTAGGTTTGTTAATCTGCTGCT
CTTATGGCCAGGTTTTCTTTTTACTTCATTATACTGGATTTGAGGACTTCGAGTTTCCCAATAAAGTAGTATTAAT
GTGCATTATCATTAAATGGCCTTATTGGAACAGTACTCTCAGAGTTCCTGTGGTTGTGGGGCTGCTTCTTACCTC
ATCATTGATAGGCACACTTGCACTAAGCCTTACAATACCTCTGTCCATAATAGCTGACATGTGTATGCAAAAGGT
GCAGTTTTCTTGTTATTTTTTGCAGGAGCTATCCCTGTATTTTTTTCATTTTTTATTGTAACCTCTCCTATGCCA
TTATAATAATTGGGATCCTGTGATGGTGGGAATCAGAAGAATATTTGCTTTTATATGCAGAAAAACATCGAATTCA
GAGAGTTCAGAAGACAGCGAACAGTGTGAGAGTCTCATTTCTATGCACAGTGTCTCAGGAGGATGGAGCTAG
TTAGCTGTCTGTTGTCTGTAGCCCAGCTTGATAATGGAACATACAGCGAAGAGACAATCTCTGGCAAGTTTTTG
TAGAAAAAATGTTTCAGTGCCTAGTCTGAAAAATAACAGTTTGAGTCTTTTGAACTCTAAAAATATATTTTTCTC
ATACCTGTTTTCTTCATTTTCATAATGAAGCACTTTGCTATGTAGCTGTGTACATATCACTACAGTTATAGGAAG
TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCCTTACACATCTCAAGGAATTCAGCTGTTGAAATCATTTGA
ACTAATCAAGGAATAAATCCTAATGTTCTGGGACTTTATTTTCACATGTTAAATGCTGGAATATATTATGAAAAT
GTTTTCAAGAAATCACTTAAGTGTTCATAGACCAGTATTTCTGACAGGTAAAATGCTAAAATAAGCTACCTGTAA
TAAGTGTGGATTATATTTTTGGGTTTTGTAGAATATTGCAAATTAACCACACAAAAAATGTTTAATTTATGCAAC
AAGCATGTTTGTGCAAATTTTCATGGGACTTTAAAAAGAATAAGTATTTGAGAAAATATCTGGTTCACTTACACTA
CATTTACTGTATTATTCTTTTATAGCATTAGGTGCCTTGATTTTAAATCTGTGACAAACCATGGCAAATTTTTTA
AAGGGGAAGTATTATTATAAAATGAAGAAATATGTATTTCTAAAGGCTATATTGCTGTAACTTAATTGATAAAG
CTCTGTTTAATTTAGAGTTTTGAAGAAATAGTCTCCCTCAATTAAGAAATTTTCATAATGGAATGATTTAAATT
GAAGTGACAAAGAGTATTATTAAAAATACAATGTTTATAAAAAAA

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FIGURE 246

MVPPRRHRGAGRPGVLSSSPFFRLRSKFSGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF
TQRRRMALGIVILLLLVDVIWVASSELTSYVFTQYNKPFESTFAKTSMFVLYLLGFIIWKPWRQ
QCTRGLRGKHAAFFADAEGYFAACTDDTTMNSSLSEPLYVPVKFHDLPSEKPESTNIDTEKTP
KKSRRVFSNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF
LANLSYQEALSDTQVAIVNILSSTSGLFLLILAAVFPSNSGDRFTLSKLLAVILSIGGVVLVN
LAGSEKPAGRDRTVGSIWLAGAMLYAVYIVMIKRKVDREKLDIPMFFGFVGLFNLLLLWPGE
FLLHYTGFEDEFEPNKVVLNCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALSLTIPLSIIA
DMCMQKVQFSWLFFAGAIPVFFSFFIVTLLCHYNNWDPVMVGIRRIFAFICRKHRIQRPEDS
EQCESLISMHSVSQEDGAS

Important features:**Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,
364-379, 399-419, 453-472

N-glycosylation sites:

amino acids 157-161, 255-259

N-myristoylation sites:

amino acids 14-20, 329-335, 404-410, 407-413, 418-424

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FIGURE 247

CGTCTGTAGAGATATCATGAACTTCAACTTAGCTTTGGTACTTTCTTCCCTGAAGACAGAGGG
CAGAACTCTGAGTTCCAGAACCATTTTCAACTGTATTGGGGACCAATCACTTGACTCTATTCT
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTTCTAAACTGAA
TCCTGCTACTAAAATAATTCAGATGATATATTTTTCCAATTCTACAATCTTGCTTTGTTTTAT
TTAGTTGTTTTCTCTCTCTCTTCCCAGTTTTCCAGAGACTGGAGCTAAACTGGGCTTTCAACA
TCATCATGAAGTTTATCCTCCTCTGGGCCCTCTTGAATCTGACTGTTGCTTTGGCCTTTAATC
CAGATTACACAGTCAGCTCCACTCCCCCTTACTTGGTCTATTTGAAATCTGACTACTTGCCCT
GCGCTGGAGTCCTGATCCACCCGCTTTGGGTGATCACAGCTGCACACTGCAATTTACCAAAGC
TTCGGGTGATATTGGGGGTTACAATCCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG
GCTATGAGAAGATGATTCATCATCCACACTTCTCAGTCACCTTCTATTGATCATGACATCATGC
TAATCAAGCTGAAAACAGAGGCTGAACTCAATGACTATGTGAAATTAGCCAACCTGCCCTACC
AAACTATCTCTGAAAATACCATGTGCTCTGTCTCTACCTGGAGCTACAATGTGTGTGATATCT
ACAAAGAGCCCGATTCACTGCAAACCTGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTCGCG
ATGCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGTGGGCATTGTGCCAGGAAGGA
GGCAGCCCTGCAAGGAAGTTTCTGCTGCCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC
TGTCTTTTGC GGATGGATGTGTTTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTTTACT
ATATACCCTGGATTGAAAATGTAATCCAAAATAACTGAGCTGTGGCAGTTGTGGACCATATGA
CACAGCTTGTCCCCATCGTTCACCTTTAGAATTAAATATAAATTAACCTCCTC

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FIGURE 248

MKFILLWALLNLTVALAFNPDYTVSSTPPYLVYLKSDYLPAGVLIHPLWVITAHCNLPKLR
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKLTAEELNDYVKLANLPYQT
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ
PCKEVSAAPAICNGMLQGILSFADGCVLRADVGIIYAKIFYIIPWIENVIQNN

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites:

amino acids 11-15, 156-160, 173-177

Tyrosine kinase phosphorylation site:

amino acids 108-117

N-myristoylation sites:

amino acids 182-188, 203-209

Amidation site:

amino acids 185-189

Serine proteases, trypsin family, histidine active site:

amino acids 52-58

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FIGURE 249

GCGAGGCGGCCGCTGTCTTCTGCTGCGGCTTCCGCGACCACAAGTACTGCTGCGACGACCCGC
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC
TGTCCGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG
TGAACTCCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATAAACATTCA
ATAAATGTCTCCATACCATCAA

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FIGURE 250

MWWLSIGALIGLSVAADVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV
NTGMAAEVPKVSPQQSYSCLPQLESNEGQAVNSKRLHHCFMATVTTSDIPGSPEEASVPN
PDL CGPVP

Important features:

Signal peptide:

Amino acids 1-26

N-myristoylation sites:

Amino acids 7-13, 11-17, 62-68, 93-99

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FIGURE 251

GTGGTTTGGATTGAGCCGGGCCCCGGCCGGGGCGCCGAGTCGGAGGGGGTGGCAGTGAGCGGCG
GCAGAGGCTACGGGGCTCGGTTTGGCTGACTGGGGAGTCGGCAGGCGGCAGGAACCATGCGAG
GCCAGCGGAGCCTGCTGCTGGGCCCCGGCCCGCCTCTGCCTCCGCCTCCTTCTGCTGCTGGGT
ACAGGCGCCGCTGTCCACCTCTACTCCGGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT
GCCTGCGCTCCCTGCTCTACAACCTCTTTGGGGGAGTGACACCGCTGTTGATGCTGCCTTTG
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTTGGAGTGGTGTTCGTGGTCCTGG
TGATCGTGCTGACAGGCTCCATTGTAGCTATCGCCTACCTGTGTGTCTGCCTCTCATCCTCC
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA
TTGTCTTCCACTACTACCAGGCCATCACCCTCCGCCTGGGTACCCACCCAGGGCAGGAATG
ATATCGCCACCGTCTCCATCTGTAAGAAGTGCATTTACCCCAAGCCAGCCCGAACACACCCT
GCAGCATCTGCAACAGGTGTGTGCTGAAGATGGATCACCCTGCCCTGGCTAAACAATTGTG
TGGGCCACTATAACCATCGGTACTTCTTCTCTTCTGCTTTTTTCATGACTCTGGGCTGTGTCT
ACTGCAGCTATGGAAGTTGGGACCTTTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC
AGACCCACCCACCCACCTTCTCCTTTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT
GGTTCCTGTGCAGTTCTGTGGCACTTGCCCTGGGTGCCCTAACTGTATGGCATGCTGTTCTCA
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGAGAGACGTCGGCTACAGG
CCAAGGGCAGAGTATTTAGGAATCCTTACAACCTACGGCTGCTTGGACAACCTGGAAGGTATTCC
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGCTCTTACCTTCTAGTCACTTGCCCC
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG
CAGTGTCAGCTGGACTGTGTGAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTTCA
AGGGCCTCCAAGGGCAGCTTTTCTCAGAATCCTTGATCAAAAAGAGCCAGTGGGCCTGCCTTA
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTTTTACCACTGCAGAAGAAAGACACAATGT
GGAGAAATCTTAGGACTGACATCCCTTTACTCAGGCAAACAGAAGTTCCAACCCAGACTAGG
GGTCAGGCAGCTAGCTACCTACCTTGCCCAGTGCTGACCCGGACCTCCTCCAGGATACAGCAC
TGGAGTTGGCCACCACCTCTTCTACTTGCTGTCTGAAAAACACCTGACTAGTACAGCTGAGA
TCTTGGCTTCTCAACAGGGCAAAGATACCAGGCCTGCTGCTGAGGTCACTGCCACTTCTCACA
TGCTGCTTAAGGGAGCACAAATAAAGGTATTCGATTTTTTAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

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FIGURE 252

MRGQRSLLLGPARLCLRLLLLLGYRRRCPLLRLVQRWRYGKVCLRSLLYNSFGGSDTAVDA
AFEPVYWLVDNVIRWFGVVFVVLVIVLTGSIVAIAYLCVLPLILRTYSVPRLCWHFFYSHWNL
ILIVFHYYQAITTPPGYPPQGRNDIATVSICKKCIYPKPARTHHCSICNRCVLKMDHHC PWLN
NCVGHYNHRYFFSFCFFMTLGCVCYSYGSWDLFREAYAAIETYHQTPPPTFSFRERMTHKSLV
YLWFLCSSVALALGALTVWHAVLISRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWK
VFLGVDTGRLHWLTRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV

Important features:**Transmembrane domain:**

amino acids 88-100,202-216,254-274

N-myristoylation sites:

amino acids 55-61,56-62,92-98,210-216,309-315,319-325,340-346

Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 201-212

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FIGURE 253

GATCAAGCGCCTTCCTTTCCCTTCCTCTCCCTACTTGCCCTTTGCCCTAAGCCAAGACCTGGCCATCAGCCTGGC
TGCAGGGGCGCTGCAGAGCCAGCTGCACTTTTTCAGGTATGGGGGAGGGCCAGGCACCATGAAGCCAGTGTGGGTG
GCCACCCTTCTGTGGATGCTACTGCTGGTGGCCAGGCTGGGGGCGCCCGGAAGGGGTCCCCAGAAGAGGCCTCC
TTCTACTATGGAACCTTCCCTCTTGGCTTCTCCTGGGGCGTGGGCAGTTCTGCCTACCAGACGGAGGGCGCCTGG
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGTCTTCACACACAGTGGGAAGGGGAAAGTGCTTGGGAATGAG
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCCAGGAGGACATCATTCTGCTGAGGGAACTGCACGTCAAC
CACTACCGATTCTCCCTGTCTTGGCCCCGGCTCCTGCCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGA
ATCGAATTCTACAGTGATCTTATCGATGCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGCACTACTGG
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAACTACTTCAGAGACTAC
GCCAACCTGTGCTTTGAGGCCTTTGGGGACCGTGTGAAGCACTGGATCACGTTCACTGATCCTCGGGCAATGGCA
GAAAAAGGCTATGAGACGGGGCCACCATGCGCCGGGCGCTGAAGCTCCGCGGCACCGGCCTGTACAAGGCAGCACAC
CACATCATTAAAGGCCCACGCCAAAACCTGGCATTCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG
GGAATTTCACTGAACTGTGACTGGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCGAGAGA
TACCTACAGTTCTGTCTGGGCTGGTTTGGCAACCCCATTTATGCCGGTGACTACCCCAAGTCATGAAGGACTAC
ATTGGAAGAAAGAGTGCAGAGCAAGGCCTGGAGATGTGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTAC
ATTAAAGGCACATCCGATTTCTTGGGATTAGGTCATTTTACTACTCGGTACATCACGGAAAGGAAGTACCCCTCC
CGCCAGGGGCCCAGCTACCAGAACGATCGTGACTTGATAGAGCTGGTTGACCCAACTGGCCAGATCTGGGGTCT
AAATGGCTATATTCTGTGCCATGGGGATTTAGGAGGCTCCTTAACCTTTGCTCAGACTCAATACGGTGATCCTCCC
ATATATGTGATGGAAAATGGAGCATCTCAAAAATTCCTACTGTACTCAATTATGTGATGAGTGGAGAATTCATAC
CTTAAAGGATACATAAATGAAATGCTAAAAGCTATAAAAGATGGTGCTAATATAAAGGGGTATACTTCCTGGTCT
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTTAACGACAGA
AATAAGCCTCGCTATCCAAAGGCTTCAGTTCAATATTACAAGAAGATTATCATTGCCAATGGGTTTCCCAATCCA
AGAGAGGTGGAAAGTTGGTACCTCAAAGCTTTGGAAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCT
TTGCTAAGTCACATGCAAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGTCCTCATCACTGCT
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCTGAGACAGGATTATCAATTTTGGAGCTTCATAAGAGAATCTT
CAGGATCTTCCTCCCTTTTCTGCTTTGAGGGTTCCATACATTGCTGTTTTCAGGTTCTACAATAATTACCTTTT
TTTCTCTTTCTCTTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAATAAAAATAAGCAGAAATTA

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FIGURE 254

MKPVWVATLLWMLLLVPRLLGAARKGSPEEASFYYGTFPLGFSWGVGSSAYQTEGAWDQDGKGPSIWDVFTTHSGKG
KVLGNETADVACDGYKQVEDIILLRELHVNHYRFSLSWPRLPTGIRAEQVNKKGIEFYSDLIDALLSSNITPI
VTLHHWDLPLQLQVKYGGWQNVSMANYFRDYANLCFEAFGDRVKHWITFSDPRAMAEKGYETGHHAPGLKLRGTG
LYKAAHHIIKAHAKTWHSYNTTWRSSKQQGLVGISLNCWGEPEVDISNPKDLEAAERYLQFCLGWFFANPIYAGDYP
QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITERNYPSRQGPSYQNDRLIELVDPN
WPDLGSKWLYSVPWGFRRLLNFAQTQYGDPIIYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIK
GYTSWSLLDKFEWEKGYSDRYGFYYVEFNDRNKPYPKASVQYYKKIIANGFPNPREVESWYLKALETCSINNQ
MLAAEPLLSHMQMVTETIVVPTVCSLCVLITAVLLMLLLRRQS

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 541-558

N-glycosylation sites:

amino acids 80-84, 171-175, 245-249

Glycosaminoglycan attachment site:

amino acids 72-76

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

amino acids 23-27, 564-568

Tyrosine kinase phosphorylation sites:

amino acids 203-211, 347-355, 460-468, 507-514

N-myristoylation sites:

amino acids 44-50, 79-85, 167-173, 225-231, 257-263, 315-321

Amidation site:

amino acids 307-311

Glycosyl hydrolases family 1 active site:

amino acids 407-416

Glycosyl hydrolases family 1 N-terminal signature:

amino acids 41-56

Motif name Glycosyl hydrolases family:

amino acids 37- 67

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FIGURE 255

CGCGAAGATGCGAAAGGTGGTTTTGATCACCGGGGCTAGCAGTGGCATTGGCCTGGCCCTCTG
CAAGCGGCTGCTGGCGGAAGATGATGAGCTTCATCTGTGTTTGGCGTGCAGGAACATGAGCAA
GGCAGAAGCTGTCTGTGCTGCTCTGCTGGCCTCTCACCCCACTGCTGAGGTCACCATTGTCCA
GGTGGATGTCAGCAACCTGCAGTCGGTCTTCCGGGGCCTCCAAGGAACTTAAGCAAAGGTTTCA
GAGATTAGACTGTATATATCTAAATGCTGGGATCATGCCTAATCCACAATAAATATCAAAGC
ACTTTTCTTTGGCCTCTTTTCAAGAAAAGTGATTCATATGTTCTCCACAGCTGAAGGCCTGCT
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTTGAGACCAATGTCTTTGG
CCATTTTATCCTGATTCGGGAACTGGAGCCTCTCCTCTGTACAGTGACAATCCATCTCAGCT
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTTAGCCTCGAGGACTTCCAGCACAG
CAAAGGCAAGGAACCCTACAGCTCTTCCAAATATGCCACTGACCTTTTGAGTGTGGCTTTGAA
CAGGAACTTCAACCAGCAGGGTCTCTATTCCAATGTGGCCTGTCCAGGTACAGCATTGACCAA
TTTGACATATGGAATTCTGCCTCCGTTTATATGGACGCTGTTGATGCCGGCAATATTGCTACT
TCGCTTTTTTGC AAATGCATTCACCTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT
TTTCCACCAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCACTGGCTT
TGGAAGAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTTTA
TCAAAAGTTACTGGAAGTGGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC
CAGGCTCAGTGGCTCATGCCTATTAAATTCCAGCACTTTGGGAGGCCAAGGCAGAAGGATCACTT
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTTGTCTCTACAAAAGAAAT
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG
GGAGGATCTCTTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC
AGCCTGGGTGACAGCGAGACCCTGTCTCAAAATATGTATATATTTAATATATATATAAAACCA
GAGCTGACAATGACACTCTGGAACATTGCATACCTTCTGTACATTCTGGGGTACATGGATTTC
TACTGAGTTGGATAATATGCATTTGTAATAAACTATGAACTATGAA

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FIGURE 256

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFQHSKG
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLLMPAILLLRF
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGGRNYIMTQKMDLDEDTAEKFYQK
LLELEKHIRVTIQKTDNQARLSGSC

Important features:**Transmembrane domain:**

amino acids 234-254

N-glycosylation sites:

amino acids 37-41,178-182,229-233,263-267

Glycosaminoglycan attachment site:

amino acids 12-16

N-myristoylation sites:

amino acids 9-15,13-19,15-21,215-221,224-230

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FIGURE 257

CGGACGCGTGGGGCCGTATGCGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCCC
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTTGGCCTGCTGGGGGAGA
AGACCCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGCCCCCTGCAGAACCTGCTTC
ATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC
TATCCCCTGAGCCCGATGGGGGCTGATGGTGCTCCCTAAGGACAGCATTTCAGTTTTCTTCTG
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC
CTTTGGGAAGACCATATCCTCCATACTCCTTGCCGATTTCTCTTGGAACAACATCACTGATT
CATTGGATCCTGCCACCCTGAGTGCCACATTTCAAGGCCACCCCATGAACGACCCTACCAGGA
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT
GCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC
AGAAGCCGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCATCCTGCCTTAG
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCCAGAATAACTTCTGTG
CCTTCAATCTGACGTTGCGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCCTGGGCA
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGĈ
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAATTAAGGCCCGCTCTCTGGAGGGAAGG
ACATTACTGAACCTGTCTTGCTGTGCCTCGAACTCTGGAGGTTGGAGCATCAAGTTCCAGCC
GGCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG
AGACCCCCAGGTGGGGCTTCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG
GGCTATTGATAAGGTCCCCTTGCTGTTGCCTTCTTGCACTCTCCACACATTTCCCTTGGATGGG
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA
TTTATTTTTTTTTCACAGGGAAAAA

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FIGURE 258

M R G S V E C T W G W G H C A P S P L L L W T L L L F A A P F G L L G E K T R Q V S L E V I P N W L G P L Q N L L H I R A V G
T N S T L H Y V W S S L G P L A V V M V A T N T P H S T L S I N W S L L L S P E P D G G L M V L P K D S I Q F S S A L V F T R
L L E F D S T N V S D T A A K P L G R P Y P P Y S L A D F S W N N I T D S L D P A T L S A T F Q G H P M N D P T R T F A N G S
L A F R V Q A F S R S S R P A Q P P R L L H T A D T C Q L E V A L I G A S P R G N R S L F G L E V A T L G Q G P D C P S M Q E
Q H S I D D E Y A P A V F Q L D Q L L W G S L P S G F A Q W R P V A Y S Q K P G G R E S A L P C Q A S P L H P A L A Y S L P Q
S P I V R A F F G S Q N N F C A F N L T F G A S T G P G Y W D Q H Y L S W S M L L G V G F P P V D G L S P L V L G I M A V A L
G A P G L M L L G G G L V L L L H H K K Y S E Y Q S I N

Important features:**Signal peptide:**

amino acids 1-35

Transmembrane domain:

amino acids 365-386

N-glycosylation sites:

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 397-401

N-myristoylation sites:

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

Leucine zipper pattern:

amino acids 371-393

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FIGURE 259

CAGGCGGGCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGGCTGAGCAAGGCGCTGCTGCGCCT
CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCTTGCTGGCCTACGTGCGCTCTGTTTG
GGGCAACTTCGTTAATATGAGGTCTATCCAGGAAAATGGTGAATAAAATTGAAAGCAAGATTGAAGAGATGGT
TGAACCACTAAGAGAGAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTTTATC
AGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTCGTGGGCTCCCATCTAACTGACAACTCAT
GATGGACGGCCACGAGGTGACCGTGGTGGACAAATTTCTTCACGGGCAGGAAGAGAAACGTGGAGCACTGGATCGG
ACATGAGAACTTCGAGTTGATTAACCACGACGTGGTGGAGCCCCTCTACATCGAGGTTGACCAGATATACCATCT
GGCATCTCCAGCCTCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAGACCAATACGATTGGGACATT
AAACATGTTGGGGCTGGCAAAACGAGTCGGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC
TGAAGTCCACCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCTACGATGAAGG
CAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAAGTGCAGTGGCCAGAATCTT
CAACACCTTTGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCAGGCGCTCCAGGG
GGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCCAGTACGTACGTCAGCGATCTAGTGAATGGCCT
CGTGGCTCTCATGAACAGCAACGTGAGCAGCCCGTCAACCTGGGGAACCCAGAAGAACACACAATCCTAGAATT
TGCTCAGTTAATTAAAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGCCCAGGATGACCCACA
GAAAAGAAAACCAGACATCAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCCTGGTCCCGCTGGAGGAAGGTTT
AAACAAAGCAATTCACTACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTACATCCCCAAACCAAAGCC
TGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTGAACTCCTCACTTTTAGGACACAAGACTACCATTGTACAC
TTGATGGGATGTATTTTTGGCTTTTTTTTGTGTCGTTTAAAGAAAGACTTTAACAGGTGTCATGAAGAACAAC
TGGAATTTCACTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCCCTCAAAAACTGCAGATTTTG
CCTTGCACTTTTGAATCTCTCTTTTATGTAAATAGCGTAGATGCATCTCTGCGTATTTTCAAGTTTTTTTAT
CTTGCTGTGAGAGCATATGTTGTGACTGTGCTTGACAGTTTTATTTACTGGTTTCTTTGTGAAGCTGAAAAGGAA
CATTAAAGCGGGACAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAATAAATGAGTCGTTATACTATGCAT
AAAGAAAAATCCTAGCAGTATTGTGAGGTGGTGGTGCCTGGCATTGATTTTAGGGCAGATAAAAGAATTCTGTG
TGAGAGCTTTATGTTTCTCTTTAATTCAGAGTTTTTCCAAGGTCTACTTTTGAGTTGCAAACCTGACTTTGAAA
TATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTTGCTGCGTATCTGGGGCGGGGCAGGT
TGGGGGGCACAAAGTTAACATATTCTTGGTTAACCATGGTTAAATATGCTATTTTAATAAAATATTGAAACTCA

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FIGURE 260

MVSKALLRLVSAVNRMRM KLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMMDGHEVTVVDNFFTGRK
RNVEHWIGHENFELINHDVVEPLYIEVDQIYHLASPPPNMYNPIKTLKTNTIGTLNMLGL
AKRVGARLLLASTSEVYGDPEVHPQSEDYWGHNPIGPRACYDEGKRVAETMCYAYMKQEGVE
VRVARIFNTFGPRMHMNDGRVVS NFILQALQGEPLTVYSGSQTRAFQYVSDLVNGLV ALMNS
NVSSPVNLGNPEEHTILEFAQLIKNLVSGSGSEIQFLSEAQDDPQKRKPDIKKAKMLGWEPVV
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

Important features:**Signal peptide:**

amino acids 1-32

N-glycosylation site:

amino acids 316-320

Tyrosine kinase phosphorylation site:

amino acids 235-244

N-myristoylation sites:

amino acids 35-41, 101-107, 383-389

Amidation sites:

amino acids 123-127, 233-237

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FIGURE 261

GCGTGGTGCGGGGCGTGGGGAAATCGGGTTGCCCCAGCCGTTACTGGTCCGCGCAGTCAGGG
CATCCTCCGCATCCTCCACATCCTTCC**ATG**GCTCTGAAGAATAAATTCAGTTGTTTATGGATC
TTGGGTCTGTGTTTGGTAGCCACTACATCTTCCAAAATCCCATCCATCACTGACCCACACTTT
ATAGACAACATGCATAGAAGCCCACAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGAC
ATGAAATACATGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAAGTGC
AAATTTGAACATAATGACTGTTTGGATAAATCATATAAATGCTATGCAGCTTTTGAATATGTT
GGAGAAAATATCTGGTTAGGTGGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGG
TATAATGAAACCCAATTTTATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT
ACACAGTTAGTTTGGGCCAATTCATTTTATGTGCGTTGTGCAGTTGCAATGTGTCCTAACCTT
GGGGGAGCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAATATG
CCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAGAAGAGAAATGTGTAAAGAAC
CTCTGCAGGACTCCACAACCTTATTATACCTAACCAAATCCATTTCTGAAGCCAACGGGGAGA
GCACCTCAGCAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTT**TAA**
TGTCATTTATATACAAAAGAAATCTCAAATGTAAATAAAGGAATAGTTTATTGCTTAATA

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FIGURE 262

MALKNKFSCWLWILGLCLVATTSSKIPSIDPHFIDNCIEAHNEWRGKVNPPAADMKYMIWDKG
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNETQFYDF
DSLSCSRVCGHYTQLVWANSFYVGCAMCPNLGGASTAIFVCNYGPAGNFANMPPYARGESC
SLCSKEEKCVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFSLGFLLLRIF

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site:

amino acids 119-123

N-myristoylation sites:

amino acids 103-109,150-156,160-166,161-167,175-181

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:

amino acids 136-156

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:

amino acids 166-178

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FIGURE 263

CGCCCTCCGACCCGCCCCGCGGCGCATTGTGGGATCTGTGCGCTTGTGAGGTGGTGGAGGAAA
AGGCGCTCCGTCA**ATG**GGGATCCAGACGAGCCCCGTCTGTGGCCTCCCTGGGGGTGGGGCTG
GTCCTCTGCTCGGCCTGGCTGTGGGCTCCTACTTGGTTCCGAGGTCCCGCCGGCCTCAGGTC
ACTCTCCTGGACCCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCCAC
AACACCAAGAGGTTCCGCTTTGCCCTGCCCACCGCCCACCACACTCTGGGGCTGCCTGTGGGC
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACACTCCTGTC
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTGTCATCAAGGTCTACCTGAAGGGTGTGCAC
CCCAAATTTCTGAGGGAGGGAAGATGTCTCAGTACCTGGATAGCCTGAAGGTTGGGGATGTG
GTGGAGTTTCGGGGGCCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTTAACATTTCAG
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAACTGGGAATGATTGCCGGCGGG
ACAGGAATCACCCCAATGCTACAGCTGATCCGGGCCATCCTGAAAGTCCCTGAAGATCCAACC
CAGTGCTTTCTGCTTTTTGCCAACCAGACAGAAAAGGATATCATCTTGCGGGAGGACTTAGAG
GAACTGCAGGCCCCGCTATCCCAATCGCTTTAAGCTCTGGTTCACCTCTGGATCATCCCCAAAA
GATTGGGCCTACAGCAAGGGCTTTGTGACTGCCGACATGATCCGGGAACACCTGCCCGCTCCA
GGGGATGATGTGCTGGTACTGCTTTGTGGGCCACCCCCAATGGTGCAGCTGGCCTGCCATCCC
AATTGGACAACTGGGCTACTCACAAAAGATGCGATTACCTACT**GA**GCATCCTCCAGCTTC
CCTGGTGCTGTTGCTGTCAGTTGTTCCCCATCAGTACTCAAGCACTATAAGCCTTAGATTTCCT
TTCCTCAGAGTTTCAGGTTTTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG
AACAATATTCCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAA
TCTCCCCGTGGCAACAGGTCCAGGAGAGGCCCATGGAGCAGTCTCTTCCATGGAGTAAGAAGG
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCCTTGATAGCATCTTACTCTCACCTT
CTTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGGTTTTACTTAAACTTCACTGTTCAA
CCTATGAGCAAATCTGTATGTGTGAGTATAAGTTGAGCATAGCATACTTCCAGAGGTGGTNTT
ATGGAGATGGCAAGAAAGGAGGAAATGATTTCTTCAGATNTCAAAGGAGTCTGAAATATCATA
TTTCTGTGTGTGTCTCTCTCAGCCCCTGCCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA
AACTGCTGTTTGTGGCANGAACCCCTGGCTGTGCAAATAAATGGGGCTGAGGCCCTGTGTGA
TATTGAAGA

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FIGURE 264

MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTR
FRFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKGVHPKFP
EGGKMSQYLDLKVGDVVEFRGPSGLLTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGIT
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIIILREDLEELQARYPNRFLWFTLDHPPKDWAY
SKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

Important features:**Signal peptide:**

amino acids 1-26

N-glycosylation site:

amino acids 214-218

N-myristoylation sites:

amino acids 22-28, 76-82, 128-134, 180-186

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FIGURE 265

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAGA
ACGCGGCTACAATTAATACATAACCTTATGTATCATAACATACGATTTAGGTGACACTATAG
AATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTCGGT
TCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACG**ATG**TTGGGGGCCCCGCTCAGG
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCC
TCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC
AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTAC
AGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGA
AGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGACCCGGAGAAC
TGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCAC
TTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTAC
TCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACCCCCATACCACGG
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGG
GCCCCGATGACCCCGGCCCCGGCCTCCTGTTACAGGAGCTCCCGAGCGCCGAGGACAACAGC
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAACACGCACGCTGGGGGA
ACGGGCCCCGAAGGCTGCCGCCCCCTTCGCCAAGTTCATC**TAG**GGTCGCTGG

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FIGURE 266

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARN SYHLQIHKN GHVDG
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGYDV
YHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIH FNTPIPRRHTRSAEDDSERDP
LNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFAKFI

Important features:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

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FIGURE 267

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGAGAGAAGCGCCTGC
AGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAAAGGCTCCACAAAGGAGTTGGGAGTTC
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGG
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTG
CCGGAGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCAGTGGAGCAGGGCTGCTTGGCAGCCACCGGCCCTGCAACT
CAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCCGG
AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGAATAACCACCATTTTGCAAGGACCATGAGG
CCACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTT
GAGGGCACTGAGGAGGGCTCGCCAAGAGAGTTTACCTTAAACAGGTACAAGCGGGCGGGCAGTCCCAGGAC
AAGTGCACCTACACCTTATTGTGCCCCAGCAGCGGGTACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG
GTGCTTCTGGAGAACCAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAG
ATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGC
CGCAACATGAACTCGCGGGTCACGCAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACCGG
TTGGAGCTCTCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG
GACCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCAACAACCAATCAGAGATCATCGCGCAGCTTGAGGAG
CACTGCCAGAGGGTGCCCTCGGCCAGGCCCTCCCCAGCCACCCCCGCTGCCCCGCCCCGGGTCTACCAACCA
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCA
CCCCCTCTGCCCCACTATGCCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGCCCATGGAGAGAC
TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACCAACCGCCTC
ATGCAGGTGTGGTGGCAGCAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTGGATGGCTCTGTT
AACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGGTTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAG
AACATTTACTGGCTGACGAACCAAGGCAACTACAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC
TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGC
AATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGATGTCTACACA
GGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCCACTCCAACCTCAACGGGGTCTGG
TACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCGAGGAGGCTCTTACTCA
CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCACTAAGCCAGCTCCCCCTCTGACCTCTC
GTGGCCATTGCCAGGAGCCACCCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTCATCCTGA
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGATACGGT
GTTTTCTGTCCCTCTACTTTCCTTACACCAGACAGCCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA
CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

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FIGURE 268

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ
RVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLEVDGGIVSEVKLLRKE
SRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLEHKYQHLATL
AHNQSEIIAQLEEHQCRVPSARVPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVLP
PPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSIIYLVKPENTNRLMQVWCDQRHDPGG
WTVIQRRLDGSVNFFRNWETKQGFQGNIDGEYWLGLENIYWLTNQGNKLLVTMEDWSGRKVF
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYQKGGWWYN
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLLKKVMMIRPNPNTFH

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites:

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 124-128

Tyrosine kinase phosphorylation sites:

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites:amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,
473-479**Amidation site:**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature:

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins:

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins:

amino acids 275-292

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FIGURE 269

GCCGAGCTGAGCGGATCCTCACATGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAA
GCGGGTCTTACCCCCGGTCCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGA
GAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC
CAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCTGGCGCACGGACTCCTGCAGCT
CGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCG
CCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCC
TGAGAGCCGGGTGGACCCTGAGGTCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG
CAGGATCCAGCAACTCTTCCACAAGGTGGCCAGCAGCAGCGGCACCTGGAGAAGCAGCACCT
GCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCATGAGGT
GGCCAAGCCTGCCCCAAGAAAGAGGCTGCCCCGAGATGGCCAGCCAGTTGACCCGGCTCACAA
TGTCAGCCGCGCTGCACCGGCTGCCCAGGGATTGCCAGGAGCTGTTCCAGGTTGGGGAGAGGCA
GAGTGGACTATTTGAAATCCAGCCTCAGGGGTCTCCGCCATTTTTGGTGAAGTCAAGATGAC
CTCAGATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC
CTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAA
GGTGATAGCATCACGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGG
CAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCCTATAGCCTGCA
GCTCACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT
ACCCTTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCT
CTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC
CATCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTA
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAGCG
TCCTGGCTGGGCCTGGTCCCAGGCCCCAGAAAGACGGTGAAGTCTTGGCTCTGCCCGAGGATGT
GGCCGTTCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAAACTTGTGGACAGAGAA
GAAGACCAGACTGGAGAAGCCCCCTTTCTGAGTGCAGGGGGGCTGCATGCGTTGCCTCCTGA
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCTTCACT
CCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTTGGGGCCAGCCAGACTGGCCTCAA
TGGCGGACTCAGTCACATTGACTGACGGGGACCAAGGCTTGTGTGGTTCGAGAGCGCCCTCAT
GGTGCTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCCAATGGTATCTGGGC
GGAGCTCACAGAGTTCTTGAATAAAAGCAACCTCAGAACAC

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FIGURE 270

MTVIRFFPAASATKRVLPVLRVSSPRTWNPVPEPRIPAPRLPKRMSGAPTAGAALMLCAA
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA
CQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLQS
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFQI
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDENRPWEAYKAGFGDPHGEFWLGLEKVHSITGD
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPSPGLSVPFSTWDQ
DHDLRDKNCAKSLSGGWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATT
MLIQPMAAEAAS

Important features:**Signal peptide:**

Amino acids 1-13

Transmembrane domain:

Amino acids 53-70

N-glycosylation site:

Amino acids 224-228

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 46-50;118-122

N-myristoylation sites:

Amino acids 50-56;129-135;341-347;357-363

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 396-409

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FIGURE 271

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG
AACAAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGCTG
CTGCTGCTGACCATGGCCTTGGCCGGAGGTTGGGGACCGCTTCGGCTGAAGCATTTGACTCG
GTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTAC
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTT
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGCT
GAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCTCTAACT
CTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTTCATGG
ACTTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCCAGAAATCCAG
TACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAAGCAAAATGTCC
TATCTGCAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGC
TTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTTGTCTCTCGGTG
ATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT
GAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAGCTAAACAGATATCCA
GCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGAAGCAGGGCCTCTACCT
ACAAAAGTGAATCTTGCTCATTCTGAAATTTTAAGCATTTTTCTTTTAAAAGACAAGTGTAATA
GACATCTAAAATTCCACTCCTCATAGAGCTTTTAAAATGGTTTCATTGGATATAGGCCTTAAG
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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FIGURE 272

MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPK
EEELYACQRGCR LFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL
RQEQLMSLMPKMHLLFPLTLVRSFWS DMMSAQSFITSSWTFY LQADDGKIVIFQSKPEIQYA
PHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVLSVMV
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVR SKTEDHEEAGPLPTK
VNLAHSEI

Important features:**Signal peptide:**

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site:

amino acids 90-94

N-myristoylation sites:

amino acids 28-34, 29-35, 31-37, 86-92

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FIGURE 273

CCCACGCGTCCGAACCTCTCCAGCG**ATG**GGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGTG
CTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGA
CCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT
GCAGGTCACCGGGCGTTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCAT
AGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACAT
CTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTT
CACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGGGCTGGTT
CATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGA
GGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCAGCCGAGAAGCA
GAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACCCGCCGACCAAGCGCACACGGCGGCCCA
GCCCCTCACG**TAG**TCTGGGAGGCAGGGGGCAGCAGCCCCTGGGCCGCCTCCCCACCCCTTTCC
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC
TGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGC
TGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTACCCCTGA
TCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGC
GACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCCTCAAATCTGCTTCTCGGATCT
CCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGTTT
GTTTGTTTGTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAGAGGGTTGTCCACTCCTCA
CATTCCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCCCGGAATAAAACCATTTTCC
TGC

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FIGURE 274

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRIS
ATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLIGKPSGKSKDCVFTEIVLENN
YTAFQONARHEGWFMATFRQGRPRQASRSRQNRQEAHFQKRLYQGQLPFPNHAEKQKQFEFVGS
APTRRTKRTRRPQPLT

Important features:**Signal peptide:**

Amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 275

TATTTACCATATCAGATTCACATTTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTCTGT
TTTTATTCTCTGTCTTATTGCCATCTCAGAAGTGCGGAGCAAGGAGTCTGTGAGACTCTGTG
GGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAAGGCATCTGG
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAACTCCTTCCAGCTCCCACATAAACGTG
AGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC
TTTGGGGTGGACAGATGCCCACTGAAGAGCTTTGGAAGTCAAAGAAGCATTTCAGTGATGTCAA
GACAAGATTTACAACTTTGTGTTGCACTGATGGCTGTTCCATGACTGATTTGAGTGCTCTTT
GCTAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTTTATCACATGTTTAATTACAGTGTT
TTACTGCCTGGTAGAACACTAATATTGTGTTATTAAATGATGGCTTTTGGGTAGGCAAAACCT
TCTTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTTCTCCCTTTGCC
AAGGTTAATGAAGTGTCTTTTCAAATTCTACTAATGCTTTGAAATTCAAATGCTGCGCAAA
ATTGCAATAAAAATGCTATAAA

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FIGURE 276

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRLHLEGIPQAQQAETGN
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKSCKHVSMSRQDLQTLCTDGC
SMTDLSALC

Important features:**Signal sequence:**

amino acids 1-18

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 107-111

N-myristoylation sites:

amino acids 3-9, 52-58, 96-102, 125-131

Insulin family signature:

amino acids 121-136

Insulin family proteins:

amino acids 28-46

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FIGURE 277

GCAGCTGGTTACTGCATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGG
CCCACAGACCAGAACTTCCACTATACTACTTAAATACATAGGTGGCTTGTCAAATTCATTTGATTAGTATTGT
AAAAGGAAAAAGAAGTTCCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAAGTCT
CAGATGAACAACTTCTACACTGATTTTAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAAC
AGACACAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATTAACCCAACGCATAGAAGAC
TTTTTTTTCTCTTCTAAAAACAATAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAAAT
GAAGACTTTTACCTGGACCCTAGGTGTGCTATTCTTCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATT
CAAAATTAATAAAATAAACCAGAGAAGATACCCCTCGTGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATA
CACATTCTGTGCTGACCTGAACAAAGAATAACAGGGCCAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCAT
TAAAGACATGATCACCAGGATGGACCTGAAAACCTGAAGGATGTGCTCTCCAGGCAGAAAGCGGGAGATAGATGT
TCTGCAACTGGTGGTGGATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACAT
GAACTCTCGTGTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCACCTGAACT
TTCCCAACTGGAAAACAAAATCCTCAATGTCAACACAGAAATGTTGAAGATGGCAACAAGATACAGGGAACCTAGA
GGTGAAATACGCTTCCTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTT
GAGGATATTTTCCCGACAAGACACCCATGTGTCTCCCCACTTGTCCAGGTGGTGCCACAACATATTCCTAACAG
CCAACAGTATACTCCTGGTCTGCTGGGAGGTACGAGATTCAAGAGGGATCCAGGTATCCAGAGATTTAATGCC
ACCACCTGATCTGGCAACTTCTCCACCAAAAGCCCTTTCAAGATACCACCGGTAACCTTCATCAATGAAGGACC
ATTCAAAGACTGTCAGCAAGCAAAGAAGCTGGGCATTCCGTCACTGGGATTATATGATTAAACCTGAAAACAG
CAATGGACCAATGCAGTTATGGTGTGAAAACAGTTTGGACCCTGGGGGTTGGACTGTTATTAGAAAAGAACAGA
CGGCTCTGTCAACTTCTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCT
TGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGA
TAAAAAGTCTATGCAGAATACAGCAGCTTTCTGTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAAC
TTACCAGGGAAATGCAGGGGATTCTATGATGTGGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGA
TATGTATGCAGGAACTGCGCCCACTTTATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCTAACCTAAA
TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCAAGATGGAATTTTCTGGGCCGAATACAGAGGCGG
GTCAATACTCCTTAAGAGCAGTTAGATGATGATCAAGCCTATTGACTGAAGAGAGACACTCGCCAATTTAATGA
CACAGAACTTTGTACTTTTCAGCTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTTCTAC
ACAGAAAGTTTTTAAATGAATTTTACCCTAATAAAGGGAACCTATAAATGTAGTTTCATCTGTCTGCTCAAT
TACTGCAGAAATTTATGTATCCACAACCTAGTTATTTTAAAAATTATGTTGACTAAATACAAAGTTTGTTC
TAAAAATGTAAATATTTGCCACAATGTAAAGCAAATCTTAGCTATATTTTAAATCATAAATAACATGTTCAAGATA
CTTAACAATTTATTTTAAATCTAAGATTGCTCTAACCTTAGTGAAAAAATATTTTTTAAATTTAGCCAAATA
ATGCATTTTATTTTATAAATAACAGACAGAAATTAGGGAGAACTTCTAGTTTTGCCAATAGAAAATGTTCTT
CCATTGAATAAAAGTTATTTCAAATTGAATTTGTGCCTTTCACACGTAATGATTAAATCTGAATTTCTAATAATA
TATCCTATGCTGATTTTCCCAAAACATGACCCATAGTATTAAATACATATCATTTTAAAAATAAAAAAAACCC
AAAAATAATGCATGCATAATTTAAATGGTCAATTTATAAAGACAAATCTATGAATGAATTTTTCAGTGTTATCTT
CATATGATATGCTGAACACCAAAATCTCCAGAAATGCATTTTATGTAGTTCTAAATCAGCAAAATATTGGTATT
ACAAAAATGCAGAATATTTAGTGTGCTACAGATCTGAATTATAGTTCTAATTTATTATTACTTTTTTTCTAATTT
ACTGATCTTACTACTACAAAGAAAAAAACCCCAACCCATCTGCAATTCAAATCAGAAAGTTTGGACAGCTTTAC
AAGTATTAGTGCATGCTCAGAACAGGTGGGACTAAAACAACTCAAGGAAGTTGGCTGTTTTCCCGATACTGA
GAATTCACAGCTCCAGAGCAGAGCCACAGGGGCATAGCTTAGTCCAACTGCTAATTTTCAATTTACAGTGTAT
GTACGCTTAGTCTCACAGTGTCTTTAACTCATCTTTGCAATCAACAACCTTACTAGTGACTTTCTGGAACAATT
TCCTTTCAGGAATACATATTCAGTCTTAGAGGTGACCTTGCTTAATATATTTGTGAAGTTAAATTTTAAAGA
TAGCTCATGAAACTTTTGTGTTAAGCAAAAAGAAACCTCGAATTGAAATGTGTGAGGCAACATATGCATGGGAAT
AGCTTAATGTGAAGATAATCATTTGGACAACCTCAATCCATCAACATGACCAATGTTTTTCATCTGCCACATCTC
AAAATAAACTTCTGGTGAACAAATTAACAAAATATCCAAACCTCAAAAAAA

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FIGURE 278

MKTFTWTLGVLFFLLVDTGHCRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGP
ICVNTKGQDASTIKDMITRMDLENLKDVLRSQKREIDVLQLVVDVDGNIVNEVKLLRKESRNM
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQ
SVMITLLEEQCLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGLLGGNEIQRDPGYPRDLMPP
PDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDP
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNYKLLIELEDWSDKK
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGWW
YNACAHSNLNGVWYRGGHYRSKHQDGIFWAEYRGGSYSLRAVQMMIKPID

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation sites:

Amino acids 160-164;188-192

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 120-124

Tyrosine kinase phosphorylation sites:

Amino acids 173-180;387-396

N-myristoylation sites:Amino acids 70-76;110-116;232-238,343-349;400-406;467-473;
475-487**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453

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FIGURE 279

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCGGC
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGCCG
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAAGCC
CGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCCAAGTCGCGAGACAGCGGACAAGCAGCGGA
GGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGGCGTCG
TGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCGAGCGCG
AGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA
ACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAGAAGAAGAC
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACCACTTGCAGC
TGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTTAACC
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA
TGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCAAATTCAAAGAAT
CAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAGCAGCAGTCAGGCC
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA
ACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC
TGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACCAAGAGCAGAAGTGTCT
CTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTCTAGCAGTCCTTCA
CCCAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGGCAGAGTTCCTATTCTATC
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 280

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGGTSCDKNKLVFSRVKLFSGSKRRRRRPE
PQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLAMN
SEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNK
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSVSGVLNGGKSMSHNEST

Important Features:**N-glycosylation site:**

Amino acids 242-246

Glycosaminoglycan attachment sites:

Amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site:

Amino acids 93-100

N-myristoylation sites:

Amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop):

Amino acids 231-239

HBGF/FGF family proteins:

Amino acids 78-94, 102-153

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FIGURE 281

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGGA
CTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGGCA
ACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCTCCA
TTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTGCCCC
AGTAGGGGTGGGATGAGCGAATATTCCTCAAAGCTAAAGTCCCACACCCTGTAGATTACAAGAG
TGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAAACCACG
TCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA
GGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGGAGTACATA
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCTGTGGAGGGG
GGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAGCGAGTCGGGG
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAGCGCGCTCCGGG
CGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGCGCTGGCCAGTAGCCTGAT
CCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCGGCGAGCGGCGCGT
GTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCTGCTGTCCAAGGTGCG
ACTGTGCGGGGGGCGGCCCGCGCGGCCGGACCGCGGGCCGGAGCCTCAGCTCAAAGGCATCGT
CACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAAGCATCCAGGG
CACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTGAGGGACTGCTCTACAG
TTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCTTTGAGAATTACTACGTCCT
GTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCCTGGTACCTCGGCCTGGACAA
GGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCCCACTTTCTGCC
CAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCCACAGTGTCCCCGAGGCCTCCCC
TTCCAGTCCCCCTGCCCCCTGAAATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA
GCCAGCCACCACCACAACCTGT

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FIGURE 282

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDRG
PEPQLKGIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTHFNLI PVGLRVVTIQSAKLGHYMA
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK
TKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

Important features:

Tyrosine kinase phosphorylation site:

Amino acids 199-207

N-myristoylation sites:

Amino acids 54-60; 89-95; 131-137

HBGF/FGF family signature:

Amino acids 131-155

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FIGURE 283

ATGCCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTGG
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACGGC
AACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGGCGC
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAA
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTTCAAC
CTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTTTAAAGAA
TCTGTTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT
AGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA
ACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAAGCACAAAGTGCG
TCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAAC**ATAG**

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FIGURE 284

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLRR
QDPQLKGIVTRLYCRQGYLQMHPDGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLYIA
MNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

Important features:**N-glycosylation sites:**

Amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site:

Amino acids 199-207

N-myristoylation sites:

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins:

Amino acids 104-155, 171-198

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FIGURE 285

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCCAGGTCCAGGTTTTGCTTTGA
TCCTTTTCAAAAAGTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCCT
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAGAGAC
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTGCAGCCAAATGAGCCTCTTCGGGC
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
GAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT
TCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCTTCAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTTGGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCT
CAGTGTCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG
GTGGGAAGTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACACCAGCAGCTCTTGCCCA
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
ACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTAT
TAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCACCTAGCTGGGTTCTGTATTTTCAGTTCTTTC
GATACGGCTTAGGGTAATGTGAGTACAGGAAAAAAGTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC
TCTAAAGCTCCATGTCTGGGCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACAT
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAAGTATGTTGCTATGAATTAACCTGT
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAATTTCTGCCATTTAGAAGAAGAGAACTACA
TTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG
TTTCATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT
ATTTTTACCAAAGGTATTTAATATCTTTTTTATGACAAGTTAGATCAACTATTTTGTAGCTGGTAAATTTTTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAAGTGAATTGGAATAGAATTGGTAAGTTGCAAA
GACTTTTTGAAAATAATTAAATTATCATATCTCCATTCCTGTATTGGAGATGAAAATAAAAAGCAACTTATGA
AAGTAGACATTCAGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAGTCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTGAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTTTATTATCTTAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTATGTACA
GAAGTATGTCTCTTAACAGTTCACTTATTGTACTCTGGCAATTTAAAGAAAATCAGTAAATATTTTGTCTGT
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAATAAAAAGA
ATGTGGCTATTTTGGGGAGAAAATTAATAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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FIGURE 286

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF
PHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS
GTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNA
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNNLLTEEVRLYSCTP
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKT
GVRGLHKS LTDVALEHHEECDVCVRGSTGG

Important features:**signal sequence:**

Amino acids 1-14

N-glycosylation sites:

Amino acids 25-29;55-59;254-258

N-myristoylation sites:

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

Amidation site:

Amino acids 229-233

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FIGURE 287

CAGCGCTGACTGCGCCGCGGAGAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCGTCCC
CGCTCGGCCTGGCCAGGCCCCGCGCT**ATG**GAGTTCCCTCTGGGCCCCTCTCTTGGGTCTGTGCT
GCAGTCTGGCCGCTGCTGATCGCCACACCGTCTTCTGGAACAGTTCAAATCCCAAGTTCCGGA
ATGAGGACTACACCATAACATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG
AGTACCAGCTGTGCCAGCCCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCCCAGTG
CCAAGCATGGCCCGGAGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTTACCCCTGGGCA
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCCAAACCCATCCACCAGCATGAAGACC
GCTGCTTGAGGTTGAAGGTGACTGTCAGTGGCAAATCACTCACAGTCCTCAGGCCCATGACA
ATCCACAGGAGAAGAGACTTGCAGCAGATGACCCAGAGGTGCGGGTTCTACATAGCATCGGTC
ACAGTGCTGCCCCACGCCTCTTCCCACTTGCCTGGACTGTGCTGCTCCTTCCACTTCTGCTGC
TGCAAACCCCG**TGA**AGGTGTGTGCCACACCTGGCCTTAAAGAGGGACAGGCTGAAGAGAGGGA
CAGGCACTCCAAACCTGTCTTGGGGCCACTTTCAGAGCCCCAGCCCTGGGAACCACTCCCAC
CACAGGCATAAGCTATCACCTAGCAGCCTCAAACGCGGTCAATATTAAGGTTTTCAACCGGAA
GGAGGCCAACCAGCCCGACAGTGCCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG
GAGACAGTCCTTTCCCACCATTCCCTGCCTTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC
CCTTAAGGCACAGTGGGAGCTGAGCTGGAAGGGGCCACGTGGATGGGCAAAGCTTGTCAAAGA
TGCCCCCTTCAGGAGAGAGCCAGGATGCCAGATGAACTGACTGAAGGAAAAGCAAGAAACAG
TTTCTTGCTTGGAAGCCAGGTACAGGAGAGGCAGCATGCTTGGGCTGACCCAGCATCTCCCAG
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTTGTAGCCAGGTACTGCATTCTCTCCCAT
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGGCTGTGCCAACCTGTTCTTAGAGTG
TAGCTGTAAGGGCAGTGCCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCCC
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTGTCTGTCTGATTTCTACAACCTGGAGTTT
TTTATACAATGTTCTTTGTCTCAAATAAAGCAATGTGTTTTTTCGG

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FIGURE 288

MEFLWAPLLGLCCSLAAADRHTVFWNSSNPKNEDYTIHVQLNDYVDIICPHYEDHSADAAM
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPQSAKHGPEKLSEKFQRFPTPFTLGKEFKEGHSYY
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHDNPQEKRLAADDPEVRVLHSIGHSAAPRLFPL
AWTVLLLPLLLLQTP

Important features:**Signal sequence:**

Amino acids 1-17

N-glycosylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 118-127

N-myristoylation site:

Amino acids 10-16

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FIGURE 289

CGGACGCGTGGGCGGACGCGTGGGCGGCCCCACGGCGCCCGGGCTGGGGCGGTGCTTCTTC
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGGGC
CTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGGCTC
CAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACCTGCCGG
GGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAGGTGGA
AACACTGCCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTGGTAGAG
GTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG
GAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCGGACCTCTTCCAGTGGCTG
TGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGCCTTCCCTGT
CCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGGGACACGAGGG
GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTT
GGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGTTTTGGCCCCCTGT
GCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGGCTGGGCCCTGCAT
CACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACTGTGGAGCTGACCAA
TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGC
ATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGGCTCCAAG
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAACAAGCAGTGTGAAAAC
ACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTG
AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTG
CTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC
TTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTGAGAG
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATAATCGCGGCCACCACCTGTAGGA
CCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCCTCCTGCTGGACACTCAGGACAGC
TTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCAGCCCAGGTACCC
AGGCCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTGGATACCATGAGCTCT
TCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAAAGTTTTTCCTTAATGGTG
GCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTGGTCCTCACAGGGGTGGGGCCATCACAG
CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTGTGTTACCCACATCCCCACACCCCA
TTGCCACTTATTTATTCATCTCAGGAAATAAAGAAAGGTCTTGGAAGTTAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT
IRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQE
APDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQCAGYGG
EACGQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDECGTE
GANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVCP
GENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVLQQMFFGIIICAL
ATLAAKGDVFTAFIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Important features:**Signal sequence:**

Amino acids 1-29

Transmembrane domain:

Amino acids 342-392

N-glycosylation sites:

Amino acids 79-83;205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 290-294

Aspartic acid and asparagine hydroxylation site:

Amino acids 321-333

EGF-like domain cysteine pattern signature:

Amino acids 181-193

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FIGURE 291

CAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTCGACCTCGACCCAC
GCGTCCGAACACAGGTCTTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTGGAAGGAGGGAGTGCGCGGGCTGCCCC
GGGCTCCTCCCTGCCGCTCCTCTCAGTGGATGGTTCCAGGCACCCTGTCTGGGGCAGGGAGGGACAGGCCTGC
ACATCGAAGGTGGGGTGGGACCAGGCTGCCCTCGCCCCAGCATCCAAGTCTCCTTGGGCGCCCCGTGGCCCTG
CAGACTCTCAGGGCTAAGGTCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGTAGC
TTGAAGGAGGCACCATGAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTGGCTCAGGCCTGCCCTG
AGCCCTGCGACTGTGGGGAAGATATGGCTTCCAGATCGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC
CTGGCTTCCCGCAATGTGACTACACTGAGCCTGTGAGCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCA
GGGAGGTGCCCTGCTGCAGTCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGAGCCCTGGCCT
CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGCACAACC
TCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGGACGCTTCCGCAGCCTCC
GTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACATTGGCCGAGGGCACCTTCACCCGCTCACCG
CGCTGTCCACCTGCAGATCAACGAGAACCCCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCC
TGACCACGGCCGTGTCCATCCCGGAGCAGGACAACATCGCTGCACCTCACCCATGTGCTCAAGGGTACACCGC
TGAGCCGCTGCCGCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGCCG
AGCTGCGGCCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCGGCCCTCAGCTTCACTGGCACA
TCCAGATACCCAGTGGCATTGTGGAGATCACCAGCCCCAACGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCC
CTGTGGCCAGCTCCAGCCGCGCTTCCAGGCCTTTGCCAATGGCAGCCTGCTTATCCCGACTTTGGCAAGCTGG
AGGAAGGCACCTACAGCTGCCTGGCCACCAATGAGCTGGCAGTGCTGAGAGCTCAGTGGACGTGGCACTGGCCA
CGCCCGGTGAGGGTGGTGGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAAGGGCTGCTATA
CGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATCATCTACCTCAGCCGTGCTGGGAACC
CTGAGGCTGCAGTCGAGAAGGGTCCCTGGGCAGCTGCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCC
TCTTCTTCTCCTCACCTCCTTCTAGCCCCACCCAGGGCTTCCCTAACTCCTCCCCTTGCCCTACCAATGCCCC
TTTAAGTGCTGCAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCTCC
TTCTAATCTCTTCTAGAGCACCTGCTATCCCCAATTCTAGACCTGCTCCAACTAGTGAAGTAGGATAGAATTTG
ATCCCTAACTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATGCCTGTGCTCTCCTCTCAGGGGCAGCATG
CTAACGGGGCGACGTCTAATCCAATGGGAGAAGCCTCAGTGGTGAATTCCAGGCACTGTGACTGTCAAGCTG
GCAAGGGCCAGGATTGGGGGAATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAG
GAGGATGGGAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCTCCTTG
CTGTTTTCTGATGATTTGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAATGTGGGGATCCAGGATGG
CCTTCCTTCTCTTACCCTTCTCCTCAGCCTGCAACCTCTATCCTGGAACCTGTCTCCTTTCTCCCCAACT
ATGCATCTGTTGTCTGCTCCTCTGCAAAGGCCAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATG
CCAAAAAAGGGCGCCGCGACTCTAGAGTGCACCT

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FIGURE 292

MQELHLLWWALLLLGLAQACPEPCDCGKEYGFQIADCAYRDLESVPPGFANVTTLSSLNRLP
GLPEGAFREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSALQL
LKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCTCGIV
WLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELRPGFV
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANGSLLIP
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFFLTSTF

Important features:**Signal peptide:**

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites:

Amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site:

amino acids 319-326

N-myristoylation sites:amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329, 334-340,
350-356, 394-400**Amidation site:**

amino acids 355-359

Leucine Rich Repeat:

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain:

amino acids 180-230

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FIGURE 293

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC
TCGCTTCCAGGCGCGGCGGCTGCAGCCTTGCCCCCTCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACGCTGGGAGGTCCATCT
CTAGGGGCGAGACACGCTCGGACCCACCCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAGCGGGCAGACC
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCAATTCTTGACATTGGTCCTGATGTCAACCCAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA
GGGAGAATGTGCCACGGGTGATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGTGCTA
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTGTGGCCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACGCTGTGCAGGTGCAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGAGAATCCAGGATCTGT
GTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACACGGATGTGAAC
ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTGCTCTTAACCCAGATGAAAAA
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACCTGCAGCCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGATTACTGCCTGCTGAGTGACCATGGTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTTGCCCTGTCACTGTCTGAGGGACACGTGCTCCGACGGATGCTCCGAGGATG
CAAAATTGGACTCTTGTGCTCTGGGGGACACGGTTGTGAACATTCTGTGTGAAGCATGAGTGAAGATTCTGTGT
GCCAGTGCTTTGAAGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGTGCTTGAGGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCCAACACATTTGTGTTA
ATAATGGGAATTCCTACATCTGCAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCG
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTGAACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
ATTCACACAGGTCCACACAGAGTTCACCTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTACCCAAG
GAGAAGGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGACGGACGGGCTCAGGATG
ACGCTCTCCGAGTGGGCGAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAATAACAAGAGATTGCCTCTGAGCCCAACAACAGCATCTCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTGAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAATGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAACGAAGAAGTAAGAAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAATAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTTGGCACAGAACAAGACAAGAAGTATACACTAATTTGTATAAATTTATCTAGGAAAAAATCCT
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC
AACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAAGTTTGCACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAAATTCACCACTTCAG

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FIGURE 294

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFIID
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAVKR
MRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI
LIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF
CINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDG
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINICALNKPGEHECVN
MEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTC
SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSCALGDHGCEHSCVSSD
SFVCQC FEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRRK
DVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENF
EVVKQFVTGIIDSLTISPAAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMT
GLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA
IEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDSPAGELPKTVQQPT
ESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM
FQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation site:

Amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 115-119; 606-610; 892-896

N-myristoylation sites:Amino acids 133-139; 258-264; 299-305; 340-346; 453-459; 494-500;
639-645; 690-694;
752-758; 792-798**Amidation sites:**

Amino acids 314-318; 560-564; 601-605

Aspartic acid and asparagine hydroxylation sites:Amino acids 253-265; 294-306; 335-347; 376-388; 417-429;
458-470; 540-552; 581-593

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FIGURE 295

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCGC
CATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCGC
GCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAA
CCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGCGGGAACACGGCTTGGGAGGAAAA
GACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATCCTGGAGGGGCTGTGCGA
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCCTGGTG
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGT
GTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC
CTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTGCCGGTG
CCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGCTCGGGCCTGAC
CAACAGAGACTGCGGCGAGTGTGAAGTGGGTGGGTGCTGGACGAGGGCGCCTGTGTGGATGT
GGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGCCCAGGAAA
CTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTG
CTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAACTGCTACAATACTCCAGGGAGCTA
CGTCTGTGTGTGCTCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGC
TGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTGTAATGTGCCGG
ACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGAAAAATGTGGCCCTGAGGATGCCGTCT
CCTGCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTCTAACGGTTGATTCTCATTTGTCCC
TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTGTATATTTTGATACAGTTCTTTGT
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAA

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FIGURE 296

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEK
TL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LKV
CCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR
NETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANG
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSY
VCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

Important features:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 190-194;251-255

Glycosaminoglycan attachment sites:

Amino acids 149-153;155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 303-310

N-myristoylation sites:Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;
252-258;313-319**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

EGF-like domain cysteine pattern signature:

Amino acids 166-178

Leucine zipper pattern:

Amino acids 94-116

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FIGURE 297

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAGAAAGAAGAGGAAG
ATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCATCATGCTGCTATTCTTGCAAATACTGA
AGAAGCATGGGATTTAAATATTTTACTTCTAAATAAATGAATTACTCAATCTCCTATGACCATCTATACATACTC
CACCTTCAAAAAGTACATCAATATTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTT
TTGGACAATGCAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCATTT
GACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTGTGGAATCCTTAAGGGC
CCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACTCCGAATTCATGTGCTACTTGGCCTAGCTA
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGT
TTACACCCAGATCCATTTATATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCA
GATTGCCAGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAGACTTTC
CAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAATATTAATGTAAAAAGATGC
CTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAAACTTACTGAACTGCCTGAAAAATGTCTGTCCGAACCTGAGCA
ACTTACAAGAACTCTATATTAATCACAACCTTGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATC
TTCTTCGACTTCATCTCAATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAG
AGATTCTGATGATTGGGGAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCAATCTTCGCA
GCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTTGGACTGGAAAACTTAGAAAGCA
TCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGTTGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGG
ATCTAAATAAAAAATCCTATTAATAGAATACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGA
TAAATAATATGCCTGAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAG
CTACTAACAACCCTAGATTGTCTTACATTACCCCAATGCATTTTTTCAGACTCCCCAAGCTGGAATCACTCATGC
TGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTGCCAAACCTCAAGGAAATCAGCATAC
ACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTGGATGAACATGAACAAAACCAACATTCGATTTCATGGAGC
CAGATTCACTGTTTTGCGTGGACCCACCTGAATTTCAAGGTGAGAATGTTCCGGCAAGTGCATTTTCAGGGACATGA
TGGAATTTGTCTCCCTCTTATAGCTCCTGAGAGCTTTTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGTTT
CCTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTGGTCAAAAACCTTTCG
CTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTAGATATAAATGGCGTAACTCCCAAAGAAG
GGGTTTTATATACTTGTATAGCAACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT
CTTTTCCACAAGATAACAATGGCTCTTTGAATATTAAAAAAGAGATATTACAGGCCAATTCAGTTTTGGTGTCT
GGAAAGCAAGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCATGCTG
CGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATCCATCAACTGAGTATAAAA
TTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAATGTGTAAATGTCACCACCAAAGGTTTGCACC
CTGATCAAAAAGAGTATGAAAAGAATAATACCACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTG
GTGTGATATGTCTTATCAGCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACT
TACAGAAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAAAGAAAAA
GTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCATAAAACCACCAAGGAAACCTA
CTCCAAAAATGAAC

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FIGURE 298

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF
PARLPANTQIILLQTNNAIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN
KLTPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDALPN
LEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLEISFYDNRLIKVP
HVALQKVVNLFKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPDLRKIE
ATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISHSNPIRCDCVIRW
MNMNKTNIRFMEPDSLFCVDPPEFQGGQNVVRQVHFRDMEICLPLIAPESFPSNLNVEAGSYVS
FHCRTAEPEQPEIYWITPSGQKLLPNTLTDFYVHSEGTLDINGVTPKEGGLYTCIATNLVGA
DLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVKTENSHAAQ
SARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLM
ACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS
LKVKATVIGLPTNMS

Important features:**Signal sequence:**

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708**Cell attachment sequence.**

amino acids 277-280

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FIGURE 299

GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTT
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCG
CCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCAT
ACCATGCCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCCA
GTCCTAGCTTACTCTGCCACCACTGCCCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT
ACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATGAACCT
TCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCCTGCACCATGACC
AGAGACACAGTGTGTCTAGTGTAAAGAAGGCACCTTCCGGAATGAAAACCTCCCCAGAGATGTGC
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGGAAACCCCAGCTGCTGAAGAGACA
ATGAACACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCT
GAAGAGACAATGACCACCAGCCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC
AGCCCCGGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA
ATTGTGCTTCTGATTGTGTTTGTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTG
AAAGGTTTCAGGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT
CTGCTGTGTTCCACAGACAGAAACGCCTGC

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FIGURE 300

MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVA PQQRHSFKGEECPAGSHRSEHT
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTRDTVCQCKEGTFRNENSPEMCR
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLI
VLLIVFV

Important features:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 240-259

N-glycosylation site:

Amino acids 77-81;140-144;156-160

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 126-130

N-myristoylation sites:

Amino acids 56-62;72-78;114-120;154-160;233-239

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FIGURE 301

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT
TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAGAGACA
GCCCTGTCTGGACACAGAGTTACTGTGGATTTTTTAAGAGACTCAGTTAAAGAATTTAGGAATT
TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAACTAAAGCAAATTGAACAGG
AAAAAAAAAAGAAGATGGGTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC
AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT
GATTACCAAACAGGATTCCCATTTGTCAAAATGTAGACTACGGAGTTCCTTTTCATCAGTAT
ACTTTAGGCTGTGTCAGTGAATGCTTCTGTCCAATACTTTCCATCATCAATGTACTGTGAT
AATCGCAAACCAAGACTATCCCAAATATTCCGATGCACATTCAGCAACTCTACCTTCAGTTC
AATGAAATTGAGGCTGTGACTGCAAATTCATTCATCAATGCAACTCATCTTAAAGAAATTAAC
CTCAGCCACAACAAAATTAAATCTCAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAT
CTACTACAACTTCATCTAGAGCATAATAATTTAGAAGAATTTCCATTTCTCTCTAAATCT
CTGGAAAGACTCCTTCTTGGTTACAATGAAATCTCCAACTGCAGACAAATGCTATGGATGGG
CTAGTAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCTCTGCTAAAAGAC
AAAATCTTTGCCAAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA
ATGCCTCCTGGTTTGCTTCTTCACTTATGTATCTGTCTTTAGAAAATAATTCAATTTCTTCT
ATACCCGAAAAATACTTCGACAACTTCCAAACTTCATACTCTAAGAATGTCACACAACAAA
CTACAAGACATCCCATATAATATTTTAACTTCCCAACATTGTAGAACTCAGTGTGGACAC
AACAAATTGAAGCAAGCATTCTATATTCCAAGAAATTTGGAACACCTATACCTACAAATAAT
GAAATAGAAAAGATGAATCTTACAGTGATGTGTCCTTCTATTGACCCACTACATTACCACCAT
TTAACATACATTTCGTGTGGACCAAATAAACTAAAAGAACCAATAAGCTCATACTCTTCTTC
TGCTTCCCTCATATACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAACAATA
CAACTAAAGACACAAGTTTTTCAGGAGATTTCCAGATGATGATGATGAAAGTGAAGATCACGAT
GATCCTGACAATGCTCATGAGAGCCCAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT
TATTATGAAAATCAAGAATAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA
TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG
AACTTACTCAAAATAATGTAAATCTTTAAAAATATAAATTAGAATGACAAGTGGGAATCATAA
ATTAAACGTTAATGGTTTCTTATGCTCTTTTAAATATAGAAATATCATGTAAAGAAAAAA
AAAAAA

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FIGURE 302

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDYDQEPDDDYQTGFPRQNVVDYGVPFHQYTLGCV
SECFCTNFPSSMYCDNRKLKTIPNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPFPLPKSLERLLGYNEISKLTNAMDGLVNLT
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSSISSIPEKY
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEKM
NLTVMCPSIDPLHYHHLTYIRVDQNKLEKEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ
VFRRFDDDDDESEDHDDPDNAHESPEQEGAEGHFDLHYENQE

Important features:**N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

Tyrosine kinase phosphorylation sites:

Amino acids 268-275;300-307

N-myristoylation site:

Amino acids 230-236

Leucine zipper patterns:

Amino acids 146-168;217-239

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FIGURE 303

GCCCCGGGACTGGCGCAAGGTGCCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC
TGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCTGGT
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTATGAT
ACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGGGGTTT
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGAAACAGT
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGGACCTCCA
TCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA
AGGAGTAGCTGAAACCTTGCACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA
CCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTTGGCTGGTT
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCCCGAGACA
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGAACCTGATGATATTAG
CACTGTGGTATTAGTGTCCAACTGACTGTCAATTGAGAAAGAAAGAAAGTAGTTTGCGATTGCA
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAACTTTGTATTTAGTTT
TTTTTGAATTATGCCACTGCTGAACTTTTAAACAACTACAACATAAATAATTGAGTTTAG
GTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGTAAGCTACTATCTGAACATT
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAGCAAATAAAAG
CTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 304

MNLVDLWLTRSLMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDLP
PETVLLYLDSDNQITSIPNEIFKDLHQLRVNLNSKNGIEFIDEHAFKGVAETLQTLDSLSDNRIQ
SVHKNAFNNLKARARIANNPWCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFLNAA
NDADLCNLPPKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKKADEP
DDISTVV

Important features:**Signal sequence:**

Amino acids 1-33

Transmembrane domain:

Amino acids 204-219

N-glycosylation sites:

Amino acids 47-51;94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation sites:

Amino acids 37-43;45-51;110-116

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FIGURE 305

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTCCACTTTGTTGAATTGTTCCCT
ATACTCAAAATTGCACCAAGACACCTTGCTCCCCAAATGCAAAATGTGAAATACGCAATGGAATTGAAGCCTGCT
ATTGCAACATGGGATTTTCAGGAAATGGTGTCACAATTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGT
CCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCA
GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAG
ATAATGTCTGTATAGCTGCAAAATTAATAAACTTTAACAAAAATCAGATCCATAAAAAGAACCTGTGGCTTTCGC
TACAAGAAGTCTATAGAAATTCTGTGACAGATCTTTACCAACAGATATAATTACATATATAGAAATATTAGCTG
AATCATCTTCATTACTAGGTTACAAGAACAACACTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTG
AATTTGTAAAAACCGTGAATAATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATA
GGAGAACACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCCAAAAGA
CCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTCTTTTTGATTATATAACATGAAACATA
TTCATCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG
GCAATGTTGCAGTTGCATTTTTATATTATAAGAGTATTGGTCTTTGCTTTCATCATCTGACAACCTCTTATTGA
AACCTCAAAATTATGATAATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAA
ACCCACCCACATTATATGAACCTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGA
GTCTATGTGCATTTTGGAAATTAACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT
ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGAATTTTGTATGTCCTCTGGTCCCT
CCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTG
CTAGCCTATTTCTTGCTGAACTTGTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATCA
TTGCCGGACTGCTACACTACTTCTTTTAGCTGCTTTGTCATGGATGTGCATTGAAGGCATACATCTCTATCTCA
TTGTTGTGGGTGTCTCTACAACAAGGGATTTTGCACAAGAATTTTATATCTTTGGCTATCTAAGCCCAGCCG
TGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAA
ACAACTTTATTTGGAGTTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGCTTTTGGAGTCATCA
TATACAAAGTTTTTCGTCACTGCAGGGTTGAAACCAGAACTTAGTTGCTTTGAGAACATAAGGTCTTGTGCAA
GAGGAGCCCTCGCTCTTCTGTTCTCTCGGCACCACCTGGATCTTTGGGGTTCTCCATGTTGTGCACGCATCAG
TGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTCAATTTTTTATTCCTGTGTGTTTTAT
CTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTAAGGTAACAT
AGAGAATGGTGGATAATTACAACCTGCACAAAAATAAAATTCAGCTGTGGATGACCAATGTATAAAAAATGACT
CATCAAATTATCCAATTATTAACCTACTAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTATAGGAACT
GTAGATAATAAGGTAATAATTATGTATCATATAGATATACTATGTTTTCTATGTGAAATAGTTCTGTCAAAAAATA
GTATTGCAGATATTTGGAAAGTAATTGGTTTCTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTA
ACACGAGAAGTATATGAATGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTGCTTTGAACT
AGTCCCCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAAACATAAGAGAATGAAGGGCAGAATATCAAA
CAGTGAAAAGGAATGATAAGATGATTTTGAATGAAGTGTTTTTCTGTAGACTAGCTGAGAAATTGTTGACAT
AAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAATTGTTCTGAACTTAAATGTCCACTAAAACAACCTT
AGACTTCTGTTTGCTAAATCTGTTTCTTTTCTAATATTCTAAAAAAGGTTTACCTCCACAAATTGA
AA

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FIGURE 306

MKRLPLLVFSTLLNCSYTNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC
TNTGESSYYCMCVPGFRSSSNQDRFITNDGTVCIEVNVNANCHLDNVCIANINKTLTKIRSIKEPVALLQEVYRNS
VTDLSPTDIITYIEILAESSLLGYKNNTISAKDTLSNSTLTEFVKTVNNFVQRTDFVVWDKLSVNHRRLTKL
MHTVEQATLRISQSFQKTTEFDTNSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAF
YYKSIGPLLSSSDNFLKPPQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNY
SPDTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLGIIISLICLAICIFTFW
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIIAGLLHYFFLAFAWMCIEGILYLVVGVYIN
KGFLHKNFYIFGYLSPAVVVGFSALGYRYYGTTKVCWLSTENNFWSFIGPACLIILVNLLAFGVIIYKVRHT
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVHVSVVTAFLTVSNAFQGMFIFLFLCVLSRKIQEEY
YRLFKNVPCCFGCLR

Important features:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 431-450;494-515;573-594;619-636;646-664

N-glycosylation sites:Amino acids 15-19;21-25;64-68;74-78;127-131;177-181;
188-192;249-253;381-385;395-399**Glycosaminoglycan attachment site:**

Amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 360-364

Tyrosine kinase phosphorylation sites:

Amino acids 36-44;670-677

N-myristoylation sites:Amino acids 38-44;50-56;52-58;80-86;382-388;388-394;
434-440;480-486;521-527**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87

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FIGURE 307

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTGAGCAGCATGGC
CCGGAGGAGCGCCTTCCCTGCGCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGA
GGCCGGGCGCGCCGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA
AGAAGATATCCTGATTGTTTTAGAGGGGAAAATGGCACCTTTTACACATGATTTAGAAAAGCGCAACAGAGAAT
GCCAGCTATTCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA
ATTCTGTCTTGGCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT
GCCTCACAAGGCATCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTGTAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCTTCTTTAAACATG
TCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTGTCTGA
TGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATGGTGGACTTTGTGTGACTCC
TGGTTTCTGCATCTGCCCACCTGGATTCTATGGAGTGAAGTGTGACAAAGCAAAGTCTCAACCACCTGCTTTAA
TGGAGGGACCTGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA
ATGCCACAACCTGTGCAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGG
AGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAACAAATGCCA
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCCTCATAATGCCCTGAGGCCAGC
AGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTA
CATCTGGTGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTAACTTTTCATGTGTT
GAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC
TGATATTTACTCTTCTTTTAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCTTGTTTCAGTGCT
TTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAT
TACAATGCATTTATGGTGTCTGGGGGAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAA
GAATTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAATTTTATTGTGATATTTAGATGTTTGTAC
ATTTTTAAAAATTGCTCTTAATTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATTCA
GTATTAAAAAATAAATTACACTGTGGTAGTGGCATTAAACAATATAATATATTCTAAACACAATGAAATAG
GGAATATAATGTATGAACTTTTTGATGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCT
AATAAACATTTTATACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTGGAAAAAATAAATAA
AAAAAA

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FIGURE 308

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGKM
APFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLLGT
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGCRNG
GFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN
GGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVCEPGCG
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDPPESNYIW

Important features:**Signal sequence:**

Amino acids 1-28

N-glycosylation sites:

Amino acids 88-92;245-249

Tyrosine kinase phosphorylation site:

Amino acids 370-378

N-myristoylation sites:

Amino acids 184-190;185-191;189-195;315-321

ATP/GTP-binding site motif A (P-loop):

Amino acids 285-293

EGF-like domain cysteine pattern signatures:

Amino acids 198-210;230-242;262-274;294-306;326-338

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FIGURE 309

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGGG
TTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGACT
CTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATCATGGAATGAACCCGAGCAATGGAG
ATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG
TGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTCGATG
ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCGGAGGGG
TTTTCTTTGAAGGCTCTGTAGCCCGATTTCCTGCGCAAGACGGATTCAAGCTGAAGGGCGCTA
CAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGATAATTCCA
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCAATAACAAGACAT
ATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATTCAAGATCCGGTACCCCGACC
TACACAATATGGTTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG
GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGCTCCAGACCTCCT
TCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAACTTGATGGGTCTGCGT
ATCTTGAGTGCTTACAAAACCTTATCTGGTTCGTCAGCCACCCCGGTGCCTTGCTCTGGAAG
CCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCTGCCACCCGCGGCCTT
GTGAGCGCTACAACCACGGAACGTGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTCTTATCAAGTCTACTGCA
TCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCTCCTGACCACGTGGAAGATTGTGG
CGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATCCTGGCCAGGATGTTCCAGA
CCAAGTTCAAGGCCCACCTTTCCCCCAGGGGGCCTCCCCGGAGTTCAGCAGTGACCCTGACT
TTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCATGACGAAGCTGTGAGTGGCGGCT
TGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAGGGCTGCCCCCTTACCCGTGGACG
ACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGACACAGGCCCAGGGGAGTCAGAAA
CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAAGTCTGTATTACCTCCCAGGTGCC
AAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATAATTGCCAGCACGGCAGAGGAGGTGG
CATCCACCAGCCCAGGCATCCATCATGCCCCACTGGGTGTTGTTCCCTAAGAAACTGATTGATTA
AAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAAATACATGTTGATCTGTGGAGTTGATTC
CTTTCCTTCTTGGTTTTAGACAAATGTAAACAAAGCTCTGATCCTTAAATTGCTATGCTG
ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCTGTTTCTTCTTGACACAGACTGATTAAA
AATTAAAAGNAAAAA

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FIGURE 310

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGIP
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRIPQ
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLPPMVS
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH
ETLLTTWKIVAFATATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVDGVPVML
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDGPGESETCDSVSGSSEL
LQSLYSPPRCQESTHPASDNPDI IASTAEVASTSPGIHHAHWVFLRN

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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FIGURE 311

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAG
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCTGG
AGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCAGGCCGCGAGGCCCCAGCTCAGGCT
CGTGCCCAACCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCCCTCACCTGGCGCT
GCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA
CCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCAGTGACT
GCTCTGGGGGAAGTACAAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCAGGCGAGC
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACT
GTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAGGGGATGCCA
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGG
GGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG
ACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCCTCCGCCCCACTGG
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGTCAGAACAGAAGACCTCGCTGCCCCTGAG
GACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA
TGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTTCTGGCCACGTGGAACC
TCGAACCCGAGCTCCTGCAGAAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAGGGGCTGGCCCCAGGCAGC
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGTCTGAGGGTGGCGA
TTAAAGTTGCTTC

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FIGURE 312

MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRT
SGLCVPLTWRCRDLDCSDGSDEEECRIEPCCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKLRN
CSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVTLES
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLLLLSW
LRAQERLRPLGLLVAMKESLLLSEQKTSLP

Important features:**Signal sequence:**

Amino acids 1-30

Transmembrane domain:

Amino acids 231-248

N-glycosylation sites:

Amino acids 126-130;195-199;213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation sites:Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

Leucine zipper pattern:

Amino acids 17-39

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FIGURE 313

CGGACGCGTGGGCGTCCGGCGGTTCGACAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGGCCCCAGCCCACAC
CTTACCAGGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTACTGCTGTTGCTGCCGCTGGCTGGCCAC
TTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGGGAGCTAGCACCGGCTCTGCACCTGCGGGGCATCCGGGAC
GCGGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTG
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC
CTCGGCGTGCCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTTGGGAACG
TACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCATGGTGGATCCAGACATGATCAAAGC
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGGCAT
TCGCTACCGCCTGGGCACCATCCGCCATCTTCCTCGGTTCATGAACATGCATGAAATTTATACAGTGTGAACCC
AGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGACCAAGG
CAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACA
CATGACGCCTGTCTGTGCGCCCAAGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCG
TCTCGATGGTGCCTGGTGGTTCCTGCGTCGCGGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGA
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGGCAAGCGCCAGGCCAC
TGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTCCAA
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT
CCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGAC
CCACTCAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC
CAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGCGTCAATGAGTGCGACATCGA
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTGAGGCTGCGGGCACACGC
GGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATGGGGCGGTGACCCAGCCTCGCCGA
CAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAATCCCGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGG
AGCCGCGGGCAGGCGAGACTGGCGGAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAG
CACAGCTGCAGATCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGCCC
CAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCGTTGCCAGGTTGGAG
TGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCAAGTGACCCTCCACCTCAGCCTCTCAAG
TAGCTGGGACTACAGGTGCACCACACACCTGGCTAATTTTTGTATTTTTTGTAAAGAGGGGGTCTCACTGTGT
TGCCCAAGGCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTCTGGGATTGCAGG
CATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAATAAAA
CCAAAGTATTGATAAAAAAAAAA

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FIGURE 314

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDCA
LPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNRCT
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

Important features:**N-glycosylation site.**

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415**N-myristoylation site.**amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448**Amidation site.**

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 315

CGGACGCGTGGGCCCCTGGTGGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT
GGCTTCTCCTGCTTGGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCAGCTGCCAGGAC
CCAGGGAAGTGAAGCCAGCAAAGTTGTCCTCCTGCCCAGTTGTCCCGGAGCTCCAGGAAGTC
CTGGGGAGAAGGGAGCCCCAGGTCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCCA
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCCACCTTGAGCGGCT
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCCAGTCTTTTGTGACATGGACACCGAGG
GGGGCGGCTGGCTGGTGTTCAGAGGCGCCAGGATGGTTCTGTGGATTTCTTCCGCTCTTGGT
CCTCCTACAGAGCAGGTTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC
ACCAGCTTACTCTCCAGGGTAACTGGGAGCTGCGGGTAGAGCTGGAAGACTTTAATGGTAACC
GTACTTTCGCCCCTATGCGACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCCTGAGCCTCCACAGTGGGAGGCCCTTTA
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG
CCCACAAATATGGCATTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC
GGATGATGCTTCGATTAGGGCACTCTGGCAGCCAGTGCCCTTATCTCTCCTGTACAGCTTCCGG
ATCGTCAGCCACCTTGCCTTTGCCAACCACCTCTGCTTGCCTGTCCACATTTAAAAATAAAAT
CATTTTAGCCCTTTCA

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FIGURE 316

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVLLPSCPGAPGSPGEKGAPGPQG
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCMDTEGGGWLVFQRRQ
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDFNGNRTFAHYATFRL
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

Important features:**Signal peptide:**

Amino acids 1-16

N-glycosylation site:

Amino acids 178-182

Glycosaminoglycan attachment site:

Amino acids 272-276

Tyrosine kinase phosphorylation site:

Amino acids 188-197

N-myristoylation sites:

Amino acids 16-22;89-95;144-150;267-273

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 242-255

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FIGURE 317

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCCGCGGGGGTGTGCGGGGCCCAACCCAGGAT
GCTCCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGGCGCTGCTACTGTTGCTCTT
GGGATCAGCTTCTCCTCAGGATTCTGAAGAGCCCGACAGCTACACGGAATGCACAGATGGCTA
TGAGTGGGACCCAGACAGCCAGCACTGCCGGGATGTCAACGAGTGTCTGACCATCCCTGAGGC
CTGCAAGGGGGAAATGAAGTGCATCAACCACTACGGGGGCTACTTGTGCCTGCCCCGCTCCGC
TGCCGTCATCAACGACCTACATGGCGAGGGACCCCCGCCACCAGTGCCTCCCGCTCAACACCC
CAACCCCTGCCCACCAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG
TGCCAGGCCCTGCACGACTGTGCGCCCGAGCCAGGACTGCCATAACTTGCTGGCTCCTATCA
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCCGAGTGTGTGGACATAGACGAGTGCCG
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCTGGCTCCTTCCGCTGCCAGTGCGAGCC
GGGCTTCCAGCTGGGGCCTAACAACCGCTCCTGTGTTGATGTGAACGAGTGTGACATGGGGGC
CCCATGCGAGCAGCGCTGCTTCAACTCCTATGGGACCTTCTGTGTCGCTGCCACCAGGGCTA
TGAGCTGCATCGGGATGGCTTCTCCTGCAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT
CTGTCAGTACCGCTGCGTCAACGAGCCAGGCCGTTTCTCCTGCCACTGCCCACAGGGTTACCA
GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCGCACCAAGTGTCTC
CGAGGCCCAAACCTGTGTCAACTTCCATGGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT
GGAGCCCTACATCCAGGTCTCTGAGAACCGCTGTCTCTGCCCCGGCCTCCAACCTCTATGTG
AGAGCAGCCTTCATCCATTGTGCACCGCTACATGACCATCACCTCGGAGCGGAGCGTGCCCCG
TGACGTGTTCCAGATCCAGGCGACCTCCGTCTACCCCGGTGCCTACAATGCCTTTCAGATCCG
TGCTGGAACTCGCAGGGGGACTTTTACATTAGGCAAATCAACAACGTCAGCGCCATGCTGGT
CCTCGCCCCGGCCGGTGACGGGGCCCCCGGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA
TTCCCTCATGAGCTACCGGGCCAGCTCTGTACTGAGGCTCACCGTCTTTGTAGGGGCCTACAC
CTTCTGAGGAGCAGGAGGGAGCCACCCTCCCTGCAGCTACCCTAGCTGAGGAGCCTGTTGTGA
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCTTGGTGGCTGAGGTGGGCGGGTC
ACACTGCAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCAGGCCAAGTTCACCTA
AATGGGGGTCTCTATATGTTTCAGGCCAGGGGCCCCCATTTGACAGGAGCTGGGAGCTCTGCAC
CACGAGCTTCAGTCACCCCGAGAGGAGAGGAGGTAACGAGGAGGGCGGACTCCAGGCCCGGC
CCAGAGATTTGGACTTGGCTGGCTTGCAGGGGTCCTAAGAACTCCACTCTGGACAGCGCCAG
GAGGCCCTGGGTTCCATTCTAACTCTGCCTCAAACGTGACATTTGGATAAGCCCTAGTAGTT
CCCTGGGCCTGTTTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAA

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FIGURE 318

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPDSSQHCRDVNECLTIPE
ACKGEMKCINHYGGYLCLPRSAAVINDLHGEGPPPPVPPAQHPNPCPPGYEPDDQDSCVDVDE
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRQCCE
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSSYSSY
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCSAQTCVNFHGGYRCVDTNRC
VEPYIQVSENRLCPASNPLCREQPSSIVHRYMTITSESVPADVFQIQATSVYYPGAYNAFQI
RAGNSQGDIFYIRQINNVSAMLVLARPVTGPREYVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF

Important features:**Signal sequence:**

Amino acids 1-25

N-glycosylation sites:

Amino acids 198-202;394-398

N-myristoylation sites:Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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FIGURE 319

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC
TCAAAGGTGCGTACCCAGCTGTGCCCCGACACCATGTACCTGCCCCTGGCCACCTCCCCGATGC
CCGCTGGGAGTACCCCTGGTGTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGGCTG
GGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCGGG
GCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGTG
AACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC
GAGGACGGCGGCTTACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCCAGCTGGGAC
TGCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA
GGAGGGGGACTGGGGACCCAGCCCCCTTCCAGCCCAAGGACCCAGTTTTCTGGCCTTGTCTCT
TCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGAGCACGGCCTGGGGACCCTGCTCGACCACC
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCCAG
CGCCGCCTGTGCCTGTCCAGGCCCTGCCCACCCTCCAGGGGTGCGAGTCCACAAAACAGTGCC
TTCTAGAGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCCAGGCCCTTGGCTGCAGGCAACACTTTAGC
TTGGGTCCACCATGCAGAACACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCAGGTA
TGGCAGAGGTGCAAGACCTAGTCCCCCTTCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT
GTCCAGGGTCCTCTAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG
CGAGCTTTCTCTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG
AGATTCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAATAATTGTTTCCTGAATACAAGCCTAT
GCGTGA

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FIGURE 320

MRGTPKTHLLAFSLCLLSKVRTQLCPTPCTCPWPPRCPLGVPLVLDGCGCCRVCAARRLGEP
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEG
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGLGTQPLPAQGPQFSGLVSSLP
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRCLSRPCPPSRGRSPQNSAF

Important features:

Signal sequence:

Amino acids 1-23

N-myristoylation sites:

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;

167-173;183-189;209-215

Insulin-like growth factor binding proteins signature:

Amino acids 49-65

von Willebrand C1 domain:

Amino acids 107-124

Thrombospondin 1 Homology Block:

Amino acids 201-216

IGF binding protein site:

Amino acids 49-58

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FIGURE 321

[illegible]

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FIGURE 322

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAVI
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

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FIGURE 323

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGGGGCGTGAGGAGCA
TGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCTGGGCTCAGTGCTGTCAGGCTCGGCCA
CGGGCTGCCCCCGCTGCGAGTGCTCCGCCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG
TCCCCGAGGGCATCCCCACCGAGACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACG
AGTTCCGCAGCTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCGCCT
TCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCGAGCAACCGCCTGAAGCTCATCCCGCTAGGCGTCTTCA
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGATCGTTATCCTACTGGACTACATGTTTCAGG
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCC
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGC
ACGGCCTCATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGCTGTACC
GACTCAAGGTCTTGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAACCTGCCTCTACGGCCTCAACC
TGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCCCTACCTGGCCGTCCGCCACCTAGTCTATCTCC
GCTTCCTCAACCTCTCCTACAACCCCATCAGCACCATGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG
AGATCCAGCTGGTGGGCGGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGC
TCAATGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTCA
TCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGCGCCGCTGGCGGCTCAACTTCA
ACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC
TGCCCAACTACTTCACCTGCCGCCGCGCCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCC
ACACGGTGCACTTGTGTGCCGGGCGGATGGCGACCCGCGCCCGCCATCCTCTGGCTCTCACCCCGAAAGCACC
TGGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCTACGCCCAGGTAC
AGGACAACGGCACGTACCTGTGCATCGCGCCAACGCGGGCGGCAACGACTCCATGCCCCGCCACCTGCATGTGC
GCAGTACTCGCCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAG
AGGCCAACAGCACCCGCGCCACTGTGCCTTTCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCT
TCATCTCTTTCCTGGGCGTGTCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACACAA
AGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCGACGCGCCCCGCAAGT
TCAACATGAAGATGATATGAGGCGGGGGCGGGGGCAGGGACCCCCGGGCGGCCGGGCAGGGGAAGGGCCTGGT
CGCCACCTGCTCACTCTCCAGTCTTCCACCTCCTCCCTACCCTTCTACACAGTCTCTTTCTCCCTCCGCC
TCCGTCCCTGCTGCCCCCGCCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCAGACCTGG
GGACCCACCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCAATAAT
TCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTTATGAAAACCTTGAAATAA
TAAAAAGAGAAAAAACTAAAAA

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FIGURE 324

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCFVAVPEGIPTETRL
LDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLSNLTKQDI
SENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRAFSGLSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHL
NINAIIRDYSFKRLYRLKVLEISHWPYLDTMTNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSGNLETILDSNPLACDC
RLLWVFRRRWRLNFRNQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFVDEGHTVQFVCRADG
DPPPAIWLSPRKHLVSAKSNRGLTVFPDGTLEVRYAQVDNGTYLCIAANAGGNDSPAHLHVRSYSPDWPHQP
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPR
KSDAGISSADAPRKFNMKMI

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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FIGURE 325

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG
AGGTGAAGAAGGAGAGAGGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAGGAG
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG
AGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGGAAAGAC
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT
TGGCATTGTTGGGGAAGTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCTTGAGGGAC
AGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGGCAGGGGTCC
CTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGCGCTGGTACTC
TGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC
TACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGCCTGGTGAATGCA
GCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGAGCTGAAGAGGGTT
CTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGGAACC
TTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCTGTGGTCAATGTGTCT
GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCTGTTTGGAGCTCGCGAC
GGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTGAGGTGCAGCTCATTAC
TTCAACCAGGAAGTCTACGGGAATTTACAGCGCTGCCTCCCGCGGCCCAATGGCCTGGCCATT
CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCAGTCGCCTCCTTAACCGC
GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG
CTCCTGTTCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC
TCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTTCAGATGCAC
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC
CGGCCCCCTGCAGCCCTTGGCCCCACAGGGCACTGAGGGGCAACAGGGACCCCGGCACCCCGAG
AGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGATGGTGTCCCCATGGTCGCTAGAGAC
TCCCCTTCGAGGATTGCACCCGCCGTCTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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FIGURE 326

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLY
SHRLSELRLLEFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLEVN
VASTSNPFSLRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSLTPPCSETVTW
ILIDRALNITSLQMHSLRLLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP
NYRLHVDGVPHGR

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 177-199

N-glycosylation sites:

Amino acids 118-122;170-174;260-264

Eukaryotic-type carbonic anhydrases proteins:

Amino acids 222-271;128-165;45-93

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FIGURE 327

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGT
TTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTGTCTGAGAACATTTACATTATAGATAA
GTAGTACATGGTGGATAAATTCTACTTTTAGGAGGACTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACT
AAGACACCAATGAAGGAGTATGTGCTCCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCA
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATGATG
ATGATGATGAGGACAACTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTCCATTTGATCTGTTTCCAA
TGTGTCCATTTGGATGTGAGTGCTATTACGAGTTGTACATTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCA
ACATTCCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAG
GACTCACTTCACTTTATGGTCTGATCCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTCTTAACCA
CAAAGAAGTTGCGAAGGCTGTATCTGTCCACAATCAACTAAGTGAATACCCTTAATCTTCCCAAATCATTAG
CAGAACTCAGAAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACAG
TTTTGGAAATGAGTGCAAACCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTTC
ATATCAGAATTGCAGAAGCAAACTGACCTCAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAG
ATTATAATAAAATTTCAACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAA
ACAACAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAACA
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATAATCTTCCTTCATTCTAATTCAA
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT
TATTCAACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTT
AGCTTGGGAACCTTTGGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACAT
TTGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCAAGTGGTAAAGTCC
ACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAACTATTGATACATAAGGGGTTGAGAGAAACA
AGCATCTATTGCAGTTTCCTTTTTGCGTACAAATGATCTTACATAAATCTCATGCTTGACCATTCCCTTCTTCAT
AACAAAAAGTAAGATATTCCGTATTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGG
AATGCTTGACTTAGCAAAATTTGTGCTCTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGTGA
AGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA
TTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGTCTTTATGTTTAAAACTAATTTCTTAAAA
TAAAGCCTTCAGTAAATGTTTCACTTACCAACTTGATAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATAT
GCTTTTTTTTTTTAATTATTACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC
CGCATTTTAAATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCCACTTCAA
CTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGGAAGAGCCTGGACACTAACAAATCTACACC
AAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT
CAAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAA
CATATGTAAATCAGAAAACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

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FIGURE 328

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPRS
HFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS
LYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT
FKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
STVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPPELKYLQI
IFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

Important features:**Signal sequence.**

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 329

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGTGT
TTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGTGTT
CAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCG
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCT
GAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC
GCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTCAGTTTGA
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA
TGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCATGCAGCAAAT
GTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTACCAAC
CTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCG
TTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGACCCATCATCATCCACACTGATGA
AGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTGAAAAGGTGAAGGA
CAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGC
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA
GAGAGCTGTGGACACATCCTTGTACATACTGCCCCAAGGAAGACAGGGAAAGTCTTCAGATGGC
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT
AATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAACCT
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA
TACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA
TGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATTTTAAATAAAGTGCCTTTATACAATG

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FIGURE 330

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRQTASLQ
PGISEDLLKKVKDRMGIDSSDKVDFILLDNVAEQAHNLPSCPMLKR FARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Important features:**Signal sequence:**

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 331

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCAGTCTTGTGGCTACAACATTTTCCCTTTCCT
AACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTTGCTGGAGAAGAAAGGGCTGAGGGCAG
AGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTGCCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT
GCAGCGGAGTGAGGTGATGGAAGTCTAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGA
CCTGGAGAGCCTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG
ACGTGCCGTTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGGTGAACCTCAACAGCCT
TTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAATAAAATTTTAA
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGG
GAGAAAGTATGTTAAAAATAGAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACC
CTGGGTGAGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTTGCAGAA
TCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCTCTC
AGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTC
TGGGTGCTGCTGGCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACC
TTCAACCACTTGACCGTCCACCAAGGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACA
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCGCCCTCATC
GTGCAGCCCTGCAGCGAAGTGCTCACCCTACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAAC
CGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG
GAGCCATCCCACAAGAAGGAGCACTACCTGTCCAGTGTCACAAGACGGGCACCATGTACGGGGTGATTGTGCGC
TCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCC
AGCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCT
CTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGACCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC
TTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAGTTCCTACTCATACGTGTCCCTGCCCTTCGGC
TGCACCCGGGCCGGGGTGAATAACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAG
GCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAGGGCAGAAGCAGTATCACCACCCG
CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCTGC
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCC
ATCGATGATAACTTCTGTGGACTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTG
TACACCACCAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG
ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCCATTCACCTCCTCAGCAAA
GAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAGGCAACTTTATTTTCTTGGGGAACAAAGGTGA
AATGGGGAGGTAAGAAGGGGTTAATTTTGTGACTTAGCTTCTAGCTACTTCCCTCAGCCATCAGTCATTGGGTAT
GTAAGGAATGCAAGCGTATTTCAATATTTCCCAAACCTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 332

MGTLGQASLFAPPGNYFWS DHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR
ALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSEN RDWTFNHLTVHQGTGAVYVGAINRVYK
LTGNLTIQVAHKTGPEEDNKSRYPP LIVQPCSEVLTLTNNVNKLLIIDYSENRL LACGSLYQG
VCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFITAVDVGKQDYFPTL
SSRKLPRDP ESSAMLDYELHSD FVSSLIKIPSDTLALVSHFDIFYIYG FASGGFVYFLTVQPE
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSL AQ
AFNITSQDDVLF AIFSKGQKQYHHPDD SALCAFP IRAINLQIKERLQSCYQGEGNLELNWLL
GKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVV FVGT
KSGK LKKVRVYEFRC SNAIHLLS KESLLEGSYWWRFNYRQLYFLGEQR

Important features:**Signal sequence:**

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site. .

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 333

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAGG
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCCAGAGCCCACACCATGCCGGGCACCTACGC
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGGCCCTGAT
GCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCA
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGACAGGCT
TAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG
GGATGCCCTGCGCCTCACCCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTC
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCAT
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCT
GGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA
GGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC
AGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAA
CAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGAT
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA
TCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA
TGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGA
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCG
GGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGGAGGACAA
GTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA
GAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGC
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGCAGTTGTGGCCACCTT
CCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC
CACAGACACCCACAAAGTTCCTGTTGTGCAGGCACAAATATTTCTGAAATAAATGTTTT
GGACATAG

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FIGURE 334

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGQ
TSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALNDTQ
KLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK
NGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY
PVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS
RLRQRQSLTSGQELTEIPIHWTAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

Important features:**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

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FIGURE 336

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEW
KKLGRSVSVFVYYQOTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQSTNSS
YTMNTKTGTLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAAGGSRGQEF

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

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FIGURE 337

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCGG
CACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCA
TGATTTCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG
CCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTCATCCC
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGGTGT
TGTCTACATCAATGGGGTCAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT
CCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTACAGCTGCT
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCTTAGAACTCA
ATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCATGTGGGGGCAA
ACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGC
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC
TCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCCAATGAGGTGGGCA
CTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAG
CTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCC
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC
TGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTACCTCCG
CACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCAGTC
TCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCCACGACAGATGGGGCCCCACCCTCAACCAA
TATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTAT**TG**ATGACCCCACTCATTGGCTAAAG
GATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAG
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACCATCTCA
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGC
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCACCCCTAT
CTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG
GTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAACTAACATGAAATATGTGTT
GTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAAAAA

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FIGURE 338

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSS
QPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPYSC
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVGVANVTLSQCSPRSKPAVQYQWDR
QLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAADVAG
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTLSSVTS
ARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSSGLSRMGAVPV
MVPAQSQAGSLV

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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FIGURE 339

CGGAGAACCTTTGCACGCGCACAAACTACGGGGACGATTTCTGATTGATTTTGGCGCTTTTCGATCCACCCTCCT
CCCTTCTCATGCGGACTTTGGGGACAAAGCGTCCCGACCGCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA
GGACAGCGTCGGGAACCCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCGTCTTCATCGTCGCGGTT
TGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTCCCCAGCAGACAGTGGCCCCACAGC
AACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC
CGTGCACAGAGGGTGTGGATTACACATTGCTTCCAACAATTTGCCTTCTTGCTGCTATGTACAGTTTGTAAAT
CAGGTCAAACAAATAAAAGTTTCTGTACCACGACCAGAGACACCGTGTGTAGTGTGAAAAAGGAAGCTTCCAGG
ATAAAACTCCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCCAGAGGGATGGTCAAGGTCAGTAATTGTA
CGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCTGGGAAAACCCAGCAGCGGAGGAGA
CAGTGACCACCATCTGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTT
TAGCTGTGGTTGTGGTTGGCTTTTTCATGTGCGAAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGT
GAGGAGGTCCCGAACCTGTGCACAGAGTCCTTTTCCGGCGGCGTTTCATGTCTTCACGAGTTCCTGGGGCGGAGG
ACAATGCCCGCAACGAGACCCCTGAGTAACAGATACTTGCAGCCACCCAGGTCTCTGAGCAGGAAATCCAAGTC
AGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAA
CTGAAGGGTGTGAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACATCAGCACCTTGCTGG
ATGCTCGGCAACACTGGAAGAAGGACATGCAAGGAAACAATTCAGGACCAACTGGTGGGCTCCGAAAAGCTCT
TTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCTGTGAAGAATCTCTCAGGAAACCAGAGCTTCCCT
CATTTACCTTTTCTCTACAAAGGGAAGCAGCTGGAAGAAACAGTCCAGTACTTGACCCATGCCCAACAACT
CTACTATCCAATATGGGCGAGCTTACCAATGGTCTAGAACTTTGTTAACGCACTTGGAGTAATTTTTATGAAAT
ACTGCGTGTGATAAGCAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGTTATACGATTGTGATTAAGG
GCTGTTTTAGGGCCACATGCGGTGGCTCATGCTGTAAATCCAGCACTTTGATAGGCTGAGGCAAGGTGGATTGCTT
GAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAACCTCCATCTCAATTTAAAAAGAAAAAAGTGGTTT
TAGGATGTCAATCTTTGCAGTCTTTCATCATGAGACAAGTCTTTTTTCTGCTTCTTATATTGCAAGCTCCATCT
CTACTGGTGTGTGATTTAATGACATCTAATACAGATGCCGCACAGCCACAATGCTTTGCCTTATAGTTTTTTA
ACTTTAGAACGGGATTATCTTGTATTACCTGTATTTTTCAGTTTCCGATATTTTGAATGATGAGATTATC
AAGACGTAGCCCTATGCTAAGTCATGACATATGGACTTACGAGGTTTCGACTTAGAGTTTGGAGCTTTAAGATA
GGATTATTGGGGCTTACCCCACTTAATTAGAGAACTTTATATTGCTTACTACTGTAGGCTGTACATCTCTT
TTCCGATTTTTGTATAATGATGTAACATGGAAAACTTTAGGAAATGCACTTATTAGGCTGTTTACATGGGTTG
CCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATAACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGG
AGGCACTTACTGCATTCCAGTTCTCCCTCCTGCGCCTGAGACTGGACCAGGGTTTGATGGCTGGCAGCTTCTCA
AGGGGCAGCTTGTCTTACTTGTTAATTTTAGAGGTATATAGCCATATTTATTTATAAATAAATATTTATTTATTT
ATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGCCTGGTATCTTTGGGAAGCCATGTGTCTGGTTT
GTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAAGTTAG
ATCCGAGACTGCCAAGAGCTTCTCTTCAAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCATTGGG
CTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGGACGGTGTGGG
AATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGCCCCCTCTCGCTTCTGGTGGTCTGTGAATGAGTCCCT
GGGATGCCTTTTAGGGCAGAGATTCTGAGCTGCGTTTTAGGGTACAGATTCCCTGTTTGAGGAGCTTGGCCCT
CTGTAAGCATCTGACTCATCTCAGAGATATCAATTCTTAAACACTGTGACAACGGGATCTAAATGGCTGACACA
TTTGTCTTGTGTACGTTCCATTATTTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACCTCT
TCTCCACAGTAGCCAGTCGTGGTAGGATAAATTACGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTC
AAGGCATTGTGTGTTTGTTCGGGACTGGTTTGGCTGGGACAAAGTTAGAACTGCCTGAAGTTTCGCACATTCAG
ATTGTTGTGTCCATGGAGTTTATAGGAGGGGATGGCCTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATC
TGGCGTCCCACACCTTGTCCCCTGCACTTCTGGATGACACAGGGTGTGCTGCTGCTCCTAGTCTTTGCTTTGCTG
GGCCTTCTGTGAGGAGACTTGGTCTCAAAGCTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTTGTCCCTTCTC
AGAGGCGTTCTTGAAGATGCATCTAGACTACCAGCCTTATCAGTGTTTAAGCTTATTCTTTAACATAAGCTTC
CTGACAACATGAAATGTGGGGTTTTTGGCGTTGGTTGATTTGTTTAGGTTTTGCTTTATACCGGGCCAAAT
AGCACATAACACCTGGTTATATATGAAATACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 340

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVPPQQTVAPOQQQR
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKN
SPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVLVIIILAV
VVVGFSCRRKFISYLGICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQEL
AELTGVTVESPEEPQRLLEQAEAGCQRRRLVPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE
EDEAGSATSC

Important features:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

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FIGURE 341

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG
CCATGCTTCGTTTCTTGCCAGATTTGGCTTTACAGCTTCCTGTTAATTCTGGCTTTGGGCCAGG
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCACCCC
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTCCAGGATCGCGAGGCAGCAGCGA
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGTACTTC
GCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCTCCTGCC
TGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGAAGTGGCTC
TGTTCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTAAAATGTTTG
TGTTGCGGTGAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGATGTAGCTAAGG
ATTGGAATGACAACCCCCGGAAAAATTTGCGGTTATTCTGGAGATACTGGTCAAAGAAGATA
GAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG
CTTCCCTGCTGGTGGTGAAGTCTCAACCCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG
CCATCCCTGTCCCCAAGCTTTCTTGTGAAGAACCTCTGCCACCGTCACCAGCTATTCATTAAGT
TCCGGGACCTGGGTGGCACAAGTGGATCATTGCCCCCAAGGGGTTTCATGGCAAATTACTGCC
ATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTCATGCAAG
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC
CCATTTCCATGCTCTACCAGGACAATAATGACAATGTCAATTCTACGACATTATGAAGACATGG
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTCTTAGGG
TAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTAGATCGAAATGTC

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FIGURE 342

MLRFLPDLAFSFLLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQVPVYILKKIFQDREAAAT
TGVSRDLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTKPGKMFVLRVWPWPQGAVHFNLDDVAKD
WNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRKRRAA
IPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAFMQA
LMHAVDPEIPQAVCIPTKLSPISMLYQDNNNDNVILRHYEDMVVDECGCG

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

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FIGURE 343

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCATTCTCTTTTCATTGACAACTGACTTTTTTTTATTTCT
TTTTTTCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTGTGTTTTACACACATAAGGAT
CTGTGTTTTGGGGTTTCTTCTTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCAGTGG
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGGTATCCTGGCGGCCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAATAACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTTCATGGAAAATAACTCAGTGCTGCTGGGAACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGTCTTAAGGCTGCCAGCGCCTTGCCAAAATGAGAGCTTGTA
AGAAGGCTCATGCCATTGACCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAAGTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCCCTGATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAAGTGTCTTTGCTTCTACTACTTCTTCTCTCCTAACATCTCTATTTCAAAGTGT
GGCGGTTACCTGGATACCTTGGAGGATCCTTACCAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGTGGCAGATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTAGAAAATAGAC
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAATCTCTGACTGTGCTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTTCTGCTTCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCACATAAAA
GACCCAACTTGACAGACCAAAATTATCAAATGTTGTGGAATTTTCTGTCCCTCTAATGGATGTGGTACAAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCAATTCA
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAATCTTTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGATGTAGTCGAGATGAAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGA
TTCCAGTTTAATGCCTTTAAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTGATATGTGAT
AGCAGTGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG
AAAACAGATTCCATCATAGGACCCATTCTGCTGAAAAGGGATCGAAGTGCAAGTGGCAATTGAGGATTTAGCAT
GAAACACATGCGGAAGAACTCAAACAGCCTTTCAACAGTGTGCATCTGTTTTCTTCATGGTTCTAGCTCTG
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAATATTAACCTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAA

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FIGURE 344

MELVRRMLPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE
RPEKNSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLTTFQ
IVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD
YKIKLNFKEIFLEIDKQCKFDFLAIDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLSTDYA
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVLIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV
VEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNSTVEIIYI
TEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPNLVVFLDT
CRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLICD
SSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFGHETHAEETPNQPFN
SVHLFSFMVLALNVTVATITVRHFVNQRADYKYQKLQNY

Important features:**Signal sequence:**

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423**Casein kinase II phosphorylation site.**amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 345

TGGGGGCCCCCAGGCTCGCGCGTGGAGCGAAGCAGCATGGGCAGTCGGTGCGCGCTGGCCCTGGCGGTGCTCTC
GGCCTTGCTGTGTCTAGGTCTGGAGCTCTGGGGTGTTCGAAGTGAAGCTGCAGGAGTTCGTCAACAAGAAGGGGCT
GCTGGGGAACCGCAATTGCTGCGCGGGGGCGCGGGGCCACCGCGTGCCTGCGCGTCCCGGACCTTCTTCCGCGTGTG
CCTCAAGCACTACCAGGCCAGCGTGTCCCCGAGCCGCCCTGCACCTACGGCAGCGCGCTCACCCCGTGTGGG
CGTCGACTCCTTCACTGTGCCCCGACGGCGGGGGCGCGACTCCGCGTTCAGCAACCCCATCCGCTTCCCTTCGG
CTTCACCTGGCCGGGCACCTTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTGATGACCTCGCAACAGA
AAACCCAGAAAGACTCATCAGCCGCTGGCCACCCAGAGGCACCTGACGGTGGGCGAGGAGTGGTCCCAGGACCT
GCACAGCAGCGGCCGACGGACCTCAAGTACTCCTACCGCTTCGTGTGTGACGAACACTACTACGGAGAGGGCTG
CTCCGTTTTCTGCCGTCCCCGGGACGATGCCTTCGGCCACTTCACCTGTGGGGAGCGTGGGGAGAAAGTGTGCAA
CCCTGGCTGGAAGGGGCCCTACTGCACAGAGCCGATCTGCCTGCCTGGATGTGATGAGCAGCATGGATTTTGTGA
CAAACAGGGGAATGCAAGTGCAGAGTGGGCTGGCAGGGCCGGTACTGTGACGAGTGTATCCGCTATCCAGGCTG
TCTCCATGGCACCTGCCAGCAGCCCTGGCAGTGAAGTGCAGGAAGGCTGGGGGGGCTTTTCTGCAACCAGGA
CCTGAAGTACTGCACACACCATAAGCCCTGCAAGAATGGAGCCACCTGCACCAACACGGGCCAGGGGAGCTACAC
TTGCTCTTGCCGGCTGGGTACACAGGTGCCACCTGCGAGCTGGGGATTGACGAGTGTGACCCAGCCCTTGTAA
GAACGGAGGGAGCTGCACGGATCTCGAGAACAGTACTCCTGTACCTGCCACCCGGCTTCTACGGCAAAATCTG
TGAATTGAGTGCCATGACCTGTGCGGACGGCCCTTGCTTTAACGGGGGTGCGTGTGCTCAGACAGCCCCGATGGAGG
GTACAGCTGCCGCTGCCCGTGGGCTACTCCGGCTTCAACTGTGAGAAGAAATGACTACTGCAGCTCTTCACC
CTGTTCTAATGGTGCCAAAGTGTGTGGACCTCGGTGATGCCTACCTGTGCCGCTGCCAGGCCGGCTTCTCGGGGAG
GCACTGTGACGACAACCTGGACGACTGCGCCTCTCCCCGTGCGCCAACGGGGGCACCTGCCGGGATGGCGTGAA
CGACTTCTCCTGCACCTGCCCGCTGGCTACACGGGCAGGAAGTGCAGTGGCCCCGTGACGAGGTGCGAGCACGC
ACCCTGCCACAATGGGGCCACCTGCCACGAGAGGGGCCACCGCTATGTGTGCGAGTGTGCCCCAGGCTACGGGG
TCCCAACTGCCAGTTCCTGCTCCCCGAGCTGCCCCGGGGCCAGCGGTGGTGGACCTCACTGAGAAGCTAGAGGG
CCAGGGCGGGCCATTCCCTGGGTGGCGGTGTGCGCGGGGTATCCTTGTCTCATGCTGCTGCTGGGCTGTGC
CGCTGTGGTGGTCTGCGTCCGGCTGAGGCTGCAGAAGCACCGGCCCCAGCCGACCCCTGCCGGGGGAGACGGA
GACCATGAACAACCTGGCCAACTGCCAGCGTGAGAAGGACATCTCAGTCAGCATCATCGGGGCCACGCAGATCAA
GAACACCAACAAGAAGGCGGACTTCCACGGGGACCACAGCGCCGACAAGAATGGCTTCAAGGCCCCGCTACCCAGC
GGTGGACTATAACCTCGTGCAGGACCTCAAGGGTGACGACACCGCCGTGAGGACGCGCACAGCAAGCGTGACAC
CAAGTGCCAGCCCCAGGGCTCCTCAGGGGAGGAGAAGGGGACCCCGACCACACTCAGGGGTGGAGAAGCATCTGA
AAGAAAAAGGCCGACTCGGGCTGTTCAACTTCAAAAGACACCAAGTACCAGTCGGTGTACGTATATCCGAGGA
GAAGGATGAGTGCGTCATAGCAACTGAGGTGTAAAATGGAAGTGAAGTGGCAAGACTCCCGTTTCTCTTAAATA
AGTAAATTTCAAGGATATATGCCCCAACGAATGTGCTGAAGAGGAGGGAGGCCCTCGTGGACTGCTGCTGAGAA
ACCGAGTTCAGACCGAGCAGGTTCTCCTCCTGAGGTCTCGACGCTGCCGACAGCCTGTGCGGGCCCGGCCGCC
TGGGCACTGCCTTCCTGACGTGCGCGTTGCACTATGGACAGTTGCTCTTAAGAGAATATATATTTAAATGGGT
GAACTGAATTACGCATAAGAAGCATGCACTGCCTGAGTGTATATTTTGGATTCTTATGAGCCAGTCTTTTCTTGA
ATTAGAAACACAACACTGCCTTTATTGTCCTTTTGTATACGAAGATGTGCTTTTCTAGATGGAAAAGATGTGT
GTTATTTTTTGGATTTGTAAAAATATTTTTTCATGATATCTGTAAAGCTTGAGTATTTTGTGATGTTCTGTTTTTA
TAATTTAAATTTTGGTAAATATGTACAAAGGCACTTCGGGTCTATGTGACTATATTTTTTGTATATAAATGTAT
TTATGGAATATTGTGCAAATGTTATTTGAGTTTTTACTGTTTTGTTAATGAAGAAATTCCTTTTTAAATATTT
TTCCAAAATAAATTTTATGAATGACAAAAA

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FIGURE 346

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPPCACRTFFRVC
LKHYQASVSPPEPPCTYGS AVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTFSLIIEA
LHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRDLDKYSYRFVCD EHYGEGCS
VFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR
YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPKNGATCTNTGQGSYTCS
CRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCADGPCFNG
GRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD
DNVDDCASSPCANGGTCRDGVNDFSTCTPPGYTGRNCSAPVSRCEHAPCHNGATCHERGHRYV
CECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGQGGFFPWVAVCAGVILVLM LLLGCAAVVV
CVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKN
GFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGS SGEEKGTP TTLRGGEASERKRPD
SGCSTSKDTKYQSVYVISEEKDECVIATEV

Important features:**Signal sequence:**

Amino acids 1-21

Transmembrane domain:

Amino acids 546-566

N-glycosylation site:

Amino acids 477-481

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 660-664

Tyrosine kinase phosphorylation sites:

Amino acids 176-185;252-261

N-myristoylation sites:

Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;
676-682;683-689;695-701

Aspartic acid and asparagine hydroxylation sites:

Amino acids 343-355;420-432;458-470

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 552-563

EGF-like domain cysteine pattern signature:

Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;
467-479;505-517

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FIGURE 347

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTTCGGTCAACA
TCGTAGTCCACCCCTCCCCATCCCCAGCCCCCGGGATTTCAGGCTCGCCAGCGCCCAGCCAG
GGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGCTGT
TCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGGACAT
CTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCACGAGG
ACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC
TTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAACTG
CCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTTATAAATCTT
CATTACGGGAAAAAGACACAGCCACCCTAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCCC
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC
CCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC
AACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTG
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTAT
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACA
AGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACC
ACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTGCTCATCATGCTCATCTTCC
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA
AGAAGGAATATTTTCATCTAGAGGCGCCTGCCCACTTCTGCGCCCCCAGGGGCCCTGTGGGG
ACTGCTGGGGCCGTCACCAACCCGGACTTGTTACAGAGCAACCGCAGGGCCGCCCTCCCGCTT
GCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT
TTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTTCCTGGCTT
CTCTGCATTTGGGTATTATTATTTTTTGTAAACAATCCCAAATCAATCTGTCTCCAGGCTGGA
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAAACAAAAACA

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FIGURE 348

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWS
NPAQQTLYFGEKRALRDNRILVTSTPHELSSISISNVALADEGEYTCSIFTMPVRTAKSLTV
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT
VSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL
HCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN
VNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIIFLGHYLI RHKGTYLTAEAKGSDDAPDADT
AIINAEGGQSGGDDKKEYFI

Important features:**Signal sequence:**

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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FIGURE 349

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAGGACAGCAGCAAAG
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA
GCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGTCATTTTGATTTTGCTGTTATTTTTTTTTTCTTTTTCTT
TTTCCCACCACATTGTATTTTATTTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGG
CTTTTTTCTGAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCCCTA
GTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCTCTTGGGATCCCGG
AGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGCTGGATTTCTGCAGAACTGCACAATGTAC
AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTCAGAG
TTCTCCATTTGCAGGAAAAAATATTACAGACCATTTTACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGC
TGCACCTGGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTCCGGGAGGCTATTAGCCTCAAAT
TGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGACTTGCAAGAGCTGAGAGTGG
ATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAATCTCACGAGCTTGGAGCGTCTTATTGTGGACG
GGAACCTCCTGACCAACAAGGGTATCGCCGAGGGCACCTTACGCCATCTCACCAAGCTCAAGGAATTTTCAATTG
TACGTAATTGCTGTCCACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACC
AGATAAACCACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC
TGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCAACCTGAAGCAGCTCACTGCTCGGAATAACCCCTGGT
TTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAAATATATCCCTTCATCTCTCAACGTGCGGGGTTTCA
TGTGCCAAGGTCTGAACAAGTCCGGGGGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCACCA
CGACCCCGGCTGCTCTCTTACCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTA
TTCAAACCCCTAGCAGAAGCTACACGCCTCCAACCTCTACCACATCGAACTTCCCACGATTCTGACTGGGATG
GCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGAATGATACTTCCATTC
AAGTCAGCTGGCTCTCTCTTACCGTGATGGCATACAAACCTCACATGGGTGAAAATGGGGCCACAGTTTAGTAG
GGGGCATCGTTCAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA
CCTATCGGATTTGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTAGAGGCCA
CCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCCACAGCATGG
GCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGCGCGGTGATATTTGTGCTGGTGGTCTTGCTCAGCGTCTTTT
GCTGGCATATGCACAAAAGGGGCGCTACACCTCCAGAAGTGGAATACAACCGGGGCGGGCGGAAAGATGATT
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAATCGTCTCCTTAA
ATAACGATCACTCCTTAAAGGAGATTTAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTACACAG
ACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTCAGCAGC
CAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAG
ATTACATTTGATAAATGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA
TGGGATTTAAAAAAGTGCTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACCTTTTGCTTTTTTAA
TCTT

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FIGURE 350

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIPE
GVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFPMNLPKNVRVLHLQENNIQTISR
AALAQLLKLEELHLDNDSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELRVDE
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPGT
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD
CSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELNMNLLSCPTTTPGLPLFTPAPSTAS
PTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVNDTSIQVSW
LSLEFVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFNRYRAV
EDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVLLSVFCWHMH
KKGRTYSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKGD FRLQPIYTP
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Important features:**Signal peptide:**

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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FIGURE 351

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCGCGCGGGGAGTAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGACGCGACCGC
GAGGGCGGGCGTGACACCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCGGGCTGGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCGCGATGAGCGCGCGGAGCCTCCGTGCGCGCGCGCGGGGTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC
GAGCGCCCATGCCCCACTACCTGCCGCTGCCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGCTT
CCCGAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAAATGAATTGGAGACCATTCCAAATCTGGGACCA
GTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTTGAAGCTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAAACTGCATTTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTTAAACTGCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCT
CTGAAAATGCAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCATAAACCTTAACAGAGATTACCAAAGGCTTACGGCTTGCTGATGCTGCAGGAACCTTCAT
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCCTGGCCTAAGCTTACTAAATACACTGCACATTGGG
AACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTTTACAAGGCAATGCATTTTACAAATGAAGAACTGCAACAATTGCATTTAAATACA
TCAAGCCTTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGGAAAAACAATTTTCAAGCTTTGTA
AATGCCAGTTGTGCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTTGCTGTTAGCCAGATGGCTTTGTGTGT
GATGATTTTCCCAAACCCAGATCAGGTTCCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTATTCCCAATGACTTTTGCTTGGAAAAAGACAATGAACACTGCGATGAT
GCTGAAATGGAAATTTATGCACACCTCCGGGCCAAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCCAATCACTTTGGTTTATCCTACTCTGTCT
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCACGCTTGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAAATGCAACTCTGACTGTC
GTAGAAACACCATCATTTTTTGGGCCACTGTTGGACCGAAGTGTAAACCAAGGGAGAAACAGCCGCTCCTCAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC
TTTTTTGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAAATACACATGTGAG
ATGTCTAACACCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCACTCCAACCTGCGACTCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTGT
GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACAAAGGCGGAGGAATGAAGATTGCAGCATTACC
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCTCAGGGAACGTTAGCTGACAGGCAG
GATGGGTACGTGCTTTCAGAAAGTGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACA
TATCATACAGGTTGAGTCCCTGACCAAGAACAGTTTAAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG
GAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCTGCGAACCGGAGCTTCAGTAATATATCGTGGCCTTCACAT
GTGAGGAAGCTACTTAACTACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
TCTTTAGATTTTAGTGAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATCTTTCATGGGTACCTTTTGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCCAAGAGCCTTTTAT
TTGAAAGCTCATTTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA
GAAATACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACATACTACTCAAGTGAAGTAACTTTTATTTAAAGAGAGAGAAT
CTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATTAC
AAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAACTATTTTTTAACCTTG
TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTTATAATGCCAGA
TTTCTTTTTATGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGATACCATTTTTTAAATAGAAGTT
ACTTCATTATATTTTGCACATTATATTTAATAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 352

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSRKRLARLPEPLPSW
VARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVEILPEHLKEFQSLETL
DLSSNNISELQTAFFPALQKLYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRN
KIKNVDGLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNLTETITKGWLYGLLMLQELHLSQNAIN
RISPDWFEFCQKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNNEISWTI
EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDSLSDNAIMSLQGNAFSOMKKLQQLHLNTSSLLCDC
QLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS
SDSPMTFAWKKNELLHDAEMENY AHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVN
MLPSFTKTPMDLTIRAGAMARLECAAVGHAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS
CTAQNAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHFFAAGNQ
LLIIVDSVDSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIAVVCVVGTSLV
WVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADLRQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGT
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDFETYHTGCSPPDRTVLMDDHYEPSYIKKKECYPCSH
PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHL
DAYSSFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQEEHNICTFKQTLNRYRTPNFQSYDLDT

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020**Glycosaminoglycan attachment site.**

amino acids 886-890

Casein kinase II phosphorylation site.amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085**Tyrosine kinase phosphorylation site.**

amino acids 667-675

N-myristoylation site.amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939**Leucine zipper pattern.**

amino acids 58-80, 65-87

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FIGURE 353

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTTCTTCTCCTTTCTGGCTTCGGACATTGG
AGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTTACTTTGTGATGAGATCGGGGATGA
ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGTCTCTTGTGTTTGCCGCTGGAAACGTTAC
AGGGGACGTTTGCAAGAGAAGATCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAA
GGGCTTCACAAGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTACCATTATTTCTGCATGGCAATTCCCT
CACTCGACTTTTCCCTAATGAGTTCGCTAATTTTATAATGCGGTTAGTTTGCACATGGAAAACAATGGCTTGCA
TGAAATCGTTCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGGCTGCACATCAACAACAACAAGATCAAGTC
TTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATAT
AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACC
TGCCAACGTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA
GGAGGTCTTGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTTGGGACTGCACCTGTGATCT
GCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCCCTGATCGGCCGAGTGGTCTGCGAAGCCCCAC
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAG
TCTCCCGCGCCCCCTGCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCA
AGAGGATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAAATCAG
ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCTTAGCTAACAGTTTACCCTGCCCTGGGGGCTG
CAGCTGCGACCACATCCCAGGGTGGGTTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTTGGCTGATTT
GAAGCCCCAAGCTCTCTAACGTGCAGGAGCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTT
TGTGGATTACAAGAACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAA
GAACCTTTTGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGAGAAATTCGCGGG
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCCTCCCGGGCATTTCATGCCAT
GCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTGCTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTC
GCTCTCTAAACTCAGCCTGCACAACAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTC
CATCATCCAGATAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCAGA
ACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGTGAACCTTTTAGAAAGGATTTTCAT
GCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTCGCCACGTTAACTTCGCACAGTAAAAA
CAGCACTGGGTTGGCGGAGACCGGGACGCACTCCAACCTCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTT
GGTCCCGGGACTGCTGCTGGTGTGTTGTACCTCCGCCTTCACCGTGGTGGGCATGCTCGTGTGTTATCCTGAGGAA
CCGAAAGCGGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGTGACTC
TTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCCACAGAGTGTATGACTGTGGCTCTCACTCGCTCTC
AGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGCACCCGGG
GGCTGGAGGGGCGTGTACCCAAATCCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTC
GCACAACCGAAAGGGCCTGACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGA
GCGCAGCCAGCTCGCTCTTTGCTGAGAGCCCCTTTTGACAGAAAGCCAGCAGACCCTGCTGGAAGAACTGACA
GTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATACATATATACATATATCCACATC
TATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAGCCCCGTGATGGCTCCCTGTTGGCTACGCAGGGAT
GGGCAGTTGCACGAAGGCATGAATGTATTGTAAATAAGTAACCTTGACTTCTGAC

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FIGURE 354

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYHL
FLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQTF
LGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDRGNRL
KTLPYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ GKDL
NETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTKIPGNW
QIKIRPTAAIATGSSRNKPLANSRPCGGCSCDHIPGSGLKMNCNNRNVSSLADLKPKLSNVQ
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE
KFAGLQNLLEYLNVEYNAIQILIPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN
YFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT
SAFTVVGMLVFILNRKRKRSDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS
LSD

Important features:**Signal sequence:**

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697**N-myristoylation site.**amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

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FIGURE 355

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGACCCAGAATAACTCAGGGCTGCACCGGGCCTG
GCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGCCGCTGGGCCCCGGGGGGATTCTTGG
CAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGGAAGGGAGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAG
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC
GGGGCCTCAGAGAAATGAGGCCGGCGTTGCGCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGCGGCGG
CGAACACCCCACTGCCGACCGTGTGCGTGTGCTCGGCCTCGGGGGCCTGCTACAGCCTGCACCACGCTACCATGAA
GCGGCAGGCGGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTCAGCACCGTGCCTGCGGGCGCGGAGCTGCG
CGCTGTGCTCGCGCTCCTGCGGGCAGGCCAGGGCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACT
GGAGCGCAGGCGTTCCCACTGCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGG
CGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGCGGTACT
CCAGGCCACCGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGTG
CAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGGGCCGCTCTAACTTGAGCTATCGCGCGCCCTT
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCC
GATCTCAGTTACTTGCATCGCGGACGAAATCGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTG
CCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCCTG
CGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCCT
TGGGGGGACCGGGTGCCCAACAGGCGCCCGCCGCGCCACTGCAACCAGCCCCGTGCCGCAGAGAACATGGCCAAT
CAGGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCCTGAACAAGACAATTAGTAACATCTATTCTGAGAT
TCCTCGATGGGGATCACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC
CCCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTTTCGACTCCTCCTC
TGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCTTGACCATGACAGTACTGGGGCTTGT
CAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCAGCCAAGGAAGGAGTCTATGGGCCCCGGGGCCTGGAGAGTGA
TCCTGAGCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCT
GCGGGACAGAGCAGAGGGTGCCTTGCTGGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGACA
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTACTTGTGTAACGACAA
TTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTTC
CCTGATGATAGAGGAAGTGAAGTGCCTTTAGGATGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATT
TTCTTATGTTTATTCGGAGAATTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATAT
AATTTACATTAAAAATAATTTCTACCAAATGGAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTATATTGG
TTCGAAATCCCAGGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

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FIGURE 356

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEEACILRGGALST
VRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLESD
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPPAPRPGAASN
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR
AGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATATSPVP
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS
KFNSTTSSATPQAFDSSSAVVVFIFVSTAVVVVLVILTMTVLGLVKLCFHESPSSQPRKESMGPP
GLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Important features:**Signal sequence:**

amino acids 1-16.

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

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FIGURE 357

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGGGAAGA
AGACTAAAAATGGTGTTCCTTCAATGTGGACACTGAAGAGACAAATTTCTATCCTTTTAAACATAATCCTAATTTCC
AAACTCCTTGGGGCTAGATGGTTTCCCTAAAACCTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTECTGGAGGTATTTCCACGAACACCACGAACCTCACCCCTC
ACCATTAACCACATACCAGACATCTCCCCAGCGTCCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC
TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAACCCAGCTACTAGAGATACCGCAGGGCCTCCCG
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
AACATAGAAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA
GATGCCTTCCCTAAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGCTCCCTACTGTT
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC
CTCAACCAATTACAAATTTCTTGACCTAAGTGGAATTTGCCCTCGTTGTTATAATGCCCCATTTCCCTTGCGCCG
TGTAATAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAAGTTTACGTCTA
CACAGTAACCTCTCTCAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC
CAAACTTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTTCTCCCGAGCCTCATCCAATTGGATCTG
TCTTTCAATTTTGAAGTTTCAAGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG
AAAATTTGCGGATCAGAGGATATGTCTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATGTCAACCTCAGCATGTTTAAACAATTTAAAGA
CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT
GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCCTGGAACAATTACATTATTTAGATATGATAAGTATGCA
AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC
TTGGATCTAAGTAAAAATAGTATATTTTTGTCAAGTCCTCTGATTTTCAGCATCTTTCTTTCCCTCAAATGCCTG
AATCTGTGAGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATCCAACCTTTAGCAGAGCTGAGATATTTG
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCCCTCCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG
AATCTGCTAAATTAGAGGAATTAGACATCTCTAAAAATCCCTAAGTTTCTTGCTTCTGGAGTTTTTGATGGT
ATGCCTCCAAATCTAAAGAATCTCTCTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT
CTAAGAACCTGGAAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAACCTGTTCC
AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTCTACAAGATGCCTTC
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTC
AACAACTCTGAAGATGTTGCTTTTGATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG
GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
CAAAGTGTGATCTCCCTGGATCTGTACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
TCTGTATCTCTCTTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAAGAGAGAAA
CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA
CAGCTTAGCAAAAAGACAGTGTGTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAGATAGCATTTTAC
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAG
TCCAAGTTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCTTGTAGTGGCCAACAACCCGCAAGCTCAC
CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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FIGURE 358

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGGI
PTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCPVPIPLGSKNNMCIKRLQIKPRSFSGI
TYLKSLYLDGNQLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYRNPC
YVYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNLNQLO
ILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWFKNINK
LQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSLKILRIR
GYVFKELKSFNLSPLHNLQNLEVLDTGNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSE
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDSLKNS
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLHSTAFEELHK
LEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESESLRTLEFRGNH
LDVLWREGDNRYLQLFKNLLKLEELDISKNLSLPSGVFDGMPPNLKNLSLAKNGLKSFSWK
KLQCLKNLETLDLSHNQLTTPPERLSNCSRLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS
NKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWVWNHTEVTIPYLATDVTCVGPGA
HKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ
RLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLENLSQ
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLEKPFQKSKFLQLRKRLC
GSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

Important features:**Signal sequence:**

amino acids 1-26

Transmembrane domain:

amino acids 840-860

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FIGURE 359

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTAC
TGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGG
AGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT
GGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCACAACA
AGGAGCGCGGGCGCCGCGGAGAACTCTGTTGCCATCACAGACGAGGGCATGGACGTGCCGC
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA
ACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC
AATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG
CTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGAAGCATCAGACT
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAACAGAGG
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCCCAACTTCCTTAG
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAACAACCTGAGGTCCCTT
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA
CCCATGTTCCCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA
GCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAGGGAACTCCTACCCCATG
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTT
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCT
CCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCC
TGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGC
TGAACCTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGG
TGTTGGCTGGAATCTTCTTGAATGGGATACCACTCAAAGGGTGAAGAGGTCAGCTGTCCTCCTG
TCATCTTCCCCACCCTGTCCCCAGCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCTG
GCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACCGGGCCCACACCTCTCCTGCCCCTCCC
TCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT
GCCACACAGCATGTGCGCTCTCCCTGAGTGCTGTGTAGCTGGGGATGGGGATTCTTAGGGG
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGCAGGGACGAGGGAA
GGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAAA

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FIGURE 360

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEEL
AAFAKAYARQCWVGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC
GHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVLCNYEPPGNVKGKRPYQEGTPCSQCPSG
YHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFLVTEVSGSL
ATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLASVFPAQD
KPGELQATLDHTGHTSSKSLPNFPNTSATA[^]NATGGRALALQSSLPGAEGPDKPSVVSGLNSGP
GHVWGPLLGLLLLPLVLGIF

Important features:**Signal sequence:**

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

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FIGURE 361

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTGG
GGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAACT
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG
AGAGGACCCCGGCGTCCGGGGCTCCCGGTGCCAGCGCT**ATG**AGGCCACTCCTCGTCTGCTGCT
CCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCCGGG
GCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCGCGATGG
CCGCGACGGCCGCGACGGCGCGCCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGG
ACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGGCCACCGG
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCG
GGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA
TTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCA
TGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTC
TTTCTTCCAGTTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAG
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC
CAGCATCAAGACAGACAGCACCTTCTCCGGATTCTGGTGTACTCCGACTGGCACAGCTCCCC
AGTCTTTGCT**TAG**TGCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGA
GGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGG
TGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGG
CAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCTGCTG
CTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGGCCGGCCCTTTTCTCAGAGAT
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 362

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG
EKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFQFFGGWPKPA
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Important features:**Signal sequence.**

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

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FIGURE 363

[illegible]

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FIGURE 364

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGRE
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD
TDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATREELT
AFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQFRDF
RDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT
NYGEDLTRHHDEL

Important features:**Signal sequence:**

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

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FIGURE 365

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAAG
GCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA
TTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG
AAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA
GACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG
CCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTTGGGAACCGGGCAGTGCTG
ACATGCTCAGAACAAGATGGTTCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG
ATGCCTACGAATCCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACA
ACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCA
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT
GTGGGGGTATCGTGGCAGCCGTCTTGTAACCCTGATTCTCCTGGGAATCTTGGTTTTTGGC
ATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG
GTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCTG
GTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACT
CTGGCCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTCTACACCCCACAGGGCCC
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTC
CCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTAAAGTGTTTATTCCCCATTTCT
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA
TGGCGGGGGTTCGAGGAATCTGCACTCAACTGCCCACCTGGCTGGCAGGGATCTTTGAATAGG
TATCTTGAGCTTGTTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCCTTCCAT
CTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTGTGGA
GAGCATAGTAAATTTTTCAGAGAACTTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAA
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGAT
CACCTGAGGTCTGGGAGTTTCGGGATCAGCCTGACCAACATGGAGAAACCCTACTGGAAATACAA
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG
CAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 366

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLS CAYSGFSSPRVEWK
FDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGNSYGEVKVKL
IVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNSSYV
LNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVT LILLGI
LVFGIWFAYS SRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291**N-myristoylation site..**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 367

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTCAATTTTTCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCAGATTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTCTTCATCAACCTCCTTTTTTTAAAT
TTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACCTGGATTTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
CCAGTTCAGCAAGGTGATTTGTGTTTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTTGTATACTTGTCTAACTGAAGGAGCTCTGGTT
GCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTTATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTGAGGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAACTGTGGATGATACAGTCCCAGAT
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGCAATCATCTAGAGCGGATACATTTACATCACAACCTTGGAAGT
TAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGGCTCCACATC
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTACAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTTACTTTTC
AACCCTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCC
AGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACACCAGAGCACAAGGTGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTGATGAAGACTACCAAAATCATCAT
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGACCA
TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCCTAAATCACTATAACTCATACAAAATCTCCCTT
CAACCACACAACAACAGTTAACACAATAAATTCAATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAAAA
GACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGCTTTTACAAAAAACAA
AAAAGAAAAGAAATTTATTTATTAATAATCTATTGTGATCTAAAGCAGACAAAA

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FIGURE 368

MLNKMTLHPQQIMIGPRFNALFDPLLVLALQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVPDGIS
TNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL
KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRYNLAMCNLREIPNLTPLIKDELD
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHH
NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKC
RASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTQDTGMYTCMVSNVGNNTASATLNVTAATTP
FSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNTVTSLTPOSTRSTEKFTTIPVTDINSGIPGIDEVMKT
TKIIIGCFVAITLMAAVMLVIFYKMRKQHRQNHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYS
YKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

Important features:**Signal sequence:**

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,
422-428, 433-439, 531-537

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FIGURE 369

CAAACTTTCGCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCCAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGTGCTGGTACTGAGCCCTGAGG
AGCCCGGGCCTGGCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCTGTTCCAGGAGGGCGCTGCTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCGTGAGCACACCAACCACCTATCTCTGCAGAACCAACCAGC
TGGAAGATCTACCTGAGGAGCTCTCCCGGTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGAAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAGATCT
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT
TCAGCGAGCTGAGCAGCTGCGCGAGCTATACCTGCAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC
CGCGCAGCCTGGTGTGCTGCACTTGAGAGAAGACGCCATCCGGAGCGTGGACGGAATGTGCTGACCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCACTGGCCTTCCAGGGCC
TCAAGCGGTTGCACACGGTGCACCTGTACAACAACCGCTGGAGCGCGTGCCAGTGGCCTGCCTGCGCGCTGC
GCACCTCATGATCTGCACAACCAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCCCAGGTGCACCGCGACGCTTCCGCAAGCTGCGCCTGCTGC
GCTCGCTGGACCTGTCCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCTGCTGCTGCGGTGGACCTCGCCCATCTGCAGCTGCTGGACA
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTGAGTACCTGTACCTGCAGAACACA
AGATTAGTGCGGTGCCGCCAATGCCTTTCGACTCCACGCCCCAAGCTCAAGGGGATCTTCTCAGGTTTAAACAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTTTCTGC
AGCACACGCCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGGCGTGTCCACGGCCAGACACATGC
ACACACATCACACCCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCCAAACCACACAGTCTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTGCCCTGGCACACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACATGCACAAGTATGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT
GTCCATCTGTCCGTCCGTTCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCCTCT
GGAACCTACAAAAGCTGGCTTTTATTCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC
TGGCCACCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT
GTTCTTCAGGCCTGTGGGGGAAGTTCCGGGTGCCTTTATTTTATTCTTTTCTAAGGAAAAAATGATAAAAT
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAGCATTATCCCTATCCCTGCAAAAAA

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FIGURE 370

MEGEEAEQPAWFHQWPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRSG
GHSLSPEENEFAEEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLPEH
TNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKA FEHLTNLNYLYLANNKLT
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDNETFWK
LSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSNQLREQG
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYFLEELNLS
YNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKNELAALARGALAGMA
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP
ANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKEE
EEEEEEEEEEETR

Important features:**Signal sequence:**

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

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FIGURE 371

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGACCTCGGAGACCGCG
CCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTACCGCCCCCACCCTCCTCTTCTGCAC
TGCCGTCCTCCGGAAGACCTTTTCCCCTGCTCTGTTTCTTACCGAGTCTGTGCATCGCCCCGGACCTGGCCGG
GAGGAGGCTTGGCCGGCGGGAGATGCTCTAGGGGCGGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCCGGCAG
GAAGATGGGCTCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCTTTGCCTCTGGCCTGGTCCT
GAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGCCGTGCGCTCCGGACCA
TGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAGGACCAGGGGCTCCCTGCTTCCCGGTGCTT
GCGCTGCTGTGACCCCGGTACCTCCATGTACCCGGCGACCGCCGTGCCCGAGATCAACATCACTATCTTGAAAGG
GGAGAAGGGTGACCGCGGAGATCGAGGCCTCCAAGGGGAAATATGGCAAACAGGCTCAGCAGGGGCCAGGGGCCA
CACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGCTTTTC
GGTGGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCGACACGGAGTTCGTGAACCT
CTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGCTACGTGCCCGGCCCTCTACTTCTTACGCCCTCAACGT
GCACACCTGGAACCAGAAGGAGACCTACCTGCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTTCGCGCA
GGTGGGGCAGCCGAGCATCATGCAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACG
CCTCTACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCACTGGCTACCT
GGTCAAGCACGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCCACCTTCCACCCCTGCGCTGTGC
TGACCCCAACCGCTCTTCCCCGATCCCTGGACTCCGACTCCCTGGCTTTGGCATTCACTGAGACGCCCTGCACAC
ACAGAAAGCCAAAGCGATCGGTGCTCCCAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAG
GGCGGGGCACCCGCGAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGG
CGAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGGCGCACCGCGGCTCCAGTCTTGGAAATAATTAGGCAATT
CTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGGTTGTTATTTTTGTCTTTCCAGCCAG
CCTGCTGGCTCCCAAGAGAGAGGCCTTTTCACTTGAGACTCTGCTTAAGAGAAGATCAAAGTTAAAGCTCTGGG
GTCAGGGGAGGGGCCGGGGGCGAGGAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTTCTGAGGG
ATAGGTGGACCTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCCAGGTGA
TGGGGGCTGGGGCCCCAGGGCTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGCTCCAGGTTGGTAGAA
GCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCAGGCCTGCAGATGTTTCTATGAGGGGCGAG
AGCTCCTTGGTACATCCATGTGTGGCTCTGCTCCACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATG
CCTGCCACCTGGCATCGGCTTTTCTGTGCCCTCCCACACAAATCAGCCCCAGAAGGCCCCGGGGCCTTGGCTT
CTGTTTTTTATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTTCCACG
TGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCCACTGCCCTCATCCAGGCCTCTGACCA
GTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAGCTGGAAGGGGCTAGAAAGCTCCCGCTTGTCT
GTTTCTCAGGCTCCTGTGAGCCTCAGTCTGAGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCA
GGATTCACTCTCAGGAGCTGGGTGGCAGGAGAGGCAATAGCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGG
TTGCGGTGTCTCCAGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCCATAGCCCC
TCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCCCCCAAACCCCCGCTGCCTCTC
TTCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGCTTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGG
TCCCTAAGTCCCTCTCTTTAAGAAGTCTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAG
CAGAGCGCCACACTCGCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

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FIGURE 372

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRPS
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGRGDRGLQGKYGKTGSAGARGHTG
PKGQKGSMSGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFYCYV
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWVRLYK
GERENAIIFSEELDTYITFSGYLVKHATEP

Important features:**Signal sequence.**

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

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FIGURE 373

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCCG
TTCTAGACGCGGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGGA
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAAATGC
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTTCAGAGG
ATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACCCCAAAG
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAGAGTTCT
TCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATGTGGTTAA
TGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTGGTTCTTCC
TTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAAAAAAGGATC
CATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCTCAATATCCCAG
AAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA
ATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAGTAG
AAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAAATCAGATGCATGTGA
TGATGTATGGGGTATACCGCCTTAGGGCATTGTTGGGCATATTTTCAATGATGCATTGGTTTTCT
TACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTTGTA
TAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAATACAGCTGTATGTTTCTT
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAGTCAGTAGTACATTTTAAA
TGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATGTGTTGGAAAGAAGTGTTTTA
AGAATAATAATTTTGCAATAAACTATTAATAAATATTATATGTGATAAATTCTAAATTATGA
ACATTAGAAATCTGTGGGGCACATATTTTGTGATTGGTTAAAAAATTTTAACAGGTCTTTA
GCGTTCTAAGATATGCAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAACTTTTAG
CTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCTAAGCCTCCCCAAGTTCCAATGGAT
TTGCCTTCTCAAAATGTACAATAAGCAACTAAAGAAAATTAAAGTGAAAGTTGAAAAAT

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FIGURE 374

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV
KPKDVSLLWAAVKETWTKHCDKAEFFSSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI
IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAV
CLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFG
HIFNDALVFLPPNGSDND

Important features:**Signal sequence:**

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,
409-413, 473-477, 729-733, 748-752**Tyrosine kinase phosphorylation site.**

amino acids 736-743

N-myristoylation site.amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,
651-657, 657-663, 672-672**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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FIGURE 375

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAAT
CTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGAAA
AAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG
GCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA
AGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAA
CCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG
GTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA
GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTCTTCAGATAT
CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC
GGTTACTTGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA
AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC
CGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACATTTCAGAAGCCAA
GGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTC
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT
GGAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA
CTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC
AGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC
TCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAG
GCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA
GAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAATTGCCTTGACAGATATTTAGG
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCACAGA
GTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAA
CAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG
GCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

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FIGURE 376

MKTIQPKMHNSISWAIETGLAALCLFQGVFVRSGDATFPKAMDNVTVRQGESATLRCTIDNRV
TRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTS
RVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ
GITREQSGDYECASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGTQLQCEASAVPSAE
FQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHTNASIMLFGPGA
VSEVSNGTSRRAGCVWLLPLLVLHLLKLF

Important features:**Signal peptide:**

amino acids 1-28

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FIGURE 377

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGAA
ATGTGGCTCAAGGTCTTCACAACTTTCCTTTTCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTGAGGCCCTCTACCTACCCGTCCAC
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCCACACA
ATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGACTTGGAATACCAACAC
AAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTTGATGAA
GGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCAGAAGATA
CAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCTCTGGGGCT
GTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC
CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTCTCCCCAAAC
AATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCTGGTGAGG
AACCCTGTGAGTGAATGGAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA
CTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGTTGACCTTGGAGAG
GCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG
ACTGACAATACTACATATATCATTAAAGCATGGGCCCTCGCTTAGAAGTTGCATCTGAGAAAGTA
GCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA
ACTCATTTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTGACAGAAAGGAAAATCA
TTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATTATATCCATGTGTCTTCTC
TTCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAACTAGAAGGCAGGCCAGAA
ACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA
TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGGATTCCAAGCAGGTCTGTTCCA
GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC
CCTGCCCAGCAGCAAGACCATCCAGAG**TGA**ACTTTTCATGGGCTAAACAGTACATTTCGAGTGAA
ATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGTATATTAATCTGGAATCAGTGAAGA
AACCAGGACCAACACCTCTTACTCATTATTCCTTTACATGCAGAATAGAGGCATTTATGCAA
TTGAACTGCAGGTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTTGGGGAA
ATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTTCCT
CATAAGTTTTGTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTTCACTATC
ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTGTTTCGATTTTTT
AGCAGACTTTGTTTTATTAAATTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTCAATTTT
ATTTCCAAATTTCTATCTTGTTATTTGTACAACAAAGTAATAAGGATGGTTGTCACAAAAACA
AACTATGCCTTCTCTTTTTTTTCAATCACCAGTAGTATTTTTGAGAAGACTTGTGAACACTT
AAGGAAATGACTATTAAAGTCTATTTTTTATTTTTTCAAGGAAAGATGGATTCAAATAAATT
ATTCTGTTTTTGCTTTTAAAAAAAAAAAAAA

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FIGURE 378

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPHTMPKYLLGSVNKS
VVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTSLASQKIQVTVDDPVTKPVVQIHPPSGAVEY
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPII
YYGPYGLQVNSDKGLKVGEVFTVDLGEAILEDSCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMD
YVCCAYNNITGRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEG
RPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTVYEVIQHIIPAQQQDHPE

Important features:**Signal sequence:**

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 379

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACAA
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTGTT
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCAAGC
GCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCTTTAA
TTAAGGGGTTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCTGCGTC
ACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAAACAGCTG
GAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAACATTGAT
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA
GATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCT
GCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG
GAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGG
GCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGACCCCCCAGCA
ATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAA
ATAG

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FIGURE 380

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLS
GATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVARR
QEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features:**Transmembrane domain:**

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

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FIGURE 381

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGCC
GCGCCGCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCGCGC
CCGCGCCCCAGGTGAGCGCTCCGCCCCGCGGAGGCCCGCCCCGGCCCCGCCCCGCCCCGCCCC
CGGCCGGCGGGGGAACCGGGCGGATTCCTCGCGCGTCAAACCACCTGATCCCATAAAACATTC
ATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCGCGCCCTCGCCCTG
TGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGAGCGGAGCG
CGCCGAGCCTCGTCCCGCGGCCCGGGCCGGGGCCGGGCCGTAGCGGCGGCGCCTGGATGCGGAC
CCGGCCGCGGGGAGACGGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGCCCCGCCCA
ACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG
CAGGCCTGGCAGGTGGCAGCCCCATGCCCAGGTGCCTGCGTATGCTACAATGAGCCCAAGGTG
ACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTGCTGCCAGCCAG
CGCATCTTCTTGACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTCCGTGCCTGCCGC
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGCGGCTGCCTTCACT
GGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCT
GCCACATTCCACGGCCTGGGCCCGCCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAG
CTGGGCCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCG
CTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCACACACCTCTTCTGCAC
GGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTC
CTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTTCCGTGACCTTGGCCGCCTC
ATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCACTGAGGGCCCTGGCCCCCCTG
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCCGGGCACGCCCCA
CTCTGGGCCTGGCTGCAGAAGTTCCGCGGCCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAA
CGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCC
ACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACCGATGAGGAGCCGCTGGGGCTTCCC
AAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGTACTGGAGCCTGGAAGACCAGCTTCG
GCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTGACAGCCCCGCCGGGCAACGGCTCTGGC
CCACGGCACATCAATGACTCACCTTTGGGACTCTGCCTGGCTCTGCTGAGCCCCCGCTCACT
GCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCA
GGCTGTTACGCAAGAACCGCACCCGCAGCCACTGCCGTCTGGGCCAGGCAGGCAGCGGGGGT
GGCGGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC
CTGGGCCTGGCGCTGGTGCTGTGGACAGTGCTTGGGCCCTGCTGACCCCCAGCGGACACAAGA
GCGTGCTCAGCAGCCAGGTGTGTGTACATACGGGGTCTCTCTCCACGCCGCCAAGCCAGCCGG
GCGGCCGACCCGTGGGGCAGGCCAGGCCAGGTCTCCCTGATGGACGCTGCCGCCCGCCACC
CCCATCTCCACCCCATCATGTTTACAGGGTTCGGCGGCAGCGTTTGTTCAGAACGCCGCCTC
CCACCCAGATCGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGA
CGTGGAATAAAGAGCTCTTTTCTTAAAAAA

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FIGURE 382

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAAASQRIF
LHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPATF
HGLGRLHTLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLELHGNR
ISSVPERAFRGLHSLDRLLHQNRAHVHHPHAFRDLGRLMTLYLFANNLSALPTEALAPLRAL
QYLRLNDNPWVCDRCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQCAVATGP
YHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH
INDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGT
GDSESGALPSLTCSLTPLGLALVLWTVLGPC

Important features:**Signal peptide:**

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

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FIGURE 383

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTCCTGAACCTTGTCTG
AAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCGAGGGACCTTTTCGCTGCTTTTGTAGGG
ACTTCTTTTCCTTGCTTCAGCAACATGAGGGCTTTTCTTGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGA
TTGGGGCTTTGATCCCTGAACCAGAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCA
AAGGAGGGGATTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA
AACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTTGA
AAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCTCTGCTCTGGGCTATGGAAAAGAAGGAAAAGTA
AAATTCCCCCAGAAAGTACACTGATATTTAATATTGATCTCCTGGAGATTGCGAAATGGACCAAGATCCCATGAAT
CATTCGAAGAAATGGATCTTAATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGT
TTGAAAACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAAGAAGATG
AAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTATAGAGATACATCTACCCCT
TTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAAAGAACATTTTATTTTTATACAATGTTCTTTCT
TGCTTTGTTTTTTATTTTTATATATTTTTCTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTT
CTTTCTGATAAGTTATTGGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTC
ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACCACGACATGA
GACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTCTCCAAGTTAGAGGTCAACATTT
GAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCATGTTATAATGAAATAGTTTATGTGTAAGTGGCTCTG
AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGAT
GTGCAATGCTGAAGTTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGA
GGCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTGAGACCGCCTGACCAACACGGAGAAACCCTATCTCTAC
TAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCAGCTACCCAGGAAGGCTGAGGCGGCAGAA
TCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAGAA
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGG
CTCCTAGTGATTGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATGTA
TCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGCTAGCGGAATATCCTT
CCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACATTGTATCATAAGATAAAGTAGTAAACCA
GTCTACATTTTCCCATTTCTGTCTCATCAAAAAGTGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCAG
CACTTTGGGGGCCAAGGAGGGTGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCT
TGTCTCTACTAAAAATACAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAGGCTGA
GACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCCACTGCACTCCAGCCTGGG
TGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGACCTACAGCAGCTACTATTGAATAAATACCTA
TCCTGGATTTT

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FIGURE 384

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSLF
HSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPESTLI
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVEDIFD
KEDEDKDGFIAREFTYKHDEL

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

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FIGURE 385

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCTC
CCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGTCC
CTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG
ATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAATGAAG
GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGAACCTC
ACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAGTCTTTA
CTGATCTCTCTGTTTCGTCTTTCCAGGACCCTGCTGTCTCCTCCCTCCCTTCTCCCACCTTCCAG
CCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCCCAGGATTG
ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGGGCTGAGGCC
CCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACACAGGAACCTCT
CCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGCTGGACTCCACC
TCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGGGTGTCCATCCCG
ATGGTCCGCATACTGGCCCCAGTCTTGGTGTCTGCTGAGCCTTCTGTGAGCCGCAGGCCTGATC
GCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG
AACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAAGGAAGCCCCCTTCCCAGGCCCT
GAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGAGCTGGGCTTCTCGAAG
TTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGC
TGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAGTCCAGCTGCCCCGACTCC
AGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCATGTTCCAGCCTGACCTAGAAGCGTTT
GTCAGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCCGGCTGGAGACTGGGACATCCCTGAT
AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCAGCAGGGCCAGACAAGGCTCAG
TGGATCTGGTCTGAGTTTCAATCTGCCAGGAATCCTGGGCCTCATGCCAGTGTGCGACCCCT
GCCTTCTCTCCACTCCAGACCCACCTTGTCTTCCCTCCCTGGCGTCTCAGACTTAGTCCCA
CGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCTGGGGTGAGACTGGGATTCTGGCTT
CTCTTTGAACCACCTGCATCCAGCCCTTCAAGGAAGCCTGTGAAAAACGTGATTCTGGCCCCA
CCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAGGACTCTGAATTCTAACAATGCCCAGT
GACTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTGATGAACGCTCACACCCCTTCAAGTTAG
AGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCCCAATAGATCTGCTCTGTCTGCGACACCA
GATCCACGTGGGGACTCCCCTGAGGCCTGCTAAGTCCAGGCCTTGGTCAGGTGAGGTGCACAT
TGCAGGATAAGCCCAGGACCGGCACAGAAGTGGTTGCCTTTNCCATTTGCCCTCCCTGGNCCA
TGCCTTCTTGCCCTTTGGAAAAATGATGAAGAAAACCTTGGCTCCTTCTTGTCTGGAAAGGG
TACTTGCCCTATGGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACCAGAGTGCACGTAGGTGT
CTAACACAGAGGAGAGTAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCCAGCCCCCTG
GAGAAGGGGTCGGGGGTGGTGGTAAAGTAGCACAATACTATTTTTTTTCTTTTTTCCATTATT
ATTGTTTTTTAAGACAGAATCTCGTGCTGCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCA
AACTCCGCCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAG
GCACGCACCAACACCTGGCTAATTTTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTG
GCCAGGCTGGTCTTGAACCTCCTGACCTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCG
GGATTACAGGCATGAGCCACTGTGTCTGGCCCTATTTCCCTTAAAAAGTGAAATTAAGAGTTG
TTCAGTATGCAAACTTGGAAAGATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCA
TAGTCTCACCAGAGACTATCATTATTTTCGTTTTGTGTACTTCTTCCACTCTTTTCTTCTTC
ACATAATTTGCCGGTGTCTTTTTTACAGAGCAATTATCTTGTATATACAATTTGTATCCTGC
CTTTTCCACCTTATCGTTCCATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTT
ATAAATAAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

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FIGURE 386

MRLLVLLWGCLLLPGYEALEGP EEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRC SG
TIYAE EEGQETMKGRVSI RDSRQELSLIVTLWNLT LQDAGEYWCGVEKRGPD E SLLISLFVFP
GPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQ
YGHERTSQYTGTSPHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRILAPV
LVLLSLLSAAGLIAFC SHLLLWRKEAQQATETQRNEKF WLSRLTAE EKEAPSQAPEGDVISMP
PLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

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FIGURE 387

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCGGGCTCCCGCCCGGCACATG
GCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCGGAGG
CGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATCGGG
ATGTCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCACACT
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCA
GAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAAGTGGTG
ATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCGAGTGGCC
TTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGCCCAGTGAT
GAGGGCCGGTACACCTGTAAGGTAAAGAATTCAGGGCGCTACGTGTGGAGCCATGTCATCTTA
AAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGT
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATTACTGGCAGCGA
ATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATTGACTACAACCAC
CCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTACCAGTGCACAGCA
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGTATGTACAAAGCATC
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCCTTGGTG
TGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT
CGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCT
CGGAGCTCACGCTCTGGTTCTTCTCCTCCTCGCTCCACAGCAAATAGTGCCTCACGCAGCCAG
CGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCACCCAGGCATACAGCCTAGTG
GGGCCAGAGGTGAGAGGTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGTCT**TGA**ATTACAATGGAC
TTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGT
CACCAGCCACACAACCAGATGAGAGGTGCTAAGTAGCAGTGAGCATTGCACGGAACAGATT
CAGATGAGCATTCTTCTTATACAATAACCAAACAAGCAAAAGGATGTAAGCTGATTCACTGTGA
AAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGGAAAGCAGGAGTCCAAATCTATTTGT
TGACCAGGACCTGTGGTGAGAAGGTGGGGAAAGGTGAGGTGAATATACCTAAAACCTTTAAT
GTGGGATATTTTGTATCAGTGCTTTGATTCACAATTTTCAAGAGGAAATGGGATGCTGTTTGT
AAATTTTCTATGCATTTCTGCAAACCTTATTGGATTATTAGTTATTCAGACAGTCAAGCAGAAC
CCACAGCCTTATTACACCTGTCTACACCATGTACTGAGCTAACCCTTCTAAGAACTCCAAA
AAAGGAAACATGTGTCTTCTATTCTGACTTAACTTCATTTGTCATAAGGTTTGGATATTAATT
TCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAGAGTGAATGAGTTTCTCCACTCTATACTA
ATCTCACTATTTGTATTGAGCCCAAATAACTATGAAAGGAGACAAAAATTTGTGACAAAGGA
TTGTGAAGAGCTTTCCATCTTCATGATGTTATGAGGATTGTTGACAAACATTAGAAATATATA
ATGGAGCAATTGTGGATTTCCCCTCAAATCAGATGCCTCTAAGGACTTCTCTGCTAGATATTT
CTGGAAGGAGAAAATACAACATGTCATTTATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAA
AAGGGATCTAGGAATGCTGAAAGATTACCCAACATACCATTATAGTCTCTTCTTTCTGAGAAA
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTA
ATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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FIGURE 388

MSLLLLLLLVSYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
ITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL
KVLVRPSKPKCELEGELTEGSDLTLCESSTGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH
PGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLIFLLV
WLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANSASRSQ
RTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Important freatures:**Signal sequence:**

amino acids 1-16

Transmembrane domain:

amino acids 232-251

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FIGURE 389

GCGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTCG
CCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCTGT
CCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCCCCA
AAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTACTCA
GCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGGAGAAC
AGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGAATGTGA
CAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAGTTTATTC
AGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCACAAAGACTGA
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACATGAAATTCA
GGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATTCAGAGAGAAA
AGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGAGATCCAGATAG
AAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAATGTGTTCTGTATA
AACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACAGCCCATATTTGAT
GAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCA
GTATTTTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGAACTAAAATGAATGG
AAATTCTTAAAAA

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FIGURE 390

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRSSWV
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Important features:**Signal sequence.**

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

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FIGURE 391

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCGGGAAAGGG
AGGGAAGAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCGCCCCGCGCCTCTGCGCGCCCTGTCCGCCCCGGCC
AGCCAGCCCCAGCCCCGCGGGCCGGTACACGCGCAGCCAGCCGGCCGCTCCCGCGCCCAAGCGCGCCGCTTG
CTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGGCGCCCCGGTGACCGTGACCT
GCCCTGGGCGCGGGGCGGAGCAGGCATGTCCCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTCCTGGC
AGTGACCCTGGCCGGGGTTCGGAGCCCAGGGCGCAGCCCTCGAGGACCCTGATTATTACGGGCAGGAGATCTGGAG
CCGGGAGCCCTACTACGCGCGCCCCGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCTGCGGGGCCCCGGGA
GGAGTGGGAGCGGCGCCCGCAGGAGCCCAGGCCGCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCCAAGAGGGA
GAAGTCGGCTCCGGAGCCGCTCCACCAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAGCTCTGAGAA
GGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGATTGCCACCTCTTGGTCTGGA
AACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCTGGGGGCACATCGAGGGAG
ACTCAACATCCAGGCGGGCATTAAATGAAAATGATTTTATGACGGAGCGTGGTGCGCGGGAAGAAATGACCTCCA
GCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCTCACTCAAGGGAGGAACCTCCCTCTG
GCTGAGTGACTGGGTGACATCCTATAAGGTGATGGTGAGCAATGACAGCCACACGTGGGTCACTGTTAAGAATGG
ATCTGGAGACATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCTACCCGTCGCCATGGT
GGCCCGCTACATCCGCATAAAACCTCAGTCCCTGGTTTGATAATGGGAGCATCTGCATGAGAATGGAGATCCTGGG
CTGCCCCTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCACTGATGACCTGGATTTTAA
GCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCCCAATATCACCAGAAATTA
CAACATTGGAAGAAAGCCACCAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATCACCTGGGGAGCATGAAGT
CGGTGAGCCCGAGTTCACATACATCGCGGGGGCCACGGCAATGAGGTGCTGGGCGGGAGCTGCTGCTGCTGCT
GGTGCAATTCTGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACCTGGTGGAGGAGACGCGGATTCA
CGTCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCTACGAAGGGGGCTCGGAGCTGGGAGGCTGGTCCCT
GGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTCTGATTTAAACACGCTGCTCTGGGAGGCAGA
GGATCGACAGAAATGCCCCAGGAAAGTTCCTCACTATATTGCAATCCCTGAGTGGTCTGTGCGGAAATGC
CACGGTGGCTGCCGAGACCAGAGCAGTCAAGCCTGGATGGAAAAATCCCTTTTGTGCTGGGCGGCAACCTGCA
GGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGGGTCCCCCTGGAAGACGAGGAAACACACCCCCAC
CCCCGATGACCACGTGTTCCGCTGGCTGGCCTACTCCTATGCCCTCCACACACCCGCTCATGACAGACGCCCCGAG
GAGGGTGTGCCACACGGAGGACTTCCAGAAGGAGGAGGGCACTGTCAATGGGGCCTCTGGCACACCGTCCGTGG
AAGTCTGAACGATTTCACTACCTTCATACAACTGCTTCGAAGTGTCCATCTACGTGGGCTGTGATAAATACCC
ACATGAGAGCCAGCTGCCCCAGGAGTGGGAGATAACCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTCTCG
TGGCATTAAAGGCTTGGTGAGAGATTACATGGAAAAGGAATCCCAACGCCATTATCTCCGTAGAAGGCATTAA
CCATGATCCGAACAGCCAACGATGGGGATTACTGGCGCCTCCTGAACCTGGAGAGTATGGGTACAGCAAG
GGCCGAAGGTTTCACTGCATCCACCAAGAACTGTATGGTTGGCTATGACATGGGGGCCACAAGGTGTGACTTCAC
ACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGGAGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGC
CAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGTGGGTGACCCCTCTGGGCCCTTGAGACTCGTCTGGG
ACCCATGCAATTAACCAACCTGGTAGTAGCTCCATAGTGGACTCACTCACTGTTGTTTCTCTGTAATTCAAG
AAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAAGTCCCAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTT
CTTTGTTCCCATTTATCCAAATAACTTGGACAGAGCAGCAGAGAAAAGCTGATGGGAGTGAGAGAAGTCAAG
CCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGGGAGCCTGTCCGTTCAAGAGCCTCTGGCTGCATAGAAAAG
ATTCTGGTGTCTCCCTGTTTGGTGGCAGCAAGGGTTCACGTGCATTGCAATTTGCACAGCTAAAATTGCAG
CATTTCCCGAGCTGGGCTGTCCCAATGTTACCATTGAGATGCTCCAGGCGTCTAAGAGAATCCACCCCTCTC
TGGCCCTGGGACATTGCAAGCTGCTACAAATAAATTCTGTGTTCTTTTGACAATAGCGTCATTGCCAAGTGACA
TCAGTGAGCCTCTGAATCTGTTTAGTCTCCTTTTCAACAAAGGAGTGTGTTGAGAAAAGGAGAGAGAGGCTGA
GATCATTCAGGAGTTTGTGGGAGCAAGCATGGAGCTTCTTGACAAAATTCTGGGTCCATAAAACACCCCAAA
GTCCCTGCTGATCCAGTAGCCCTGGAGGTTCCCGAGGTAGGAGAGCCAGAGGTGCCAGCCTTCTGAAGGGCCA
GAAAATTTAGCCTGGATCTCCTCTTTTACCTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTC
TCTCTGCTTGAAGTATTGCCCTGTGTGGAATTGAGTGCTCATGGGTGGCCTCATATCAGCCTGGGAGTTATTT
TTGATATGTAGAATGCCAGATCTTCCAGATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGGAGCAT
CAGTTTGGGAAGAATTATTGAATTATCTTGAAGAAAAAAGTATGTCTCACTTTTGTAAATGTTGCTGCTCAT
TGACCTGGGAAAAATGAAAAAATAAAGCAAATGGTAAGACCCTTAAAAAATAAAGAAAAAATAAAGAAAAA
AAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAA

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FIGURE 392

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLPA
GPGEEWERRPQEPRPPKRAKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDHHSVR
VAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCAGRN
DLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIFEGNS
EKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRRNEMTTTDDL
FKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGA
HGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPBGYKAYEGGSELGGWS
LGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAAETRAVIAW
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSASTHRLMTDARR
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNR
ESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLNPGYVVTAKA
EGFTASTKNCMVGYDMGATRCDFTLSTNMARIREIMEKFGKQPVSLPARRLKLRGRKRRQRG

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FIGURE 393

GTCCACATCCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGTCATCATTGCTGAAGTGACCAAC
TAGTTCCCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGCTTGGGGTCTGCTTGTTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACTGGAGGACTTGTCAGCCTTGAAAGAACTCTAGTGGTT
TCTGAATCTAGCCCACTTGCGGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTAGGGGATTGTCAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCCGGGAGGAGGCGGAGGCAAGCTGGGGCCGCTT
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCACTTCAAGTGGACTCTGAGGAAGGCTTGTGACACAGGCGAGCG
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGACTCCCTGCTGGTTTCTTGTATGTGCTTGCCACAGGGGATT
GGCTCTGATCCATGTGGAGATCCAAGTGTGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGGA
GCTGGAATCTCTGAGAGCGCTCTCTGCAACCCGGATCCCTTGGACAGAGCTCTTGACCCAGACACAGGCCC
TAACACCTGACACCTACACTCTGTCTCCAGTGAGCACTTTGCCTTGATGTGATTGTGGGCCCTGATGAGAC
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTTGATCTGGTGTTAACTGC
CTATGACAATGGGAACCCCCCAAGTCAAGTACCAGCTTGGTCAAGGTCAACGTCTTGACTCCAATGACAATAG
CTGGCTGAGCCAAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC
CACACTGGACAGAGAGCAGTGGCCCAATATACCCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAAGAAACAGCTCAGCATTGATCAGTACATCAACGACAATGCACCTGTGTTTGAAGAAAGCAGGTATGA
AGTCTCCACGCGGGGAAAACAACCTTACCCTCTCTTACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
GGTCACTGCTCAGAGGTCACTGAATATGAAGAGTGGCCGGCTTTGAGTTCAGGTGATCGCAGGACAGCGG
GCAACCCATGCTTGATCCTGATGCTCTGTGTGGGTGAGCCTCTTGATGGCAATGATAATGCCAGAGGTTGGT
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGTCCCGGCCATT
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAATGGAGAGCCCTCTACAGCATCCGCAATGG
AAATGAAGCCCACTCTTCACTCAACCCCTCATACGGGGCAGCTGTTCTGTCATGTACCAATGCCAGCAGCCT
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT
GAGGGTCTATGTTTGTACCAAGTGTGGACCACTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT
GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCTGGCTTTGTTGATGTCCATCTGCCG
GACAGAAAAGAAGGACAACAGGGCCTACAACCTGTGCGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGAGGTGAGCCTTGTGAAGT
CGGGCAGTCCCAAGATGTGGACAAGGAGCGGATGATGAAGCAGGCTGGGACCCCTGCCTGACAGGCCCCCTT
CCACCTCACCCCGACCTGTACAGGACGCTGCGTATCAAGGCAACCAAGGAGCAGCCGCGGAGCAGGAGGT
GCTGCAAGACAGGTCACCTCTTTTCAACCATCCAGGCAGAGGAATGCCTCCCGGGAGAACCTGAACCTTCC
CGAGCCCCAGCCTGCCACAGGCCAGCCAGCTTCCAGGCCTCTGAAGTTGCAGGCAGCCCCACAGGAGGCTGGC
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACAGCCTCTCTGCAACCTGAGACGGCAGCGACATCT
CAATGGCAAAGTGTCCCTGAGAAAGAATCAGGGCCCCGTGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC
TGCTTTCGCGGAGCGGAACCCGTGGAGGAGCTCACTGTGATTCTCTCTGTTTACGAAATCTCCAGCTGCT
GTCCTTGCTGCATCAGGGCCAATTCCAGCCCCAAACCAACCCAGGAGAAATAAGTACTTGGCCAAAGCCAGGAGG
CAGCAGGAGTGCAATCCAGACACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCCAGAACAGGAGGA
AGGGCCTTTGGATCCTGAAGAGSACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC
CAGCACAGGTCTGGCCCTGGACCGCTGAGCGCCCCCTGACCCGGCCTGGATGGCGAGACTCTTTTGCCCTCAC
CACCACCTACCGTGACAATGTGATCTCCCCGATGCTGAGCCACGGAGGAGCCGAGGACCTTCCAGAGCTTCGG
CAAGGCAGAGGCACAGAGCTGAGCCCAAGGCACAGGCTGGCCAGCAGCTTTGTCTCGGAGATGAGCTCACT
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGCCCTCCGAGGCGCTGCGCGGCTCTCGGT
CTGCGGGAGGACCTCAGTTTAGACTTGGCCACCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG
AAAGACGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGCTGCTGTAACATACCTCAGACGCCT
CTGGATCCAAGAACCAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTCTAAAATCTTGTAACTCACTAGCTAG
CGGCGGCTGAGAACTTTAGGGTGAATGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC
TGACCAAGACACCCCTTTAAGCAGCTCTGAGTCTTTTGGAGGACAGGACGCTTTGTGGCTGAGATAAGTGT
TCCTGGCAAAACATATGTGGAGCACAAGGGTCACTGCTTGGCAGAACAGATGCCACGGAGTATCACAGGAGG
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAAGGGGCTGTACCCTGGGGGTGCCAGGAATGCTCTCTGACCTAT
CAATAAAGGAAAAGCAGTAAAAA

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FIGURE 394

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQAG
AAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQVL
DINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIVGPD
ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESSLALE
IQEDAAPGTTLLIKLTATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPLDYEKN
PAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSFIALVMA
DDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS
AKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVSRYRIQDSPV
AHLVAIDSNTGEVTAQRSLNYYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLLDANDNAPEVVQ
PVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTTIVARDADSGA
NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGSPPLQTRALLRV
MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE
STYRQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEAGWDPCLOAPFHLT
PTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLEPPQPATGQPRSRPLKV
AGSPTGRLAGDQGSEEPQRPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAAFAE
RNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKPGGSRSAIPDTDGPSARAGG
QTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRD
NVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSLLEMLLEQRSSMPVEAASE
ALRRLSVCGRTLSLDLATSAAAGMKVQGDPPGGKTGTGEGKSRGSSSSSRCL

Important features:**Signal peptide:**

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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FIGURE 395

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG
CTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAATC
AGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGTGCG
GCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAG
GAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGGCCTTG
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTTACAGCT
GCCCCTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAATAAAGAT
GGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACAGCAGCGAT
GTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTCC
AAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCA
GGCTGGGGCACTGTCACCAAGTCCCCGAGAGAATTTTCCTGACACTCTCAACTGTGCAGAAGTA
AAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC
TGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGT
GATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCT
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTCTGGTTC

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FIGURE 396

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV
GGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNDLMLLQL
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENF PDTLNCAEVKIFPQKKCEDAYP
GQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLDWI
KKIIGSKG

Important Features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

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FIGURE 397

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTCGGACCTGCTAC
TACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGGGT
ACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCACTG
TGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGCTGCA
GCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCCCCCTG
ATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCCCTGAGC
TCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGCCATGTGG
TGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCGTGTCCATC
CTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACC
AGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTATGTGCCTGAGA
TGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCCCTGGCAGCCGGG
AGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGATGACGGTGACACCC
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGAGGAGCTGGACTTGG
AGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGCCCCTGGGGACTACCA
AGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAGTAACCCATGGCCTGCACCCTCC
TGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTCTTCCTCCT
TCCTCTGGGGGAGGAGGGGTTCTTGAGGGACCTGACTTCCCCTGCTCCAGGCCTCTTGCTAAG
CCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCAGGGACTATTTTCTGCACCA
GCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTCACAGTGAGCTTCCAGGACC
CAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAAAAAAAAAAAAAAAA

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FIGURE 398

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGRL
FTESCSISPKLRSIAVYYDNPHMVPPDKCRAVGSI SEGEESPSPELIDLYQKFGFKVFSFP
APSHVVTATFPYTTILSIWLATTRVHPALDTYIKERKLCAYPRLEIYQEDQIHMCPLARQGD
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSATLSPGASSRGW
DDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEKGKE

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FIGURE 400

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHEG
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWLPL
AHQLYTDVANNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI
TGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDFQPGC
GLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLQNQDKPSFAFQCTDSNRFKKGICLSCRKNR
CNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:**Signal peptide:**

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

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FIGURE 401

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCTG
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCTGT
CAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGGCTC
AACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTTGGTACC
AGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCTGTGTCC
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT
TTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCTGCCCTGA
CCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGGTTAATAATA
TTCAACATGTCAACAAC

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FIGURE 402

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS
APRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

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FIGURE 403

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGAAAGCAGCGAGTTG
GCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCTCACAACAAGATGCTCAAGGTGTCAGC
CGTACTGTGTGTGTGTGCAGCCGCTTGGTGAGTCAGTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGG
GCGGTCCGACGGCGGTAATTTTCTGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGG
ACAGTGGAACAAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCCTTCGATCA
GGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATTC
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG
GAGGGGTCCCATATTATCCACCTGCAAGCAGTGCCAGTGGTCTATCCAGCCCTGTTTGTGGTTCAGATGGTCA
TACCTACTCTTTTCAGTGCAAACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG
ACATTGCCCATGTCTTCAGATAAGCCCACCACTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT
CAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAAGTCAAACAAGAAGACAAA
AACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATCTTGCCAATTTGCAAGGACTCACTTGGCTGGAT
GTTTAAACAGACTTGATACAACTATGACCTGCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAA
TGAACAGTGTAACCAAGGCATTCTTCAATTCTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTG
CTACTGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCAAGGGGTAAA
GAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCATGGCAGTGT
TGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTCATGGGATCCAGAATAAATGGTGTGTCAGATTGTGC
TATAGATTTTGAGATCTCCGGAGATTTTGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGA
CGATATTATGAATGATGAAGATGAAATGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTATGA
CCATGATGTATACATTGATTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTACAAAAATGATAG
CCTATTTAAATATCTTCTTCCCAATAACAAAATGATTCTAAACCTCACATATATTTGTATAATTATTTGAA
AAATTGCAGCTAAAGTTATAGAATTTATGTTTAAATAAGAATCATTTGCTTTGAGTTTTATATTCCTTACACA
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTCACGAGA
ACAACTTTGTAAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAGAT
AATTCTAAGTGAAATTTAAATAAATAAATTTTAAATGACCTGGGTCTTAAGGATTTAGGAAAAATATGCATGCT
TTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA
AAAAAAAAAAAAA

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FIGURE 404

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFRD
EVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEAGV
DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPSPDK
PTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPICKDS
LGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQRQQDP
PCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGCWCVDYRGNEVMGSRINGVA
DCAIDFEISGDFASGDFHEWTDDEDDDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

Important features:**Signal peptide:**

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 405

[illegible]

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FIGURE 406

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRCSQRNQTHRSSLHYKPTPDLRISIENSEE
ALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLSDKASSLLCFQHQE
ESLAQGPPLLATSVTSWWSPQNISLPSAASFTHSFHSPHTAAHNASVDMCELKRDQLLSQF
LKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQDLHIH
SRQEEEQSEIMEYSVLLPRTLQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGEKVLGI
VVQNTKVANLTEPVVLTQHQQLQPKNVTLCVFWVEDPTLSSPGHWSSAGCETVRRETQTSCE
CNHLTYFAVLMVSSVEVDVAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRVPPLPCRRKPRDY
TIKVHNNLLAVFLLDTSFLLSEPVALTGSEAGCRASAIHLHFSLLTCLSWMGLEGYNLYRLV
VEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDS
LVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLGLPWALIFFSF
ASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLPISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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FIGURE 407

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGAG
CCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTCGC
TCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA
CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC
TGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAAAGCTC
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAGCAGGGC
TCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGCTCAGCTG
CCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTGCTACATGA
CTTCGGGCTGGACGGATAACGGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTTAC
AAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAACGTGTGCCGGAT
GTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC
CCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT
CACTGAATGGGTGGATGGCTGTGACTTCTTAGGATGGACGGAACCATGCACAGCAGGCTGGGAA
ATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG
TGAAA

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FIGURE 408

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALDY
EADGSTNNGIFQINSRRWCSNLTPNVPNVCRMVCSDLLNPNLKDTVICAMKITQEPQGLGYWE
AWRHHCQGKDLTEWVDGCDF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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FIGURE 409

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC
GCTCTGCCCTCCGGTGCTGCTGCCTGGGGCGGCCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCTT
CCCCCGGCCAGAAAGGAGTGCTTCTACCAGCCCATGCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTA
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA
TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTAGCACCATT
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAGATTGGAAAG
AAATATATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC
AGACTAAGCAAAAGTGGGCACATACAAATTTCTGCTTAGAGCATTGAAAGCTCGTGATCGAAACATACAAGAAAGC
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAGTAGAACTTAAACTCCAACTAGAGTACGTAACATTGAAA
AATGAGGCATAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA
AAAGTAGGAAACAGGTATAATTTTAAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG
TTGTACTTAAAGTGTAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATACTGCAT
TTTCCTAACCTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC
AGTCTGTTTTTAAACAGGTTCTATTACCCAGAACTTTTTTGTAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT
TCAGTTTTTAAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCCAA
CTTTTCTCTATTTACATATGCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG
AGATTTTTTATAACCAAATACATTTTCAGTGTAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
CCAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG
AAATGAAGAATATAGTTTAAAGCTTCTCTCCATAGGGACACATTTTCTCTAACCCTTAAGTAAAGTGTAGGA
TTTTAAATTAATGTGAGGTAAAATAAGTTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
TAATCATGTTATGTTAATTTAACATGATTGCTGACTTGGATAATTCAATTATTACCAGCAGTTATGAAGGAAATA
TTGCTAAAATGATCTGGGCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAAATCACTTAAGTAGAACTATAAATAAATATCTAGA
ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
AAACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTGAATTATTTTTGTAAGCAGGTACATTTTATA
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAATAAATTTTATTATAACAACCTTTTAT
TAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTAA
CACCTAAATGTGAATAACCCATATATAACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAAATTTTAAAGTTATGCCCATTTATAACGTTGTTTAT
GACTACATTGTGAGTTAGAAACAAACTTAAATTTGGGGTATAGAACCCTCAACAGGTTAGTAATGCTGGAATT
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC
TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAATGAGGTAAATGCCGTAT
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAAGACAA
AGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTGGCGCTGTTAAATTTGCAATGAGAAGCAAATTTACA
GTACCATAACTAATAAAGCAGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAGAATTCTA
CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCT
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACCTCTTACCATATAAAAACGATAATTGCTT
TATTTGGAAGAATTTAGGAATACTAAGGACAATTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
CATAACCAAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTAAATTTCTAAAGACATACTGTTTATCTGCTT
CATATGCTTTTTTTAATTTCACTATTCATTTCTAAATTTAAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT
AACAGCTCATTTTGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTT
CATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCTAGAGTTTGTCTGATATGCATTTGGATGATTAAT
GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGTGTTTGTAAATTTTATGGTAAATTAATCCTTCTTA
CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATTTGATGTCTCCTCAAATGAAGATTCTTTAT
GTGAAATTTTAAAGACATTGATTCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACATCAGTGTTG
CTCAAACTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATA
AAATTATCAAAGGAAAA

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FIGURE 410

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLSDSDFTFITLPAGQKECFYQPMPLKASLEIEYQ
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFELIL
DNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE
SNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

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FIGURE 411

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCCAGAGTCA
GTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCCACGGGCTTGGGGGAAAAGATGGTGGGGACCAAG
GCCTGGGTGTTCTCCTTCTGCTGCTGGAAGTCACATCTGTGTTGGGGAGACAGACGATGCTCACCCAGTCAGTA
AGAAGAGTCCAGCCTGGGAAGAAGAACCCACAGCATCTTGGCAAGCCTGCCGACACCCTGGAGAGCCCTGGTGAG
TGGACAACATGGTTCAACATCGACTACCCAGGCGGGAAGGGCGACTATGAGCGGCTGGACGCCATTCTGCTTTCTAC
TATGGGGACCGTGTATGTGCCCCTGCCCTGCGGCTAGAGGCTCGGACCCTGACTGGACACCTGCGGGCAGCACT
GGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTTCTGGTGCCTCAACAGGGAGCAGCGGCTGGCCAGAACTGC
TCTAATTACACCGTACGCTTCTCTGCCACAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGAGCCCATGG
TCTCCCTGGAGCAAGTGTCTAGCTGCCTGTGGTCACTGAGGCTGGGGTCCAGACTCGCACACGCATTTGCTTGGCAGAG
ATGGTGTGCTGTGCGAGTGAGGCCAGCGAAGAGGGTCACTGATGGGCGCAGGACTGTACAGCCTGTGACCTG
ACCTGCCCAATGGGCGAGGTGAATGCTGACTGTGATGCTGATGCTGCGCAGGACTTCATGCTTCATGGGGCTGT
TCCCTTCCCGGAGGTGCCACAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAGCTGCTGACCCAG
ACAGACAGTGATGGGAGATTCCGAATCCCTGGCTGTGCTGCTGATGGCAAAAGCATCTGAAGATCACAAAGGTC
AAGTTTGGCCCATGTGTACTCACAAATGCCCAAGTATAGCCTGAAGGCAGCCACCATCAAGGCAGAGTTTGTGAGG
GCAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGCACGGAGAGCTGGGAGAGCGTGTCTCTGTGCTGT
AAGGCCACAGGGAAGCCAGGCCAGACAAGTATTTTGGTATCATAATGACACATTGCTGGATCCTTCCCTCTAC
AAGCATGAGAGCAAGCTGGTGTGAGGAACTGCAGCAGCACCCAGGCTGGGGAGTACTTTTGAAGGCCAGAGT
GATGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTACAGCATCTGATGAGACTCCTTGAACCCAGTT
CCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCAGAATGCCACCAACTCCTTCTACTATGACGTGGGA
CGCTGCCCTGTTAAGACTTGTGACAGGCGAGCAGGATAATGGATCAGGTGCCGTGATGCTGTGCAAGTGTGCT
GGCATCTCCAAGACAGAGGAAAGGGAGATCCAGTCAAGTGGCTACACGCTACCCACCAAGGTGGCCAAGGAGTGC
AGCTGCCAGCGGTGTACGGAACCTCGGAGCATCGTGGGGGCGGTGTGCTGCTGCTGACAATGGGGAGCCCATG
CGCTTTGGCCCATGTGTACTGCGGAACAGCCGTGTAGCCTGAAGGCAGCCACCATCAAGGCAGGTTTGTGAGG
CCCCAGGACACTGAGAGGCTGGTGCTCACATTTGTGGACAGGCTGCAGAAAGTTGTCAACACCACCAAGTGTGTA
CCTTTCAACAAGAGGGGAGTCCCGTGTTCATGAAATCAAGATGCTTCGTCGGAAGAGCCCATCACTTTGGAA
GCCATGAGACCAACATCATCCCCCTGGGGGAGTGGTGGTGAAGACCCCATGGCTGAAGTGGAGATTCCATCC
AGGAGTTTCTACAGGCAGAAATGGGGAGCCCTACATAGGAAAAGTGAAGGCCAGTGTGACCTTCTGGATCCCCG
AATATTTCCACAGCCACGCTGCCAGACTGACCTGAACCTCATCAATGACGAAGGAGACACTTTCCCTTCCG
ACGTATGGCATGTTCTGTGAGACTTCAGAGTCAAGTCACTGACGACCTTAATGCTGGCAAGTGAAGGTC
CACCTTGACTCGACCCAGGTCAAGATGCCAGAGCAGATATCCACAGTGAACCTCTGGTCACTCAATCCAGACACA
GGCTGTGGGAGGAGGAAGGTGATTTCAAATTCAGAAAGGAGGAGCAAAAGAGAGACAGAACCTTCTCTG
GTGGGCAACCTGGAGATTGCTGAGAGGAGGCTTTAACTGGATGTTCTCTGAAAGCAGGCGGTGCTTTAAG
GTGAGGGGCTACCGGAGTGAGAGGTTCTTGCTAGTGAGCAGATCCAGGGGTTGTGATCTCCGTGATTAACTG
GAGCTAGAACTGGCTTCTTGTCCAACCCTAGGGCTGGGCGGCTTGTGACAGTGTATCACAGGCCCAAGCGG
GCCTGTGTGCTGCTTCTGTGATGACCACTGCCCTGATGCCTACTCTGCCTATGTCTTGGCAAGCCTGGCTGGG
GAGAACTGCAAGCAGTGGAGTCTTCTCCTAAATTCACCCAAATGCAATTGGCGTCCCTCAGCCCTATCTCAAC
AAGCTCAACTACCGTCCGACGGACCATGAGGATCCACGGTTAAAAAGACAGCTTCCAGATTAGCATGGCCAAG
CCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGCCATCTATGCCTTTGAGAACCTCCGGGCATGTGAAGAGGCA
CCACCCAGTGACGCCCACTTCCGGTCTTACCAGATTGAGGGGGATCGATATGACTACAACACAGTCCCTTCAAC
GAAGATGACCCATGAGCTGGACTGAAGACTATCTGGCATGGTGGCCAAAGCCGATGGAATTCAGGGCCTGCTAT
ATCAAGGTGAAGATTGTGGGGCCACTGGAAGTGAATGTGCGATCCCGCAACATGGGGGGCACTCATCGCGGACA
GTGGGGAAGCTGTATGGAATCCGAGATGTGAGGAGCACTCGGGACAGGGACCAGCCCAATGTCTCAGCTGCCTGT
CTGGAGTTCAAGTGCAAGTGGGATGCTCTATGATCAGGACCGTGTGGACCGCACCCCTGGTGAAGGTCACTCCCCAG
GGCAGCTGCCGTCGAGCCAGTGTGAACCCCATGCTGCATGAGTACCTGGTCAACCACTTGGCACTTGCAGTCAAC
AAGCACCCAGTGAGTACACCATGCTGGCACCTTGGACCCACTGGGCCACAACATATGGCATCTACACTGTCACT
GACCAGGACCCCTCGCACGGCCAAGGAGATCGCGCTCGGCCGGTGTGTTGATGGCACATCCGATGGCTCCTCCAGA
ATCATGAAGAGCAATGTGGGAGTAGCCCTCACCTTCAACTGTGTAGAGAGGCAAGTAGGCCGCCAGAGTGCCTTC
CAGTACCTCCAAAGCACCCAGCCAGTCCCTGCTGCAGGCACTGTCCAAGGAAGAGTGGCCTCGAGGAGGCAG
CAGCGAGCGAGCAGGGGTGGCCAGCGCCAGGGTGGAGTGGTGGCCTCTCTGAGATTTCTAGAGTTGCTCAACAG
CCCCTGATCAACTAAGTTTTGTGGTACTTCACCCTCTTCTGCCCTCATTTGATGTGACAGCCATTGTGAGACTGA
TGCACAACTGTCACTTGGTTAATTTAAGCACTTCTGTTTTGCTGAATTTGCTTGTGTTTTCTTCTATGCTTTA
CTTACTTTTGTCCCATGCTACTGATTGGCACGTGGCCCCACAATGGCACAAATAAAGCCCTTTGTGAACTGTTT
TTTAAATGAAACACAAGAAATTGGCCACTGGTAAAACCTCTGCAGCTTCAACTGTACTTCAATTTAATGCCATTAAT
GCAATATACTTCTCTTTTGTGATGGTTTGGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAA
ATAACCAATATAAAGCATATTTCTTGGCCTTGTCCACAGGACATAGGCAAGCCTTGATCATAGTTTATACATAT
AAATGGTGGTGAATAAAGAAATAAACAATACTTTTACTTGAAATGTAATAACTTATTTATTTCTTTGCTA
AATTTGGAATTTAGTGACATTTCAAAGTTAAGCTATTAATATAGGGTGATCATAGTTTCTTACCAAGTCTGG
AAAGAACATCTCCTGGTATCCCAATTACACAGGTTGCTAACTGTATTTGTACATTTCCCTTTGCATTCGCTTT
TGTTCTTGCTAGAAACCCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTGAAAAA

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FIGURE 412

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNID
YPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQRP
GQNCSNYTVRFLCPPGSLRRDTERIWSWPWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS
EEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTKTPKL
LTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPYMVMNP
ETKARRAGQSVSLCCATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAGEYFCKA
QSDAGAVKSKVAQLIVTASDETPCNVPESYLIRLPHDCFQONATNSFYDVGRCVPVKTCAGQQ
DNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRVSAADNGEP
MRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNNTTKVLPFNKKGSASFHE
IKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKVKASVTFLDPR
NISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHLDSTQVKMPEHI
STVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLENLDVPESRRCFVKV
RAYRSEFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGACVPAFCDDQSPDA
YSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPRVKKTAFQISMAKPR
PNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFNEDDPMSWTEDYLAWW
PKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF
KCSGMLYDQDRVDRTLKVIPOGSCRRASVNPMLEHYLVNHLPLAVNNDTSEYTMLAPLDPLG
HNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALTENCVERQVGRQSAFYLO
STPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVAQQPLIN

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FIGURE 413

GCCACGTTGTCTTCTTTCCTTCACCACCACCCAGGAGCTCAGAGATCTAAGCTGCTTTCCATC
TTTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGGCCGTCCTCTTGCCTCCTTCTC
ATCCTAATCCCCCTTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTTCCCTTAGACTCCGTT
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG
AAGCTCTCGTGTGCTAGTGTCAAAGCCAAGGCAGACCGTCCTCCTGCCCTGCTGGGATGGCT
GTCAGTGGCTGTGCTTGTGGCTATGGCTGTGGTTCGTGGGATGTTTCAGCTGGAAACCACCTGC
CACTGCCAGTGCAGTGTGGTGGACTGGACCACTGCCCCTGCTGCCACCTGACCTGACAGGGA
GGAGGCTGAGAACTCAGTTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT
CTAACTCAAACGTCCCACTTCATTTGTTCCATTCTGATTCTTGGGTAATAAAGACAACTTT
GTACCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 414

MGPSSCLLLILIPLLQLINPGSTQCSLDSVMDKKIKDVLNSLEYSPSPISKKLSCASVKS
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

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FIGURE 415

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGTG
AGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAGGA
GTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTTGCC
TGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTGGGGG
TGCCTCGAAGTGCCTCTATAAAGGATATTA AAAAGGCCTATAGGAACTAGCCCTGCAGCTTC
ATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTGCTGCTT
ATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAAGGATTAA
AAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATTTTGGTTTCA
TGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATTGTAG
ATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAACAAAC
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGATGCGGACCACCC
AGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA
AACTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGG
AGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCC
GAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGA
CAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACA
AGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG
GGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATT
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT
CAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTGGACTTTGTTT
AAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTTGTGTGTGTTTTTGTTTTTA
TTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGATCATCATGAAATGAATAAGAGG
GCTTAAGAATTTGTCCATTTGCATTTCGGAAAAGAATGACCAGCAAAGGTTTACTAATACCTC
TCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGTTTCAAGAATTAAAGCTGCAAGAGG
ACTCCAGGAGCAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCAATTTCAATTCAAAATG
CCAACCTGGAGAAGTCTGTTTTTAAATACATTTTGTGTTATTTTTTA

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FIGURE 416

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYE
VLSDSEKRKQYDITYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPRGSDIIVDLEVTLEEVYAGNF
VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFI
GEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLW
KKGEGLPNFDNNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

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FIGURE 417

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGGA
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGGCCAGCCCCGCGGGGCGAG
GATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCTGCT
GATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCTCTAG
GCCGCACACGGGGCCCGCTGCCACGCCCCGGGCCGACAGGGACAGGGAGCTCACGGCCGA
CTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCC
CAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA
CTGGTCCCCGCGCAGCCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAGCGGAGGAG
CGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCATTCGA
CGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGGCCATCTACTG
CTACGTGCCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCT
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAACGC
CAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCTCCCGCCACCTCAT
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCCTTCGTGCGCCTGAT
CTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCGCCGTGCC
CATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCTCGGCGCGCGAGGCCTTCCGCGC
TGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT
GGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTA
CGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCA
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGGACCGCCAGCAGCTGGGAGGA
GGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCTACGAGGCCGA
CTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCCGAGACTTGAAAGCTTTCGCGTTG
CTTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCCAGTTTTTTTATGACCTACGATTT
TGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTT
TTTTAAGATTAATATATTTTCAGGTATTTAATACGA

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FIGURE 418

MTKARLFRLWLVLGSVFMILLIIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRELTAD
SDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAERRS
VLRGFCANSSLAFTKERAFFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIIVLSGSL
LHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLLI
SAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL
APFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRRTASSWEE
DWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:**Signal peptide:**

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

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FIGURE 419

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG
GCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGACT
GTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGCTGA
AGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATCATCA
ACACCATTGAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAAGATCA
ACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGTCGGGCA
CGGAATGCACCATCTTACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAATGCCATCG
TGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTTG
GGCTGTTAGGGGGCTCCAAGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCT
GGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGATCGCAAGACGG
TTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTGATTCACTGTG
AGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCCGGGCCAAGGGGC
TGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCT
TGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTCAGAAATAATGAAAATCCAA
CACTGCTGGGAGTCTAAACGGAAAGAAATACCATGCAGATTTGTATGTTAGGAGGATCCCAC
TGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAGCTCTACCAGGAGA
AGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGAGACGCCCATGGTGCCCC
CCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCTCGCTGGTGCTCTACCCTTTCT
TCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCCTCG
TCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAAATTGACAAGGGCT
CTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACTGACTCAGGGAGGTGTCACCAT
CCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCTCCTTAGTGGGACACGGTGACAA
AGGCTGGGTGAGCCCCTGCTGGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT
CTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTTTTTTCCCATGTGCTTTAGTGGGC
TTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGCTGTGTGGTGAAGTGTGAAGTGTGTTT
TGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGGACCGAAGGGGACA
AGTTCCCTTTTCATCCTTTGGTGCTGAGTTTTCTGTAACCCTTGGTTGCCAGAGATAAAGTGA
AAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAAATTAAAGTGCTTTTCT
GGGTCAAAAAAAAAA

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FIGURE 420

MDLAGLLKSQFLCHLVFCYVFIA SGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLVM
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLLGGSKVLAKKEL
AYVPIIGWMWYFTEMVFC SRKWEQDRKTVATSLQHRLDYPEKYFFLIHCEGTRFTEKKHEISM
QVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKKYHAD
LYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVNWLFWA
SLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND

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FIGURE 421

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATC
GCC**ATG**GACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGCCC
TGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTCACC
ACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCGGCG
CTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGGGTGCC
CTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTGCAGACC
ACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAA
CTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACGTCCGCACT
GAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCTGCGAGCCGTGCCCCACG
TCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGACGTGGGCGGCG
GCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCCTGGATGAGCAG
GGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGGGCTGTGCGCCAT
CTGGGCAAGGTTACAGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAAC
CAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGCTGCACACGGGGCTG
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACCTGC
TGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTATCCTGGGGGCTGCTCA
CCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTTCTTCCTCATCCACCGCTGCTGAG
TCTCAGAAACACTTGGCCCCAACATAGCCCTGTCCAGCCCAGTGCCTGGGCTCTGGGACCTCCA
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACCTCCACTAGCTCCAAAATCC
CTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAACCAAGGTTAGGTGACTGAGG
ACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGAAGCTGTTTTTGCAGCCTGAGG
AAGCATCAATAAATATTTGAGAAATGAAAAA

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FIGURE 422

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAAL
LDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTTAEELGEAQAKLMEQESALREL
RERVTOGLAEAGRGREDEVTELFRALAEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTWAAA
QDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGRLAVRHLGKVQGYQWVDGVSLSFHWNQ
GEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:**Type II transmembrane domain:**

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

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FIGURE 423

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGGC
GAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCGGC
GCCAACATGGCGGGTGGGCGCTGCGGCCCCGAGCTAACGGCGCTCCTGGCCGCCTGGATCGC
GGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGGTCCA
GCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTTTACGC
CCCATGGTGTCCATCCTGCCAGCAGACTGATTCAAGATGGGAGGCTTTTGCAAAGAATGGTGA
AATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTGGCCGCTT
CTTTGTCAACACTCTCCACGATTTTTTTCATGCAAAGGATGGGATATTCCGCCGTTATCGTGG
CCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATCAGTCGAGCC
TCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTCTTTTATGCAT
CTCTGGCAAGATATGGCATCTTCACAACTATTTTACAGTGACTCTTGGAATTCCTGCTTGGTG
TTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTATGGGTCTGGTCTTGGT
GGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGCGTTCTGAGCAGAA
TCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAGGAGGAAAAAGATGA
TTCAAATGAAGAAGAAAACAAAGACAGCCTTGTTAGATGATGAAGAAGAGAAAGAAGATCTTGG
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTGCTGGTGTGGATGAGGA
GAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTAGA
GCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGCTGACACAGAGGTGGTGGGA
AGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGACTGTAGATTTAATGATGCGT
TTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGGCCTGCAGTTTGTACCAAATC
CTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCTCTCTAGTCATTTGGTCTCATG
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGTGACAATCAGGATATAGAAAAAC
AAACGTAGTGTGGGATCTGTTTGGGAGACTGGGATGGGAACAAGTTCATTTACTTAGGGGTCA
GAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATCAGCACCTTCCAGAGACAAGGCTGC
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCTCCTGAGCATCCCCAAAGTGTAACGT
AGAAGCCTTGATCCTTTTTCTTGTGTAAAGTATTTATTTTTGTCAAATTGCAGGAAACATCAG
GCACCACAGTGCATGAAAAATCTTTCACAGCTAGAAATTGAAAGGGCCTTGGGTATAGAGAGC
AGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTGTGCTATGTTTTATTTCTTACCTTTAATT
TTTCCAGCATTTCCACCATGGGCATTGAGGCTCTCCACACTCTTCACTATTATCTCTTGGTCA
GAGGACTCCAATAACAGCCAGGTTTACATGAACTGTGTTTGTTCATTCTGACCTAAGGGGTTT
AGATAATCAGTAACCATAACCCCTGAAGCTGTGACTGCCAAACATCTCAAATGAAATGTTGTG
GCCATCAGAGACTCAAAGGAAGTAAGGATTTTACAAGACAGATTAAAAAAAATTGTTTTGT
CCAAAATATAGTTGTTGTTGATTTTTTTTTTAAGTTTCTAAGCAATATTTTCAAGCCAGAAG
TCCTCTAAGTCTTGCCAGTACAAGGTAGTCTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTT
ATCTCAAGGGGTCCCTGGGTCTTGAACACTTTAATAATAACTAAAAAACCTTCTGATTT
TCCTTCAGTGATGTGCTTTTGGTGAAAGAATTAATGAACTCCAGTACCTGAAAGTGAAAGATT
TGATTTTGTTCATCTTCTGTAATCTTCAAAGAATTATATCTTTGTAAATCTCTCAATACT
CAATCTACTGTAAGTACCCAGGGAGGCTAATTTCTTT

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FIGURE 424

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAPW
CPSCQQTDSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRGPG
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY
VFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEEKDDSN
EENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTREEVEPE
EAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide
isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

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FIGURE 425

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG
CTGGGCGCGTCGGAGAGTGCCTGTGCTTCTCTCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGTCCGCGCCA
GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCATGGCAAGGTATATTTTGTGGAATGAAAAGGA
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTGGGGACAGATTTGTGATGCTTGATTACCCCT
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
TTAAATCAGAACTTGCCATAAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGG
AGTGTCCAAAACGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA
AAACCCGAATAACCCAAATGCACATGGCGATTTTAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
CTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC
TGCTGTTAATTCTGGAGAAGTGTGGTTTGTAAATTTTACTCCCCAGGCTGTTCACTGCCATGATTTAGCTCC
CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAAT
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCAATTTTCGGTCTGGAATGGCCCCAGTGAAATA
TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTGAATGACAGCATGTTAGAAGTACAGTGACAGAACTTG
GACAGGAAATTTGTCAACTCCATACAACTGCTTTTGTGCTGGTATTGGCTGGCTGATCACTTTTGTTCAAA
AGGAGGAGATTGTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAA
AGAAATATATTTGGAAGTAATACATAATCTCCAGATTTTGAACACTTTTCGGCAAACACACTAGAGGATCGTTT
GGCTCATCATCGGTGGCTGTTATTTTTCATTTTGGAAAAATGAAATTCAAATGATCCTGAGCTGAAAAAACT
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTCTCTGACACAGACATCTGTAGTAA
TCTGTATGTTTTTCAGCCGCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA
GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTCATGTTACCACGCTTGGACCTCAAAA
TTTTCTGCCAATGACAAAGAACCATGGCTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTCGAGCTTTACT
ACCAGAGTTACGAAGAGCATCAAATCTCTTTATGGTCAGCTTAAGTTGGTACACTAGATTGTACAGTTCATGA
GGGACTCTGTAACATGTATAACATTCAAGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTCATGAGTA
TGAAGGACATCACTCTGCTGAACAAATCTGGAGTTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
ACCCACCACCTTCAACGAAGTGTACACAAAGAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGAAAAGAATGGCCCGGACATTAAGTGGACTGATCAACGTGGG
CAGTATAGATTGCCAACAGTATCATTCTTTTGTGCCAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT
TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCTGAGAAT
CTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACCTCAGACTTTCAGTGAAAAAGTTCTACAAGG
GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGAGGACCTTGCCAGAATTTTGCTCGAATTTGAGCT
CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA
AGCTGGGATCAGGGCTATCCAAGTGTAAAGTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA
GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAATAATGGAAACTCTCCGAAATCAAGGCAA
GAGGAATAAGGATGAACCTTGATAATGTTGAAGATGAAGAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA
GAATTATCTACAGCACTGGTGTAAGGAAGGGTCTGCAAACTTTTCTGTAAAGGGCGGTTTATAAATATTTTA
GACTTTGCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCT
TTTAACAACCTTTAAAAAATATTAACAGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTGAGTCCATG
GACCATAGATTGCTGTCCCCCTCGACGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAC
TAGTTTTTGGTCACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTGTTTTAAAAACACCCAT
GATGTGGCACAGTAACAAACCCCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCTCTCA
AAGGTTGAAAAAATGCTTTTAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGCTGATCATCCAGGAAAACCTGAGGGAAAAAATTA
TAGCAATTAAGTGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA
TGTGTTTCATGTATTTTCTGAAATTGCTTTTCATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT
TTACATATTTGCCTTCTGAACTTGTTTTGACCTGTATCCTTATTTACATTGGGTTTTTCTTTTCATAGTTTTGG
TTTTTCACTCTGTCCAGTCTATTTATTATTAACAAATAGGAAAAATTAACAGTTGTTTTTACTGTAGCTTAT
AATGATACTGTAGTTATTCCAGTTACTAGTTTACTGTCAGAGGGCTGCCTTTTTTCAGATAAATATTGACATAATA
ACTGAAGTTATTTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGATCTTCTAGTTTCTGTGTTGTTTGA
CTCAAAGAATCAAAATTTGTCAAGTAAATGATGTTGTTTGTATTAATTCAGAGTGTACAGAAATGGTAAAAAT
CCAATCAGTCAAAGAGGTCAATGAATTAAGGCTTGCAACTTTTTCAAAAAA

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FIGURE 426

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDDQDFYSLLGVSKTASSREIRQAFKKLALKLH
PDKNPNNPNAHGDFLKNRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYYRYDFGIYD
DDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDD
RMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTA
FAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSANTLEDR
LAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQPSLAVFK
GQGTKEYEIHGKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWCPPCRALL
PELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHSAEQILEFT
EDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGS
IDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLGFLPQVSTDLT
PQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDCQAYAQTCQKAG
IRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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FIGURE 427

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGCA
CGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTCTCCCTCTTGA
GTCCTTCTGAGGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTCGCGATGGTAG
CGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTCAATT
CCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTCTGCAG
TCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACAACTACC
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC
GCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACGCTGCATGC
GTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTTCTGATCAAA
ATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGATCATAGCACCT
TGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAAAGGACAAGAAG
GTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTAGACACTTCTGGT
CCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCATAGGAGAAAAGGCT
CTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTCTTGCCGGATACAGA
AAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGAGACACTTAAACCAGCT
ATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATC
AACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCCAATAACACCTTCCA
AAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTGTGATTGCAGTAAATTACT
GTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGAACTTTTAATTATTTTTCT
AAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTTTGTACACATTGATTGTTAT
CTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTTCAGCTTATAGTTCTTAAAAG
CATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTTGGAATGACAAAT
GATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATTTTCTGAAATGTACTATCTTAATG
CTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGAATAAAATTTAACATTTAAAAAA
AAAAAA

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FIGURE 428

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSAA
PGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRHAM
CCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTLSSKMYHTKGQEGSVC
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQKDHH
QASNSSLHTCQRH

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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FIGURE 429

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCC
TTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGACCC
CAGCGTTACCAATGCATCCTGCCGCTTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCT
CCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGAATAT
AGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGTCTGTTT
CAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATTTCCAAA
TGAAATCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA
CAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATA
CAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAGTGACCCCAT
TCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAAATATCATTGG
ATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCGAATATTTTGCA
TGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAGATATAGTGGCGA
CAACATAATCTACAAACCACAGGGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC
AAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTTGTCGAGAAATAAC
ATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCATACTCTTTCACATGAA
AGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGCAATTAATAAGTGAAAA
AGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACATCCTCTTCTGCACATACA
GAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAGGCATATGTATGTGTTTGG
AGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCGTATTTGACTTACATTCTGG
AAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGATACAGCCCCAGGAGAGCAAGC
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAACTAGCACCCAGTGAATATAG
GTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAACTTGAAAAACAGTTTGTAAGCCTTTC
AACAGCAGCATCAACCTACGTGGTGAAATAGTAAACCTATATTTTCATAATTCTATGTGTAT
TTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 430

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQM
LHPIFEEASDVKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYRGQ
RSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILHDDC
AFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNW IQDKCVPLVREITFEN
GEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP
ADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPGEQAQDV
ASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:**Signal peptide:**

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

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FIGURE 431

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGCA
GGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGCGTG
GACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG
CGGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGCTTCTG
GCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTCACCTCG
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCCCAACGGCGTGGAGTGCTACAGC
TGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCGTGAGCTGCTACAAC
GCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCAGCTAATGTG
ACTGTGTCCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA
GGCCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACCTCTGACCTCCGC
AACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCTCCAGAGCCCACG
ACTGTGGCCTCAACCACATCTGTCACTTCTACCTCGGCCCCAGTGAGACCCACATCCACC
ACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAGAACACGAGGCCTCC
CGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGACCGCAGCAATTCAGGG
CAGTATCCTGCAAAAGGGGGGGCCCCAGCAGCCCCATAATAAAGGCTGTGTGGCTCCCACAGCT
GGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTGAGCTTCTCCACCTGGA
AATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCTCATCACTTCTGTTCCCA
CCACTGGACTGGGCTGGCCCAGCCCTGTTTTTCCAACATTCCCCAGTATCCCCAGCTTCTGC
TGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATATATTCTGCCAGGGGTGTTCTA
GCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTCTCCGCTTGTCTCTTGTGATG
TTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTGAGAGAGAGGATGCTAAGCTTCC
TACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGGTGGGTGGGACAATGGCTCCCC
ACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGGGAATCGGTTCCCCATATGTCTTCC
TTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTACCCAATTCGCCCTATAGTGAGTCGTA

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FIGURE 432

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCTE
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNALNLTSRALDP
AGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCFDGNVTLTAAANVTVSLP
VRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTTVAST
TSVTTSTSAVRPTSTTKPMPAPTSQTPRQVEHEASRDEEPRLTGGAAGHQDRSNSGQYPAK
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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FIGURE 433

CGGGACTCGGCGGGTCTCTCCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCCATGGAGTT
GGTGCTGGTCTTCTCTGACGCTGCTGGCCCCATGGTCTTGGCCAGTGCAGCTGAAAAGGA
GAAGGAAATGGACCTTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGTTCGC
TGTGGTCTTCTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTTTCAA
TCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACGCCAATGC
AACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAACCTGAG
GCGGCTGCTTGAACCTTTGGATGCAAATGTCGATGCTTAAGAAAACCGGCCACTTCAGCAACA
GCCCTTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCTATCCCCTCTAACACCATT
CCTCCACCTGATGATGCAACTAACACTTGCTCCCCACTGCAGCCTGCGGTCTGCCACCTC
CCGTGATGTGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTGGTCTTTGTGG
CTACTTGTGTTGTGGATGGTATTGTGTTTGTAGTGAAGTGTGGACTCGCTTTCCAGGCAGGG
GCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCCGTGGCCCTCCATCACCTTCTGCTCCTA
GGAGGCTGCTTGTGTTGCCGAGACCAGCCCCCTCCCCTGATTTAGGGATGCGTAGGGTAAGAGC
ACGGGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCACTTTGTCATCATTCT
TCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTTATCCCACCTGATCCCAGTCT
GAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCCCAGCGTTGACGTCAGG
CAGGCTATGCCCTTCCGTGGTTAATTTCTTCCCAGGGGCTTCCACGAGGAGTCCCCATCTGCC
CCGCCCTTCACAGAGCGCCCCGGGGATTCCAGGCCCAGGGCTTCTACTCTGCCCTGGGGAAT
GTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGGGACCCTACCCCTTCCAACC
TTCCCTGCTTCTGAGACTTCAATCTACAGCCCAGCTCATCCAGATGCAGACTACAGTCCCTGC
AATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCCGTTGGGGCCAGCACACCGGGA
TGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTCTGCCTACGTCCCCTTAGATGGGCAGCAGAG
GCAACTCCCGCATCCTTTGCTCTGCCTGTGCGTGGTCAGAGCGGTGAGCGAGGTGGGTTGGAG
ACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAGGTTGAAGGTCATAACGAGAGTGGG
AACTCAACCCAGATCCCGCCCCCTCCTGTCTCTGTGTTCCCGCGGAAACCAACCAAACCGTGC
GCTGTGACCCATTGCTGTTCTCTGTATCGTGATCTATCCTCAACAACAACAGAAAAAAGGAAT
AAAATATCCTTTGTTTCCT

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FIGURE 434

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKC
SFNQKPRAPGDEEAQVENLITANATEPQKQRTQTEVQPSGGSLWNLRRLLEPLDANVDA

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FIGURE 435

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTGTTTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

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FIGURE 436

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFH
YDCGNKTVTPVSPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

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FIGURE 437

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAGCTCTTGTGGCAGG
TAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTCTGTCTACCTCACGGCGCAAGTGTGGATTCTGT
GTGCAGCCATCGCTGTGCCGCCTCAGCCGGGCCCCAGAAGTGGCCCTCCGTTTGCTCGTGCAGTAACCAGTTCA
GCAAGGTGGTGTGCACGCGCCGGGGCCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACC
TCATGGAGAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGTTGG
GCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAACACCCTGGAGCTGTTG
ACAAGTGGCTGACAGTCATCCCTAGCGGGCCTTTGAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGCAACA
ACCCCATCGAAAGCATCCCTCTTACGCCTTCAACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCA
AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAAGTTGGGCATGTGCA
ACATTAAAGACATGCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACTTCCCTG
AGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTGAAGTACAGGTCAGCCTGA
TTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAGTCAACTTGGCCCACAATAACCTCTCTCTTTG
CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCCTTGGAAGTGTGATTGTG
ACATTCTGTGGCTAGCCTGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTC
CCATGCACATGCGAGGCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTCTGCTGCCCCCTTCATCATGG
ACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGTGCGACTCCCCCTATGTCCTCCG
TGAAGTGGTTGCTGCCAATGGGACAGTGCTCAGCCACGCCTCCCGCCACCAAGGATCTCTGTCCTCAACGACG
GCACCTTGAAGTTTTCCACGTGCTGCTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCA
ACTCCAACGCCTCGGCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAAGTACAGCTTCTTCACCACAG
TAACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTTCCTACCACGTCCACTG
GTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTGAGTACCCGTGTGCCAAGCAGGTGGCAGTAC
CCGCGACAGACACCACTGACAAGATGCAGACCAGCCTGGATGAAGTCATGAAGACCACCAAGATCATCATTGGCT
GCTTTGTGGCAGTGACTCTGCTAGCTGCCGCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGC
GGAGTACAGTCACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGCAG
CAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCACAATTATGACCATATTAAGT
ACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGCCTGGGGAACTCTCTGCACCCACAGTCA
CCACTATCTCTGAACCTTATATAATTCAGACCCATACCAAGGACAAGGTACAGGAACTCAAATATGAAGTCCCCT
CCCCCAAAAACTTATAAAATGCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTT
TTCTTGATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAACAGATTATATTAATTTAAAGACAAAA
AGTCAAAACA

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FIGURE 438

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTR
RGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLN
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISE
GAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLEEELEMSGNHFP EIRPGSFHGLSSLKKLWVMNS
QVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHPWNCDCDILWLAWWL
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP
MSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTVNAVAGNSNASAYLNV
STAE LNTSNYSFFTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQTTRVPKQV
AVPATDTTDMQTSLEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAARTVE
IIQVDEDI PAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHW TENS LGNSLHPT
VTTISEPYIIQHTKDKVQETQI

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FIGURE 439

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG
TCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGC
CCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAA
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTGCACC
GATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAATTAGTAAAAAAT
GTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTCAACGACACCCTGATC
TTCATAAAAAATTGTAAAGGTTTCAACAGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 440

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEVK
HCTDQISFKKRLSLKKSWWK

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FIGURE 441

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG
GGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC
ACCTCCGCCAGGAACTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGG
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAG
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCAGCCAA
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGAAGGGGC
AGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGGGAAGAGGC
CAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTAAGTTTAGA
AGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG
AGGCGAATAAATGTTCAAACGTGA

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FIGURE 442

MPSPGTVCSELLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG
QAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 443

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTCG
TGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGTTT
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTGCTC
CTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT
ATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATCTTACA
CCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCAGCCTGGGGCCAGAGTCTTTGTCCCC
CGTGTGCGCATGTGTTTCAAGGTTCAGCCTCTCCCAGAAGTGAGATCATGGACAAAAAGGGCAA
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAACTCACGCCG
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGAGACAATGGA
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAAACAC
AAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCAACAACCTGAAG
CGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTGAGTCATGTTGCT
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGTAACAACAACCTCC
CTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAGCGTCTTCCATTCTCTG
GGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGACACGGGCAGCAGAGTG
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCAACCCCTGGTCAGGGCA
GAGGGAGTTGGGTGGGTTCAGGCTCTGGGCTCACCTCCATCTCCAGAGCATCCCCTGCCTGCAG
TTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGAGCCTCCTTGTTCATAACC
ACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGATGTTTTAAACACACACCTC
TAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGAATTTTTTTTAAATGAAAGTGC
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

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FIGURE 444

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLS PRSPQGWV
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQAQ
QEAELTTPRPAGVVPGA

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FIGURE 445

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTGC
TGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGA
GGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCCTCACCAGGTGCCACTGGACCTGG
TGTCACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG
CCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCTGTGGA
TGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCCGTATCC
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACCATGCAGG
AGGACCGCAGCATGGTGAGCGTGCCGGTGTTACGCCAGGTTCCCTGTGCGCCGCCGCCTCTGCC
CGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT
GCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGACCATCCTCCT
TGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

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FIGURE 446

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYE
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGC
VNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

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FIGURE 447

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAGA
TGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGGTGC
CCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTGGATG
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGACCGGT
TCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAGAACCAG
GGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC
TGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAAGCGGTTGA
TGGAGAAGGCTTCCCTCCCCCTCCCCTCCCCTTGGGGCTTTGTGGCAAAAATCCTATGGTTATCC
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCTACTAACAGAC
TTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTGCTGTTTCCTCT
GTCCTGTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTCTTCCAAGCGACT
GTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAATTATGGCTGGGCCTTCTACATG
GCCTGGCTCTCCTTCACCTGCTGCATGGCGTGGCTGTCAACCACCTTCAACACGTACACCAGG
ATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAACCCGAACCTGCCTACCA
CATCACCATCAGTGTTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCCACCCTGGGTCTTTGACC
AGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGGGAGTCGACTTCTACTCC
GAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA
TCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGAGTAGGCTTGAGCCCTACCT
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTCTTGAGCATGGTTTTTA
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTCCTAAGGGATTCTGGGTGCCA
CTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTACCCACCCACATCTCACACATCCAGAA
TTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGCTAAACCATGGAGATAAAAAGAAG
AGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 448

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMPV
SLDGD TNTSTQEVVQYNWETGDDRF SFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKRGE
KGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQ LPPA
TNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRL ETTCLELWLG
LLHGLALLHLLHGVGCHHLQH VHQDGAGVQVQA

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FIGURE 449

[illegible]

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FIGURE 450

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN
LSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQIT
QLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRI FQDCRSLKF
LDIGYNQLKSLARNSFAGL FKLTELHLEHNDLVKVNFAHFPR LISLHSLCLRRNKVAIVVSSL
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKS LTSITLAGNL
WDCGRNV CALASWLSNFQGRYDGNLQCASPEYAQGEDVLD VYAFHLCEDGA EPTSGHLLSAV
TNRSDLGPPASSATT LADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGT MALIFSFLI
VVLVLYVSWKCFPASLRQLRQCFVTORRKQKQKQTMHQAAMSAQEYYVDYKPNHIEGALV I I
NEYG SCTCHQQPARECEV

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FIGURE 451

TTGAGCGCAGGTGAGCTCCTGCGCGTTCGGGGGCGTTCCTCCAGTCACCCTCCCGCCGTTAC
CCGCGGCGCGCCCCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAAACTAATACGGA
CTGAACGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT
ACCATCCATAGCCAGATAGATTATCTTACACTGAACTGATCAAGTACTTTGAAAATGAACTTCG
AAATTTATCTTGGTGTCTTCATACTTGCTGCACTGAGTCTTCAACCACCTTTTCTCTCCAA
CTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACTTATATAAA
GTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTACGTGAAGCAAGTTACTAAT
GTTTTTATTACAAAACCTACCCTAACCATTAATCTTTGGTAACTGGCCTCTTTGCAGAGAAT
CATGGGATTGTTGCAAAATGATATGTTTGATCCTATTTCGGAACAAATCTTCTCCTTGGATCAC
ATGAATATTTATGATTCCAAGTTTTGGGAAGAAGCGACACCAATATGGATCACAAACCAGAGG
GCAGGACATACTAGTGGTGCAGCCATGTGGCCCCGAACAGATGTAAAAATACATAAGCGCTTT
CCTACTCATTACATGCCCTTACAATGAGTCAGTTTCATTTGAAGATAGAGTTGCCAAAATTGTT
GAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCTGATGAC
ATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCATTTAGATATTGACAAG
AAGTTAGGATATCTCATACAAATGCTGAAAAGGCAAGTTGTGGAACACTCTGAACCTAATC
ATCACAAGTGATCATGGAATGACGCGAGTGTCTGAGGAAAGGTTAATAGAAGTTGACCAGTAC
CTGGATAAAGACCACTATACCCTGATTGATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAA
GGTAAATTTGATGAAGTCTATGAAGCACTAACTCACGCTCATCCTAATCTTACTGTTTACAAA
AAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCAACCAATCATAGCA
GTGGCTGATGAAGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACCAC
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTCTGCCTTCAGA
AAGAATTTCTCAAAAGAAGCCATGAACTCCACAGATTTGTACCCACTACTATGCCACCTCCTC
AATATCACTGCCATGCCACACAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCA
ATGCCAAGGGTGGTCCCTTATACACAGAGTACTATACTCCTCCCTGGTAGTGTTAAACCAGCA
GAATATGACCAAGAGGGGTACATACCCTTATTTTCATAGGGGTCTCTCTTGGCAGCATTATAGTG
ATTGTATTTTTTTGTAATTTTCATTAAAGCATTAAATTCACAGTCAAAATACCTGCCTTACAAGAT
ATGCATGCTGAAATAGCTCAACCATTAATTACAAGCCTAATGTTACTTTGAAGTGGATTGTCAT
ATTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATCTGGGAAACCAGTT
CCAAACATCTGCAGAAACCATTAAAGCAGTTACATATTTAGGTATACACACACACACACACA
CACATACACACACACGGACCAAAATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGT
CTCCATTGTTCACTGTAGCATAGGGATAGATAAGATCCTGCTTTATTTGGACTTGGCGCAGAT
AATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATATATTGCACTTTAAATTTCT
CTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAACTTGATTG
AAAATGACAACTTTTTGCACCCATGTCACAGAATACTTGTTACGCATTGTTCAAACCTGAAGGA
AATTTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAA
GGTGATAAGTGTTGAAAATTAAATGTGATAACCTTTGAACCTTGAATTTGGAGATGTATTCC
CAACAGCAGAATGCAACTGTGGGCATTTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCA
TTTATTTTTTCCCTCAAAAGAGAGTCAAATACTGACAGATTCGTTCTAAATATATTGTTTCTGT
CATAAAATTATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCATAATAATGAAGACAC
CATGAATATACTTTTTCTTCTATATAGTTTACGAATGGCCTGAATAGAAGCAACCAGGCACCAT
CTCAGCAATGTTTTCTTCTTGTGTTGTAATTATTTGCTCCTTTGAAAATTAAATCACTATTAATT
ACATTAAAAATCAAATTGGATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 452

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVKQ
VTNVFITKTPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIWIT
NQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED
PDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEERLIEL
DQYLDKDHYTLDQSPVAAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYNRIQP
IIA VADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTDLYPLLC
HLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPPYFIGVSLGS
IIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Important features:**Signal Peptide:**

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

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FIGURE 453

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGAC
TATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTGCT
GATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGACCAA
CCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGCTGGA
TGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGGCAGGC
TGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAAACCTCCA
ATATGAGGACAAGTTCCGAAATAATTTGAAAGGCCAAAAGGCTGGATATCAACACCAACACCTA
CACATCTCAGGATCTCAAGAGTGCCTGGCAAAATTCAGGAGGGGGCAGAGATGGAGAGTTC
AAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAGCGGCTCTTCCGCCCCATTGAGGAACTGAA
GAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGGTACGGCTGAT
CAACAAGTTCAATAGTTCCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTCTTTGATCTTGA
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGTGGT
GATCAATGGGCTGAACAGCACAGAGCCCCTCGTGAAGGAGTATGCTGCGTTTGTGCTGGGCGC
TGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGAGCCCTGCAGAAGCT
GCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGTCCTGTTTGCCTGTG
CTCCCTGCTGCGCCACTTCCCCTATGCCCAGCGGCAGTTTCTGAAGCTCGGGGGGCTGCAGGT
CCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTGCGCGTGGTCACACTGCT
CTACGACCTGGTCACGGAGAAGATGTTGCGCGAGGAGGAGGCTGAGCTGACCCAGGAGATGTC
CCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAGGCCTGTGGGAACAGGGCTG
GTGCGAGATCACGGCCCACCTCCTGGCGCTGCCCGAGCATGATGCCCGTGAGAAGGTGCTGCA
GACACTGGGCGTCCTCCTGACCACCTGCCGGGACCGCTACCGTCAGGACCCCCAGCTCGGCAG
GACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCAGCCTGGAGCTGCAGGATGGTGA
GGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAACAGCTTGCTGAAGGAGCTGAGAT**AG**
AGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGAGGCTGAGGGGTGCCAGCGTGGGTG
GGCTTCTCAGGCAGGAGGACATCTTGGCAGTCTGGCTTGGCCATTAAATGGAAACCTGAAGG
CCAAA
AAA

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FIGURE 454

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEELD
AEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTY
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI
NKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYA AFVLGA
AFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKLGGLQV
LRTLQVEKGTEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPGLWEQGW
CEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE
DEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

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FIGURE 455

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAGT
GGCCAGGAAGGCACAGGCCTGAGAACTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCTA
CCTGGGGGACAGGGCAAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGGTGT
CTGTGCGTCTTGACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCTAGAC
TCCTATCTTCTGAATTCTATAGTGCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGTCCTTG
TGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCCCCTGGA
TGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTTCTCGCCA
ACAATGATGTTTCCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG
GAGCTGGGGCCGGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCAATGGATCCG
ACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAACCAGCTCTACT
GCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAGGAAGAAAGTTT
TCAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGATGTTCC
AGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCTAACGACCTCATGC
TCATCAAATGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCATCAACGTCTCCTCTC
ATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAACCAAGAGCCCCAAG
TGCATTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT
CCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCT
GGGGAGATTACCCTTGCGCCCGGCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTCA
CCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCAGGACTCAGCACACCGG
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTCCCAGAGA
TGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCC
CCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGGGAACAATTTCCAAAATGTCCAG
GGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGCTCAGGGCCCATCCCTT
CTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAAAAAAAAA

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FIGURE 456

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS
SSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPV
YESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCP SAGTKCLVSG
WGTTKSPQVHF PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGR DSCQGD SGGPVVCN
GSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 457

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTTGCTTCCTGAACT
AGCTCACAGTAGCCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCACCCTGTAGGAATCCAGATGCAGG
CCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG
CCACAACCTCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGA
CCCTGCTGACTTTGTGCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGC
TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTC
TTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTGCTGAGCTGTATAACA
AAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATA
AAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAAC
AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCC
CTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAATAGATG
TCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGA
AGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG
AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAG
ACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTCTCGTGTTCCTGTT
CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCAC
CAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAA
TGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAA
TACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTCCCAGATTGTAC
CAGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCC
CATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCCAGGAAAGAAATAT
ATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCTTCAGAGAGATTAAAGACCAGAAAAAGT
GAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGT
ACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

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FIGURE 458

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 459

GTTGATGGCAAACCTTCCTCAAAGGAGGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCCAC
TGGCGGGCCCGCAACACTCCGTCTCACCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCTGT
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGTGGT
CAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGGAA
GTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAGGATGA
GAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGATGTTTA
TTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC
CCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCAACT
ACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCTGGGCCCTACTATGTGCTTTGAAG
ACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATCGCCCTGGTGA
ATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGGAGATGTTATGC
ACCTAGTGAAATTCTTAAAGAAATTCCGGGGGGTGCCTGGTGTGGTGGCCTCCTACGACG
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTGGGGAGTTCCTACG
CAAAACAACCTGGGCTTCGGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAAA
GCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAATACGAGGGATGGCCAGAGC
TGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTTTAGGGTGGCTGTGGCTCTTCCTCAG
CCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCGGCAGGGGCTGAGGAGGA
GGAGCAGGGGGTGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGACGCTGTGTGCGCCTCTCCTC
CTCGGAAACAGAACCCTCCCACAGCACATCCTACCGGAAGACCAGCCTCAGAGGGTCCTTCT
GGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGGACTGCTGACGGCTGGTCCTG
AGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTATTTTGTGGTTTTGAAAAAA
AAAAAAAAAAAAAA

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FIGURE 460

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKYKCGLIKPCPA
NYFAFKICSGAANVVGPPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV
MHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRLKFLSDLGSSYAKQLGFRDSWVFIGAKDLRG
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

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FIGURE 461

AAACTCAGCACTTGCCGGAGTGGCTCATTTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGGA
AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCCTC
TAGAACCCGACCCACCACTATGAGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGGCGT
CCAGTGGTCCCTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTATTAA
GGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA
GTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA
GCCAGCGCCAGAGAACAAATGCCCTCAACACACAAACCCAGCCCAAGGCCCACACCACCGGAGA
CAGAGGAAAGGAGGCCAACCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCACACAGCACA
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCACCCAGAGG
GCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA
GACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTGAGAGAA
GCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCCAAAAGTCAGCACAGAATGCT
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCACAGCAGTCATCCC
ACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAGAGCCCCACGACGCA
GAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTGGGATTTTGAGGAAAA
ATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTGTGAAGATCAAAGCCTC
CAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCCAACCTCACTCTCTTCTGACTCCAGACA
CTTCAACCAGAGTGAGTGGGACCGCTGGAACACTTTGCACCACCCTTTGGCTTCATGGAGCT
CAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAGTGCCCCAGCAGCAGCTGCT
CCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGTGCCGTGGTGGGCAACGGGGG
CATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCACGACTACGTGTTCCGATTGAG
CGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTCGGACATCCTTCTACGGCTTTAC
CGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAATCGGGGTTTCAAGAACGTGCCTCT
TGGGAAGGACGTCCGCTACTTGCACTTCCCTGGAAGGCACCCGGGACTATGAGTGGCTGGAAGC
ACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTTTCTGGTTCAGGCACAGACCCAGGA
AGCTTTTGGGAAGCCCTGCACATGGACAGGTACCTGTTGCTGCACCCAGACTTTCTCCGATA
CATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGATGGTGCCCACTGGAGGATATACCGCCC
CACCCTGGGGCCCTCCTGCTGCTCACTGCCCTTCAGCTCTGTGACCAGGTGAGTGCTTATGG
CTTCATCACTGAGGGCCATGAGCGCTTTTCTGATCACTACTATGATACATCATGGAAGCGGCT
GATCTTTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAGCGGCTACACGATGA
AGGGATAATCCGGCTGTACCAGCGTCCTGGTCCCGGAACTGCCAAAGCCAAGAACTGACCGGG
GCCAGGGCTGCCATGGTCTCCTTGCTGCTCCAAGGCACAGGATACAGTGGGAATCTTGAGAC
TCTTTGGCCATTTCCCATGGCTCAGACTAAGCTCCAAGCCCTTCAGGAGTTCCAAGGGAACAC
TTGAACCATGGACAAGACTCTCTCAAGATGGCAAATGGCTAATTGAGGTCTGAAGTTCTTCA
GTACATTGCTGTAGGTCTGAGGCCAGGGATTTTAAATTAAATGGGGTGATGGGTGGCCAATA
CCACAATTCTGCTGAAAAACACTCTTCCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCC
TGGATTTACAGAAACATATAGATCTGGTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCT
TGAAGGTATTACTTAACTTCACTACAGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTC
TAGAAGGTCTATACTTGTCTTGAAGCTATTTGACAACTCTACGTGTTGTAGAAAAC
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAAA
AAAAAAA

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FIGURE 462

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK
SQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS
PEKEKTMVNLTSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQGKAA
TTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPKEKKPQATPPPAPFQSPTTQRNQRK
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHFNQSEW
DRLEHFAPPFGFMELNYSLVQKVVTFRPPVPQQQLLASLPAGSLRCITCAVVGNGGILNNSH
MGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVPLGKD VRY
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFLRYMKNRFL
RSKTL DGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSWKRLIFYINH
DFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Important features:**Cytoplasmic Domain:**

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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FIGURE 463

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGGCGCAAGGGTGAGGGCGGCCCCAGAAC
CCCAGGTAGGTAGAGCAAGAAGATGGTGTCTTCTGCCCCCAAATGGTCCCTTGCAACCATGTC
ATTTCTACTTTCCTCACTGTTGGCTCTCTTAACCTGTGTCCACTCCTTCATGGTGTGACAGCAC
TGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCTTGGGAATAAAATACGACTTCCTGA
GTACGTCATCCCAGTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACCTTCTG
GGGAACCACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCCTGCATAGTCA
CCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAACC
CCTGCAGGTCCCTGGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCCGAGCCCCCTCT
TGTCGGGCTCCCGTACACAGTTGTCACTTACTATGCTGGCAATCTTTCCGAGACTTTCCACGG
ATTTTACAAAAGCACCTACAGAACCAAGGAAGGGAACTGAGGATACTAGCATCAACACAATT
TGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTCAAAGCAAGTTT
CTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCCATTGGTGAAATC
TGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGAAGATGAGCACCTA
TCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTGACGAAGATAACCAAGAGTGGAGTCAA
GTTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGCACTGGATGCTGCGGT
GACTCTTCTAGAATTTTATGAGGATTATTTTACGATACCGTATCCCCCTACCCAAACAAGATCT
TGCTGCTATTTCCGACTTTCAGTCTGGTGTATGGAAAACCTGGGACTGACAACATATAGAGA
ATCTGCTCTGTGTTTATGATAAGGGAGCTTCTTGCATCAAGTAAGCTTGGCATCACAGTGAC
TGTGGCCCATGAAGTGGCCACCAGTGGTTTGGGAACCTGGTCACTATGGAATGGTGGATGA
TCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTGTCTGTGAGTGTGACCCATCC
TGAAGTGAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGACGCAATGGAGGTAGATGCTTT
AAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTGCTCAGATCCGGGAGATGTTTGA
TGATGTTTTCTTATGATAAGGGAGCTTGTATTCTGAATATGCTAAGGGAGTATCTTAGCGTGA
CGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAGCATAGCTATAAAAATACAAAAACGA
GGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAGATGGTGTAAAAGGGATGGATGGCTT
TTGCTCTAGAAGTCAACATTCATCTTCATCCTCACATTGGCATCAGGAAGGGGTGGATGTGAA
AACCATGATGAACACTTGGACACTGCAGAGAGGGTTTTCCCCTAATAACCATCACAGTGAAGGG
GAGGAATGTACACATGAAGCAAGAGCACTACATGAAGGGCTCTGACGGCGCCCCGGACACTGG
GTACCTGTGGCATGTTCCATTGACATTCATCACCAGCAAATCCAACATGGTCCATCGATTTTT
GCTAAAACAAAAACAGATGTGCTCATCCTCCCAGAAGAGGTGGAATGGATCAAATTTAATGT
GGGCATGAATGGCTATTACATTGTGCATTACGAGGATGATGGATGGGACTCTTTGACTGGCCT
TTTAAAAGGAACACACAGCAGTCAAGCAAGTATGATCGGGCAAGTCTCATTAACAATGCATT
TCAGCTCGTCAGCATTGGGAAGCTGTCCATTGAAAAGGCCTTGGATTTATCCCTGTACTTGAA
ACATGAAACTGAAATTATGCCCGTGTTCAGGTTTGAATGAGCTGATTCCTATGTATAAGTT
AATGGAGAAAAAGAGATATGAATGAAGTGGAACTCAATTCAAGGCCTTCCTCATCAGGCTGCT
AAGGGACCTCATTGATAAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCG
GAGTGAACCTACTACTCCTCGCCTGTGTGCACAACTATCAGCCGTGCGTACAGAGGGCAGAAGG
CTATTTTCAGAAAGTGAAGGAATCCAATGGAACTTGAGCCTGCCTGTGACGCTGACCTTGGC
AGTGTGTTGCTGTGGGGGGCCAGAGCACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTT
TTCTTTGTCCAGTACTGAGAAAAGCCAAATTTGAATTTGCCCTCTGCAGAAACCCAAAAAAGGA
AAAGCTTCAATGGCTACTAGATGAAAGCTTTAAGGGAGATAAAATAAAAACTCAGGAGTTTCC
ACAAATTTCTTACACTCATTGGCAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAG
GAAAACTGGAACAACTTGTACAAAAGTTTGAACCTGGCTCATCTTCCATAGCCACATGGT
AATGGGTACAACAAATCAATTCTCCACAAGAACACGGCTTGAAGAGGTAAAAGGATTCTTCAG
CTCTTTGAAAGAAAATGGTTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATGAGA
AAACATCGGTTGGATGGATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAAAGCT
TGAACGTATGTAAAAATTCCTCCCTTGCCCGGTTCTGTTATCTCTAATCACCAACATTTTGT
TGAGTGTATTTTCAAACCTAGAGATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTC
AACTCATTTTTTGTACTATCCCTGTGAAAAGAATAGCTGTTAGTTTTTCATGAATGGGCTTTTT
CATGAATGGGCTATCGCTACCATGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAACGTAAACC
CAAGTGTGGGTTCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 464

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVHY
DLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLEHP
PQEQIALLAPEPLLVLGYPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM
AFPCFDEPAFKASFSEIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVAFIIS
DFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAAIPDFQ
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDLWLNELF
AKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVSYDKG
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDFGFCRSQHS
SSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPDTGYLWHVPL
TFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTGLLKGHTA
VSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMEKRDMN
EVETQFKAFILRLRLDLIDKQTTWTDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALCRTQNKEKLQWLLD
ESFKGDKIKTQEFQIILTIGRNPVGYPLAWQFLRKNWNKLVQKFELGSSSIAHMVMGTTNQF
STRTRLEEVKGGFFSSLKENGSQLRCVQQTETIETIENIGWMDKNFDKIRVWLQSEKLERM

Important features:**Signal peptide:**

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

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FIGURE 465

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCACT
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCCGA
CCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGACAC
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC
CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTA
CACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCTTTGGGC
CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG
TCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGATGGCCTCCT
CAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGAACTGCAATAG
GAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAACTTGGCTCAAGA
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGAC
GCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAGGCTGCAGCACTGT
TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGGGTGCTTGTGGCCTC
CTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA
CTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTA
TGATGGGTACATTCTCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTTCAGGGCTGCGT
GGCCCAACCTTCAGCTTCTTGTGTAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA
GAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC
TCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGGCCCTTC
CTGCTTAACTCTATTACCCCCACGATTCTTCAACGCTGCTGACCACCCACACTCAACCTCCCTC
TGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTCCCATCTGTCCATGAATCATCTT
CCCCACACACAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATC
CGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC
CCTGTCCTTTCA

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FIGURE 466

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLIE
SGPQVSLVLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPA
DPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRRLRGGGIFSNLRVQGCMPPQPGCNLLN
GTQEIGPVGMTENCNRKDFTLCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETLLLID
VGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLNSLPPQ
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSS
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

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FIGURE 467

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTTG
AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGGCCCTTCG
AGGAGCTTCTGCATTGCTGTTTCTGTTCCCTTGACAGCTTTTCTGCCCCCGCCGACGTGTACCCA
GGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGGAAAA
ATGTACCCAAGCAACGAGGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATATCTGT
CATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAAGTGGCACT
GAGAGTTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTGACGAGTG
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAAA
GATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTCTTTGAAAAT
AGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAAGATGCTGTCTATAACTCTCCAAA
GGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAACATACGGGCATT
CATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTCCTGGCAGGGAAC
AGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTTCTAATGAGATAAT
CAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCAGGAGGGGTAGGCCG
AGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT
CTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCACAAAGATTGAGCCGGG
CACACTGGGAGTGGAGCATTCTATGGGATACCCCATGCAGAAGCCAGGATGCTGAAGCCTCATT
CCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCAGGGCCCTCATCGCATCAC
CTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACTTGTTCTTCCCCAA
GAGACCAAGAAGTCACTCCATGATCCATTACAACCCCAAGAGATAAGCAGCTCTATGCCTGGAA
TGAAGGAAACCAGATCATTTACAACTCCAGACAAAGAGAAAGCTGCCTCTGAAGTAATGCAT
TACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC
CCCTTACAAATATAGTATCCCTCTAATCACACACAGGAAGAGTGTGTAGAAGTGGAATACGT
ATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTCCAAGAGCTTAGATGAGAGCATATC
ATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAACCTCCTGGCTCTCAAGGATGACCAC
ATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTACTGCTCCCCAGCATTTACTGTAACCTCTG
CCATCTTCCCTCCCAATTAGAGTTGTATGCCAGCCCCTAATATTACCACTGGCTTTTCTC
TCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTCAAATGTCTATTGATATTCTCCCATTTT
CACTGCCCAACTAAAATACTATTAATATTTCTTTCTTTTCTTTTCTTTTTTTTGGAGACAAGGT
CTCACTATGTTGCCAGGCTGGTCTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCT
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTTAAAATACTATTTCTTATTG
AGGTTTAACTCTATTTCCCCTAGCCCTGTCTTCCACTAAGCTTGGTAGATGTAATAATAAA
GTGAAAATATTAACATTTGAATATCGCTTTCCAGGTGTGGAGTGTTTGCACATCATTTGAATTC
TCGTTTACCTTTGTGAAACATGCACAAGTCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGT
AACACAATTACAAAGTGAAAGATACAGCTAGAAAATACTACAAATCCCATAGTTTTTCCATTG
CCCAAGGAAGCATCAAATACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTCATCGTT
TCAGCCTAAAAATAATAGTCTGTCCCTTAGCCAGTTTTCATGTCTGCACAAGACCTTTCAAT
AGGCCTTTCAAATGATAATTCCTCCAGAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCC
TCCTCTTGTCTTGCTGTCCCTCTGTTTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTG
AGCAAAAAAAAAAAAAA

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FIGURE 468

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQEF
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQE
AEEKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNPKVYLLIGSRNNTVWEF
ANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMLL
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSWDTPCRSQ
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK
QLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 469

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC
AGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTC
CTAGTAACCTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGTGGG
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCTGGGG
CGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCAAGCAC
CACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTACCGCTGC
TCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCCTGGTCTCAGGATACCCACCATCCT
TTTCCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGACTCTCCCAG
TCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGGCTGTGGTGTG
AAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA
GGACATTCCCCCTCCCCCTCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTGCCCTCTCCCCA
CATGTATCCCTCGGTCTGAATTAGACATTCCCTGGGCACAGGCTCTTGGGTGCATTGCTCAGAG
TCCCAGGTCCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGT
AGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTT
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCC
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCA
GAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGTTAACCCTGAAGCCCCCA
ATTCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAATCTAATCTGATATTGACAT
ATTAGAAGGCAATTAGGGTGTTTCCTTAAACAACTCCTTTCCAAGGATCAGCCCTGAGAGCAG
GTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGGAGC
AGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGGCAACTACACACCAACATGCTGG
CTTTAGAATAAAAGCACCAACTGAAAAA

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FIGURE 470

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHPG
SHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Important feratures:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 471

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTCC
TCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTG
CTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGGCCC
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAA
AGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCCTCT
GTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCC
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAG
GAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTA
TGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAGGCTTCTCTG
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTTCGTGGTGGGATCAGGAAAGCAGG
GCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACTTTCTGTTCTGG
AAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGATTGTGTGAAACTG
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTG
TCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAA
TATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAA
CTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAATTGACTGCCAGGCTGG
GTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAG
GTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAA
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGGAGGCTGAGGCAGGAGAA
TCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG
GGTGA CTGAGACTCTAACTAA

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FIGURE 472

MSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPRT
FKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFVVG
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 473

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTTT
TGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTGGT
ATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATC
AAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC
CAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT
AATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATGATTGTA
AATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATATATACAA
TAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAT
TTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT
TTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAAATGCGATACA
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA
TGTTGCCAAGGAAAAA

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FIGURE 474

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG
IVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 476

MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRVI
VVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRILHK
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMALNQ
ALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALRAHSC
LSDR LQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKVLKA
DVVLLTASGPAVKRITFS PPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGHSNTDR
PSRMIFYPPPPREGALLLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWWETAVKSALRAAIKI
NSRKG PASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQNTTHTRTSH

Important features:**Signal peptide:**

amino acids 1-21

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FIGURE 477

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA
GAACCTCAGAGCCGGGAAGCCCCATTCACTAGAAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCT
GCTGCTGTTCCACAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCCACTTCCGACCCCGGCGTTGATCTGCAT
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTCCAGAGAACAATGACCTAACAAAGTTGCTG
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG
ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTCT
CTGTCTCTTGATAAAGGTTATAAATCATCACCAGACCAAGTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG
GATCATCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC
CATCGTACATATTGTCAACAAGGCTGATATCGCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT
AGGGAATGTAGAGAAAGGCTTACCCCGAGCCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA
GCAAGAGGGGAGAAGAGTGGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG
AAAACCTGTGCTCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAGG
AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAAGAGATTGTACAGGCTGTTGTGTA
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
CACATTGTTTCCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCT
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGTTTCGTGTAATTGTCACCTGGAGC
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGGTACGTTGGGGTGGCCCTGGC
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACCTTTACAGTGAATAATGAAGGAGAGGTCTGCAT
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
GCTTCACACAGGAGACATTTGGTCTGCTGGCTCCCGAATGGAACCTGGAAGATCATCGACCGTAAAAAGAACATTTT
CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAAATATCTACAACAGGAGTCAACCAAGTGTACA
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCTGACACAGATGTACTTCCCTC
ATTTGCAGCCAAAGCTTGGGGTGAAGGGCTCCTTTGAGGAAGTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACCTTTTGAACAGGTCAAAGCCATTTTTCTTCATCC
AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG
TGCATGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTGCCTTTCCTCCTATTTTTTTTTTAAAC
TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAAATAAATCA
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTCAA
GATCCCAGTTTATGTTCTGTGTCTTCCCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
CAAAGGGACCCCTCTGTGCCTTCTTCTTTGTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA
TCTTCTACTGTTCAAATAAGAGATTTTTAAATCTGAAAACTGCTTACAATTCATGTTTTCTAGCCACTCCAC
AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
CTGCGTAAATTAAATTGTGTACTGAAGGGAAAAGTTTGATCATACCAAAACATTTCTAAACTCTCTAGTTAGATA
TCTGACTTGGGAGTATTAAAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATATTTA
CAGTAGGAAGTGGGGAGTAAATCTGTTCCCTACAGTTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA
GGTGGGCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTCCTGAAGTGGGAACAAAGATCT
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTCTGTGAAGGAACCAACTGATCTCCCCACCCCTTGAGATT
AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC
TATTACAGATAAAAAA

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FIGURE 478

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFKLLFTKMLFIFNF
LFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTSCC
FSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQ
FVGIFAQNRPEWIISELACYTYSMAVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG
NVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC
FTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYSC
GARVGFFQGDRLRLADDMLKPTLFPVPRLLNRIYDKVQNEAKTPLKKFLLKLAVSSKFKE
LQKGIIRHDSFWDKLIFAKIQDSLGGVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTEC
TGGCTFTLPGDWTSGHVGVPPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFKGYLKDPEKT
QEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPVQLQIFVH
GESLRSSLVGVVVPDPTDVLPSFAAKLGVGKSFEELCQNQVVREAILEDLQKIGKESGLKTFEQ
VKAIFLHPEPFSIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

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FIGURE 479

GGAGGCGGAGGCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGGC
CCGGGGCCCCCTAAGCCATTTCCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAATCC
GGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGGAGC
TGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCTAGACA
GGGGCCGTGCTTTTCCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACACTCGG
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC
CGCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCCTGGACGTAGAGGTGTAT
TCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATGAGGCCCCG
GAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGCCACGTGATGGCAAAA
CGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCAACATGGTA
GCGCCCGGGCAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACCTCAAGGACACA
GCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGCTGGAGGGACACA
TGGGCCTTCGTGGGACGAAAAGGAGGTCCTGTCTTCGGGGAGAAACATTCTAAGTCACCTGCC
CTCTCTTCCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAAGAG
GCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGCTTCTGCAGCAAAGTT
GAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGAGTTCAGCCCTGACCCA
CTCCAGACAACAAGGTCCTCAATGTGCCTGTGGCTGTCAATTGCAGGGAACCGACCCAATTAC
CTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCAGGGGGTGTCTCCTCAGATGATAACAGTT
TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACTGTTTGGTCTGAGGGGCATC
CAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGCACTACAAGGCCAGCCTCACT
GCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGTGTGGTTCTGGAAGAGGACCTGGACATT
GCTGTGGATTTTTTTCAGTTTCCTGAGCCAATCCATCCACCTACTGGAGGAGGATGACAGCCTG
TACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCACTACTG
TACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTCAGGAGGTCCTTGTAACAAGGAGGAG
CTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGATTGGGACATGTGGATGCGGATGCCT
GAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACGTTTCCCGATCCTACCACTTTGGCATC
GTCGGCCTCAACATGAATGGCTACTTTCACGAGGCCTACTTCAAGAAGCACAAGTTCAACACG
GTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCTGAAGAAAGAAGCTTATGAAGTGGAAAGTT
CACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCCTTGTGAAGACTCTTTC
CTGCCAGACACAGAGGGCCACACCTACGTGGCCTTTATTTCGAATGGAGAAAGATGATGACTTC
ACCACCTGGACCCAGCTTGCCAAGTGCCCTCCATATCTGGGACCTGGATGTGCGTGGCAACCAT
CGGGGCCTGTGGAGATTGTTTCGGAAGAAGAACCCTTCCTGGTGGTGGGGGTCCCGGCTTCC
CCCTACTCAGTGAAGAAGCCACCCTCAGTCACCCCAATTTTCCTGGAGCCACCCCAAAGGAG
GAGGGAGCCCCAGGAGCCCCAGAACAGACAT**AG**AGACCTCCTCCAGGACCCTGCGGGGCTGGGT
ACTGTGTACCCCCAGGCTGGCTAGCCCTTCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTA
GGGGCTGGGGCTACCTTGTTTTTAACATGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCC
CTGCTCCAACACCCCGTTCCCTGAGTTAAAAGTCTATTTATTTACTTCTTGTGGAGAAGGGC
AGGAGAGTACCTGGGAATCATTACGATCCCTAGCAGCTCATCCTGECCTTTGAATACCCTCAC
TTTCCAGGCCTGGCTCAGAATCTAACCTATTTATTGACTGTCCTGAGGGCCTTGAAAACAGGC
CGAACCTGGAGGGCCTGGATTTCTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTC
TACTCAGGAACTGCTGTGCCCAACCCATGGACAGGCCCAGCTGGGGCCCACATGCTGACAC
AGACTCACTCAGAGACCCTTAGACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGA
TTTCCAAAGCTGGATAAGTTGGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAA
AAAAA

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FIGURE 480

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVIVNIKLILDTRR
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEARE
QGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLKDTA
KALLRSLGSQAGPALGWRDWFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSSAEEA
ECHWADTELNRRRRRFC SKVEGYGVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGNRPNYL
YRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHYKASLTA
TFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLVCISAWNDQGYEHTAEDPALLY
RVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVSRSYHFGIV
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLSAEVLDHSKNPCEDSFL
PDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVRGNHRGLWRLFRKKNHFLVVGVPASP
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

Important features:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

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FIGURE 481

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCA
GGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT
GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTT
CCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGTATCA
TTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCA
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCTCTGGAA
TTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATT
ATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATC
TGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA
AACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGGGGCATATTA
ATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC
CTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT
CATATATTTTGTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAG
CAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAATATTCTAA
AATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAA
GCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAA
ATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTT
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA
AATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCA
ACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT
TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTTTAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN
REATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFL
KIPSTLAPPMDPSPVIWIIIFGVIFCIIIVAIALLLSGIWQRRRKNKEPSEVDDAEDKCENM
ITIENGIPSDPLDMKGGILMMPS

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FIGURE 483

CGTCTCTGCGTTTCGCCATGCGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGGC
CCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGTGT
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCACCCG
GGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGGGGAA
CAAGATCAACCTCCTCGGCTTCTTGGGCCTTGCTCCACTGCCTTCCCTGCAAAGATTTCGTGCGA
CGGCGTGGAGTGCGGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCGCCCGCGCTGCGAGTG
CGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA
CCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGCGTCATGTA
CCGGGGCCCGCTGCCGCAAGTCCTGTGAGCACGTGGTGTGCCCCGCGGCCACAGTCGTGCGTCTG
GGACCAGACGGGCAGCGCCCACTGCGTGGTGTGTCGAGCGGCGCCCTGCCCTGTGCCCTCCAG
CCCCGGCCAGGAGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGCCACATGCGCCA
GGCCACCTGCTTCCCTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTGCGCAGGCACCCC
TGAGGAGCCGCCAGGTGGTGAAGTCTGCAGAAGAGGAAGAGAACTTCGTGTGAGCCTGCAGGAC
AGGCCTGGGCCTGGTGGCCGAGGCCCCCCATCATCCCTGTTATTTATTGCCACAGCAGAGTC
TAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTTGGGGATCCCAGAACC
TCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCGGGCTGGTGGGTGGGAT
AGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCTAGGATGCCCCAGCCCT
ACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTTTGGGGATAAACCTATTAA
TTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGCATGACTGC
TTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGTGTACGGA
GGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGT
GAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGGGTGAGTATGGAGGGTCT
AGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTAT
GGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTG
GGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGACCTCAGAACACTGTGACCTTAGCCC
AGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGCCACCATTCCTTGCCAGCCCCAAGAACT
CCAGCTTCCCCACTGCCTCTGTGTGCCCCCTTTGCGTCTGTGAAGGCCATTGAGAAATGCCCA
GTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCCTGACACGGGCTGTGCTTGGCCACAGAAC
CACCCAGCGTCTCCCCTGCTGCTGTCCACGTCAGTTCATGAGGCAACGTCGCGTGGTCTCAGA
CGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGCACTGTGTCCGGCGGAGCCAAGTCCACTCTG
GGGGAGCTCTGGCGGGGACCACGGGCCACTGCTCACCCACTGGCCCCGAGGGGGGTGTAGACG
CCAAGACTCACGCATGTGTGACATCCGGAGTCTTGAGCCGGGTGTCCCAGTGGCACCCTAG
GTGCTGCTGCCTCCACAGTGGGGTTACACCCAGGGCTCCTTGGTCCCCCACAACCTGCCCC
GGCCAGGCCTGCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTG
GCGACACCAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCACGACGGCTCACCTCCCCCTCCAT
CTGCGTTGATGCTCAGAATCGCCTACCTGTGCCTGCGTGTAACACAGCCTCAGACCAGCTA
TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGC
TTGGGCATCCTCCTCCAGCCTCCTGCAGCCCCCAGGCAGTGCCTTACCTGTGGTGCCAGAAA
AGTGCCCTAGGTTGGTGGTCTACAGGAGCCTCAGCCAGGCAGCCACCCACCCTGGGGCC
CTGCTCACCAAGGAAATAAAGACTCAAGCCATAAAAAAA

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FIGURE 484

MRPGAPGPLWPLPWGALAWAVGFVSSMSGGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC
CA
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVECGPGKACRMLGGRPRCECAPDCS
GLPARLQVCSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEHVVCPRPQSCVVDQTGS
AHCVVCRAAPCPVPSSPGQELCGNNNVTYIISCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG
GESAEEEENFV

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

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FIGURE 485

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCCC
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGGGA
AACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATCATC
GTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGATCATG
GAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGAAGAAC
GAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGCCACAAC
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAATAACATC
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC
GGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAGAGGAAGTTC
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA
ATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAAACAAC
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCTG
CCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAAGTCCCAGACACCA
GCCCCCAGTTCCGAAGTGTTTTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAAACCAATGAG
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGGAGCAG
GTGGTGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGGAGAACTGGGCCAGACC
CCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA
GACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGGAAGGGAGAAAC
CAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA
GACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTTAATGTTGAAGATCAG
AAAAGAGACACCATAAAATTTACTTGATCAGCGTGAAAAGCGGAATCATACACTCTGAATTGAA
CTGGAATCACATATTTTACAACAGGGCCGAAGAGATGACTATAAAATGTTTCATGAGGGACTGA
ATACTGAAAACCTGTGAAATGTACTAAATAAAATGTACATCTGA

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FIGURE 486

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGAV
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT
LQRYNGRLQODVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD
LSENNDQRQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLD SKRQVEK
EETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQENPEM
EGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF
NVEDQKRDTINLLDQREKRNHTL

Important features:**Signal peptide:**

amino acids 1-29

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FIGURE 487

AACTCAAACCTCTCTCTGCGGAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGGG
TGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGTAT
GGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGGCCT
ATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGCTCGG
TTAAATGCACCTTTCTCCAGCTTTGCCCCGTGTTGGGTGATGCTCTAACAGTGACCTGGAATTTT
CGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCC
ATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC
ATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATAACCTGCCAGGTGAAGAACCCA
CCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCT
GAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT
GTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTCATAAAGTGGTG
GAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAA
GACACAGACTTAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAAGAACCCTAGTATT
TCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTCCAACCAGTTC
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATAT
CACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAGAGTGTAATTTTTTCAA
GTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCCTTAAGACACTACTTACAGTGT
TATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTTACATTT
CCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCC
TTCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAAACAGTAAATC
CTAAATTCAAACGTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACTATGAGACACATC
TTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATTTTTGTCTG

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FIGURE 488

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTW
NFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVK
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFFQHYRKKRWAERAHK
VVEIKSKEEERLNQEKKVSVYLEDTD

FIGURE 489

[illegible]

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FIGURE 490

MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHPGSQVVKLPFINFM
KTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF
GKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNWLRK
EAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLSEMHP
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIYSSDHG
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSVLDIYPTMLDIAGIPLPQNLSG
YSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGASILPQLFD
LSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIGQYNSNVIA
NLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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FIGURE 491

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATGGC**
CTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT
TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTGTGACAGCAGT
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA
CATCTATAGCACCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGAC
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTT
CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGG
AGGCCTCCTGGGATTCTATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC
ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTTC
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCCCAGAGAAATCG
CTCCAATACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG
TCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGTATGTG**TGA**AGAAC
CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCA
CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG
CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA
GGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCC
AACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGT
TTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTGACTGACCCTCTGTGATCAA
AGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT
GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC
TGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTG
AAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA
GGCAGCCTGGGACATTTAAAAAATA

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FIGURE 492

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFI
LGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR
NRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

Important features:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 493

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGCT
TATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAGAA
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAGTGC
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCACCTTC
TGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCCTTTGGCCTCACAAACGATTTTGTGTGAAG
CTGAAGGTTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGTGAAAGC
AGAAGACGTTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATCTCAGAAA
CATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATGATGCAGCT
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA
GGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 494

MVPRI FAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSET
RQCGPPCTFWPCFELCCLDSFGLTND FVVKLVQGVNSQCHSSPISSKCESRRRFP

Important features:

Signal peptide:

amino acids 1-25

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FIGURE 495

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTT
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGA
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTTGCT
ATGATGATGCCGTCGTGCCCTTGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGAGTCT
GCTTTGAGCAGTGCTGCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGACTCAG
CCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCAGCTTAATGGAACATCAGGGGAACGATGA
CTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGATCTGGGA
TGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATTCTGTGACC
TGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAGAATTCTGGA
CAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGATGACCCCTATG
GCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCTTCACCCTTCTGTGAGATT
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTA
CTTTATAAATGAAAA

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FIGURE 496

MAPRGCIVAVFAIFCISRLCSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPL
ARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Important features:

Signal peptide:

amino acids 1-24

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FIGURE 497

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACTC
CTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTGGC
ACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCCTCAGTCGCCAGAGACCCCAGCCCCCTCA
GAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG
CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTTGCCAA
GGAGACTTCAAACCTTCGGATTACAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGGCAACAT
GGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCC
GACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAGCCCGGGCT
CCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAACCTGGGCCTCTC
ACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCTTCAATTTATC
CAAGAGGTATTTTGATACAGAGTGCCTGATGAATTTTCGCAATGCCTCACAGGCCAAAAG
GCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTTCCCAAACCTGTTTGATGAGAT
TAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGAAATGGTTGACCCC
ATTTGACCCTGTCTTACCCGAAGTCGACACTTTCCACCTGGACAAGTACAAGACCATTAAGGT
GCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAATTTTCGTTGTCATGT
CCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCCCTCATGGAGAAAATGGGTGA
CCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACATGGCTCAGAAACATGAA
AACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCAGAAGTATGAGATGCATGA
GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCTTTGCTGACCTTAGTGAACCTCTC
AGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGAACAGTGATTGAAGTTGATGA
AAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTACTGCTTATTCCATGCCTCCTGT
CATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT
TCTGGGCAGGGTGGTGAATCCGACTCTCCTATAATTCAGGACATGCATAAGCACTTCGTGCTG
TAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGATACCAGCAATGGATGGCAGGGGAG
AGTGTTCCTTTTGTTCTTAAGTGTAGGTTGTTCTCAAATAAATACAGTAGTCCCCACTTA
TCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGCCTGAAACGGTGGACAGTGCTGAACCT
TATATATATTTTTTCTACACATACATACCTATGATAAAGTTTAATTTATAAATTAGGCACAG
TAAGAGATTAACAATAATAACAACATTAAGTAAATGAGTTACTTGAACGCAAGCACTGCAAT
ACCATAACAGTCAAACCTGATTATAGAGAAGGCTACTAAGTGACTCATGGGCGAGGAGCATAGA
CAGTGTGGAGACATTGGGCAAGGGGAGAATTCACATCCTGGGTGGGACAGAGCAGGACGATGC
AAGATTCCATCCCACTACTCAGAATGGCATGCTGCTTAAGACTTTTAGATTGTTTATTTCTGG
AATTTTTCATTTAATGTTTTTGGACCATGGTTGACCATGGTTAACTGAGACTGCAGAAAGCAA
AACCATGGATAAGGGAGGACTACTACAAAAGCATTAATTTGATACATATTTTTTAAAAAAA
AAAAAAA

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FIGURE 498

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E E
E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I K R
G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F D T E
C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P V F T E
V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L A L E D Y
L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A T G R N L Q
V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F L G R V V N P
T L L

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FIGURE 499

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGC GGCTGCGGGGAGCTCCCG
TGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTTCCTTGCGGAAAATGCTGATCTCAGTCG
CAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCCGGGAGAGC
GGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAGGCGG
CCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAACGTGG
CCTGGAGGAAGAACTGGATGGTTGGCGGCGAAGGCGGCGCCAGCGGGAGGTCACCGTTGAGACC
GGACTTGCCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCCTTTTCTCC
TTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATAACCATGCCAGGACTCTCCGGGGTCCTGTGA
GCTGCCGTGCGGGTGAGCACGTTTCCCCCCAAACCCTGGACTGACTGCTTTAAGGTCCGCAAGGC
GGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAACTGAAAGAACCAATAAAATCATGTTCTT
CCAAA

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FIGURE 500

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRRKQEMLKEMPLQDPRSREEAARTQQLLAT
LQEAATTQENVAWRKNWMVGGEGGASGRSP

Important features:

Signal peptide:

amino acids 1-18

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FIGURE 502

MGPSTPLLILFLLSWGPLQGQQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKML
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGRRN
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF
TLAMAARKASRVVPFPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLANRTVV
DSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDEQQWDTP
CPRENAEAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAHASLRYN
PRERQLYAWDDGYQIVYKLEMRKKEEEV

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

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FIGURE 503

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGT
CTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGGCC
CTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAA
CGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTCAGCA
CGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGGGTGTT
TGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGACTATGC
CATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCT
GACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTT
CCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTG
AGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCC
ACCTCGCTCAGCGGCTCCCGGGGCCCAGCACCAGCTCAGAATAAAGCGATTCCACAGCA

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FIGURE 504

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTL
TPENNLRTLSSQHGLGGCDQSVMDLIKRN'NSGWVFENPSIGVLELWVLATNFRDYAIIIFTQLEF
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Important features:

Signal peptide:

amino acids 1-20

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FIGURE 505

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA
GCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC
CTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAGTGC
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGGGGCG
ACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACATAGTT
CACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG
TCCTTCCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG
CTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCA
CGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCCAG
TTACGCCTGCCTCACACCTTGCATGCGCCAACATCACCATCATTGAGCACCAGAAGTGTGAG
AACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAG
GACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATC
TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAA
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCA
TCACCCTCCATTTCCACTTGGTGTGTTTGGTTCCCTGTTCACTCTGTTAATAAGAAACCCTAAGCC
AAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATC
AACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTG
GGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT
ATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA

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FIGURE 506

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHC
LKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV
RPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIHQKCENAYPGNITDTMVCA
SVQEGGKDSCQGDSSGGLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

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FIGURE 507

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACCATGAGG
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCCTGTC
CAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCATCCTT
CCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCTGAGTCCCAGAGCCC
GACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCCCCGGTTG
TGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACATCTACCAC
CCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGGCTGTTGGGA
CTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCAAAAAAAAAAAAAA
AAAAAA

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FIGURE 508

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVLF
PVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEERP
RLWVMPNHQVLLGPEEDQDHIYHPQ

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FIGURE 509

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCCC
ACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCGCG
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCCATG
GCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAACAGAG
ACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAACCACCA
ACTTCAGTTGCCTCAGACTCCAGTAATAACAACGGTCACCACCATGAAACCTACAGCGGCATCT
AATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTCTACACCC
AAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC
AATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCATTCTGAAGCA
AAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAACGCTGGGAGTT
TTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTGGGTATCGAACC
ATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGAT
GCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCTTTTTTGGAAATA
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGG
TAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGTTCATACAATGGTTTT
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCTGGGGTGGGGGCATTGG
TCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAATGCCATCTGGGCATACA
AATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGTAGCTCACATAAAGAACTT
CAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAATTATACAATCAAA
CTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTGTGCTTTAACTGTAGTAGTT
GGTCTAGAAACAAAATACTCC

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FIGURE 510

MGLGARGAWAALLLGTLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPDHT
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQNTS
QISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGFSFVGGIVLTLGVLSILYIGCKM
YYSRRGIRYRTIDEHDAII

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FIGURE 511

GACTTTGCTTGAATGTTTACATTTTCTGCTCGCTGCCTACATATCACAATATAGTGTTTACGTTTTGTAAAAAC
TTTGGGGTGTGAGGAGTTGAGCTTGCTCAGCAAGCCAGCATGGCTAGGATGAGCTTTGTTATAGCAGCTTGCCAA
TTGGTGCTGGGCCTACTAATGACTTCATTAACCGAGTCTTCCATACAGAATAGTGAGTGTCCACAACCTTTGCGTA
TGTGAAATTCGTCCCTGGTTTACCCACAGTCAACTTACAGAGAAGCCACCACTGTTGATTGCAATGACCTCCGC
TTAACAAGGATTCCCAGTAACCTCTCTAGTGACACACAAGTGCTTCTCTTACAGAGCAATAACATCGCGAAGACT
GTGGATGAGCTGCAGCAGCTTTTCAACTTGACTGAACTAGATTTCTCCCAAACAACCTTTACTAACATTAAGGAG
GTCGGGCTGGCAAACCTAACCCAGCTCACAACGCTGCATTTGGAGGAAAATCAGATTACCGAGATGACTGATTAC
TGTCTACAAGACCTCAGCAACCTTCAAGAACTCTACATCAACCACAACCAAATTAGCACTATTTCTGCTCATGCT
TTTGCAGGCTTAAAAAATCTATTAAGGCTCCACCTGAACTCCAACAAATTGAAAGTTATTGATAGTCGCTGGTTT
GATTCTACACCCAACTTGAAATTCTCATGATCGGAGAAAACCTGTGATTGGAATTCTGGATATGAACTTCAAA
CCCCTCGCAAATTTGAGAAGCTTAGTTTTGGCAGGAATGTATCTCACTGATATTCTTGAAATGCTTTGGTGGGT
CTGGATAGCCTTGAGAGCCTGTCTTTTTATGATAACAACTGGTTAAAGTCCCTCAACTTGCCCTGCAAAAAGTT
CCAAATTTGAAATCTTAGACCTCAACAAAAACCCATTCAACAAATCCAAGAAGGGGACTTCAAAAATATGCTT
CGGTTAAAGAAGTGGGAATCAACAATATGGGCGAGCTCGTTTCTGTGACCGCTATGCCCTGGATAACTTGCCT
GAACTCACAAGCTGGAAGCCACCAATAACCTAACTCTCTTACATCCACCGCTTGGCTTTCCGAAGTGTCCCT
GCTCTGGAAGCTTGATGCTGAACAACAATGCCCTGAATGCCATTTACCAAAGACAGTCGAATCCCTCCCCAAT
CTGCGTGAGATCAGTATCCATAGCAATCCCTCAGGTGTGACTGTGTGATCCACTGGATTAACTCCAACAAAACC
AACATCCGCTTCATGGAGCCCTGTCCATGTTCTGTGCCATGCCGCCGAATATAAAGGGCACCAGGTGAAGGAA
GTTTTAATCCAGGATTCGAGTGAACAGTGCCTCCCAATGATATCTCACGACAGCTTCCCAAATCGTTTAAACGTG
GATATCGGCACGACGGTTTTCTTAGACTGTCTGAGCCATGGCTGAGCCAGAACCTGAAATTTACTGGGTCACTCCC
ATTGGAATAAGATAACTGTGGAACCCCTTTCAGATAAATACAAGCTAAGTAGCGAAGGTACCTTGGAATATCT
AACATACAAATTGAAGACTCAGGAAGATACACATGTGTTGCCAGAATGTCCAAGGGGCAGACACTCGGGTGGCA
ACAATTAAGGTTAACGGGACCCCTTCTGGATGGTACCCAGGTGCTAAAAATATACGTCAAGCAGACAGAATCCCAT
TCCATCTTAGTGCTTGGAAGTTAATTCGAATGTCATGACGTCAAACCTAAAAATGGTCGTCTGCCACCATGAAG
ATTGATAACCCCTCACATAACATATACTGCCAGGGTCCCAGTCGATGTCCATGAATACAACCTAACGCATCTGCAG
CCTTCCACAGATTATGAAGTGTGTCTCACAGTGTCGAATATTATCATCAGCAGACTCAAAAGTCATGCGTAAATGTC
ACAACCAAAAATGCCGCCTTCGCAGTGGACATCTCTGATCAAGAAACCAGTACAGCCCTTGCTGCAGTAATGGGG
TCTATGTTTGCCGTATTAGCCTTGCGTCCATTGCTGTGTACTTTGCCAAAAGATTTAAGAGAAAAAACTACCAC
CACTCATTAAAAAAGTATATGCAAAAACCTCTTCAATCCCACTAAATGAGCTGTACCCACCACTCATTAAACCTC
TGGGAAGGTGACAGCGAGAAAGACAAAGATGGTTCTGCAGACACCAAGCCAACCCAGGTGACACATCCAGAGC
TATTACATGTGGTAACTCAGAGGATATFTTGCTTCTGGTAGTAAGGAGCACAAAGACGTTTTTGTCTTATTCTGC
AAAAGTGAACAAGTTGAAGACTTTTGTATTTTGTACTTTGCTAGTTTGTGGCAGAGTGGAGAGGACGGGTGGATA
TTTCAAATTTTTTAGTATAGCGTATCGCAAGGGTTTGACACGGCTGCCAGCGACTCTAGGCTTCCAGTCTGTGT
TTGGTTTTTATTCTTATCATTATTATGATTGTTATTATATTATTTTATTATTAGTTGTTGTGCTAAACTCAAT
AATGCTGTTCTAACTACAGTGCTCAATAAATGATTAATGACAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 512

MARMSFVIAACQLVLGLLMTSLTESSIONSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRL
TRIPSNLSSDTQVLLQLSNNAIAKTVDLQQLFNLTELDQSNNFTNIKEVGLANLTQLTTLHL
EENQITEMTDYCLQDLSNLQELYINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDS
TPNLEILMIGENPVIGILDMNFKPLANLRSLVLAGMYLTDIPGNALVGLDSLESLSFYDNKLV
KVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDYALDNLPELT
KLEATNNPKLSYIHLAFRSVPALESMLNNAALNAIYQKTVESLPNLREISIHNSNPLRCDV
IHWINSNKTNIRFMEPLSMFCAMPPEYKGHVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV
QGADTRVATIKVNGTLLDGTQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDNPH
ITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQQTQKSCVNVTTKNAFAVDISDQETST
ALAAVMGSMFAVISLASIAVYFAKRFRKKNYHHSLLKKYMQKTSSIPLNELYPPLINLWEGDSE
KDKDGSADTKPTQVDTSRSYMW

Important features:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 508-530

N-glycosylation sites:

Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;

582-586;611-615

Tyrosine kinase phosphorylation site:

Amino acids 573-582

N-myristoylation sites:

Amino acids 16-22;224-230;464-470;637-643;698-704

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FIGURE 513

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCT**TAA**ACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 514

MHLARLVGSCSLLLLLGLSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 515

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCTT
TTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCGAA
CCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCGGAG
AAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTTGGGG
CCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCGGTGTG
CGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGGTTCGCCG
GCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCGCTGCTACCCCTGCGCCCCG
TGCGAGCCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTGGCGGCGGC
GCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCCGCCCCGCGCGG
GACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCAGTTCCCTCCT
GGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAGAAGCTGGCCCA
GGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGGCCCCGGGGCGGGT
GAACGAGCTCGGGCGCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACTGGAAGAGCAAGAG
CGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCCAGGG
CGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACACCCCGCAGGCGGAAGC
CCTGGCCGCAGCCGCCCAGGACGCGATTGGCCCCGGAACTCGCGCCCACGCCCCGAGCCACCCGA
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAGAGCGGCTTCGTGTACGC
GATCGGGGAGAAGTTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCTGTGCACCGAGGAGGGGCC
GCTGTGCGCGCAGCCGAGTGCCCCGAGGCTGCACCCGCGCTGCATCCACGTGACACGAGCCA
GTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTCCGGGGCAAGACCTATCAGAC
TTTGGAGGAGTTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTGTGAAGCCAACGGTGAGGTGCT
ATGCACAGTGTACGCGTGTCCCCAGACGGAGTGTGTGGACCCTGTGTACGAGCCTGATCAGTG
CTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAAACCGCGGTGATCCCTGCTGGCAG
AGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT
CGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGACGCTTCCCAGAACACA
AACTCTGACTTTTTCTAGAACATTTTACTGATGTGAACATTCTAGATGACTCTGGGAACTATC
AGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAATTGTTGGTACTTTTCCTTTTCTTGATA
ACAGTTACTACAACAGAAGGAAATGGATATATTTCAAACATCAACAAGAACTTTGGGCATAA
AATCCTTCTCTAAATAAATGTGCTATTTTACAGTAAGTACACAAAAGTACACTATTATATAT
CAAATGTATTTCTATAATCCCTCCATTAGAGAGCTTATATAAGTGTTTTCTATAGATGCAGAT
TAAAAATGCTGTGTTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 516

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNELG
RPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALAAA
AQDAIGPELAPTPEPP EYVYPDYRGKGCVDES GFVYAIG EKFA PGPSAC PCLCTEEGPLCAQ
PEC PRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVS PCERCRC EANGEVLCTVS
ACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYE EGTWRIERQA
MCTRHECRQM

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites. .

amino acids 10-15, 102-107, 103-108.

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

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FIGURE 517

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT
TTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC
GGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTGTGC
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATACAAG
TTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATCTAACT
CTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTACACATG
GAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACAACCTTCC
CTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCCATTTCTGGT
CGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTGAAAATGAAG
AGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATGTTGCCAGTTG
TTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCACCACTTTAGATA
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCTCAGGTGAACTG
CGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAATGATGACATTTTGA
AAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGACACCAGCAACCCAG
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCCTTGCTCTAGCAGCAG
CAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA
ATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTCTAGATCTAACTCTATG
AATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA
CATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTAAAGTTTATTAAACAATAA
TATAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGATTTAAGCAAACCTGCATTTTT
TCACAGGAGAAATAATCATATTCGTAATTTCAAAAGTTGTATAAAATATTTTCTATTGTAGT
TCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACAATTTTCATATGCACTAAAAACC
TAATTTAAATAAAATTTTGGTTCAGGAAAAAA

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FIGURE 518

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPKH
VYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTGGFTPEIGKKKHTESTPFWSIKP
NNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDKSTG
IEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNPAYRE
DIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD
IKCVPEMREKAATVFNTLKNMCRSRRVTALLKVY

Important features:**Signal peptide:**

amino acids 1-19

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FIGURE 519

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTG
GATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTACTG
GATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTGGGT
GATTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGAC
TGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC
AGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGCAATGAT
GGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTTCCAGAGCACAGAA
GTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTA
TTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGGGCCACTTCCAG
AATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATGCTTCAAGGAGTG
AGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAA
ACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG
CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTG
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAGTGAATTCT
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCTGCCATTTT
GAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA
GAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTG
AGGTCAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA
GCCTTTTGAGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCCTGTGTGT
GTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCCTCCTGTCTCATT
GTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGA
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTG
GGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTTGGATCAGACCTCCTGTGGGCAGGG
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAAACCAACCCAAATCAA

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FIGURE 520

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPGE
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQV
FKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL
RMSVEYSQSWGHEFQNRVNLVGDI FRNDGSIMLQGVRES DG GNYTCSIHLGNLVFKKTIVLHVS
PEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPV LILIVKKT CGNKSSVNSTVLVKNT
KKTNP EIKEK PCHFERCEGEKHIYSPIIVREVIEEEE PSEKSEATYMTMHPVWPSLRSDRNN
LEKKS GGGMPKTQQAF

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FIGURE 521

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATGG
TTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA
ACTACATTTTGC AAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCAGGA
TGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTGGCCC
TGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGGATGGT
TGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGATGAGAA
TGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGGTAAAACA
ATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAACTGGAGATA
TTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAGTAAGCAGTA
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA
AGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAATGAGGTCTGGAA
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGATGGAAAAGGAAA
TATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA
TTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCTTAATGCAAAGAGGT
GGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA
GCTGAAAAAAAAAAAAA

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FIGURE 522

MQDEDGYITLNIKTRKPALVSVGPASSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYLQ
DENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHCSPCDTNWRYYGDSYGFRRHNLWEES
KQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDG
KGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

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FIGURE 523

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGGC**
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA
GAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAAT
TGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAG
AACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGT
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTT
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA
AAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAAT
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGA
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTA
TTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG
ACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCCGCATGCTGGGGAGGGT
CTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATATAATAAATGCATGCTATT
CAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAA

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FIGURE 524

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPPKKAYD
MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQI
KVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKN SKILEICDNVTMYWINPT
LISVSELQDFEEEGEDLHF PANEEKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG
IEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWWVARMLGRV

Important features:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
242**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

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FIGURE 525

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGTC
TCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACAT
ACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACCGAGA
GCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCATGGAC
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC
TTTCAGTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAAT
GGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTT
TAACACGTCAATAAAAAAATAATCTCCCAGA

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FIGURE 526

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE
CHLCTESLKSNGRVQFLHDGSC

Important features:

Signal peptide:

amino acids 1-19

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FIGURE 527

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGG
CTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTTCTAGAGCCGAGGGACCCGGTGGCCT
CGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGT
CGGGCCCCGAGGCTCCGTGGCGGGACCCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGC
TGGTCGCCCCTCATTCGCCACGGCACCCGCTACCCACCGGTCAAACAGATCCGCAAGCTGAGGC
AGCTGCACGGGTGCTGTCAGGCCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCGGCAGCC
GCGACCTGGGTGCAGCGCTGGCCGACTGGCCCTTTGTGGTACGCGGACTGGATGGACGGGCAGC
TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGG
CCCTTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGCACCGCTGCA
TGGATAGCAGCGCCGCTTCCTGCAGGGGCTGTGGCAGCACTACCACCTGGCTTGCCGCCGC
CGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTG
ATCACTGTGAGAAGTTTTTAAGTAGAAAAAATGCTACAGCTCTTTATCACGTGGAAG
CCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGC
CAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTCACCTGTTCAATTTGACCTGG
CAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATGATGCAAAGGTATTAG
AATATTTAAATGATCTGAAACAATATTGGAAGAGGATATGGGTATACTATTAACAGTCGAT
CCAGCTGCACCTTGTTTTAGGATATCTTTAGCACTTGGACAAAGCAGTTGAACAGAAACAAA
GGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATGCAGAGACTCTTCTCCAC
TGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAAC
AAATGCATCGGAAGTTCCGAAGTGGTCTCATTGTACCTTATGCCTCGAACCTGATATTTGTGC
TTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAAATCCGAGTGCAGATGTTATTAAATG
AAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACC
ACTACAAGGACATCCTTCAGAGTTGTCAAACAGTGAAGAATGTGAATTAGCAAGGGCTAACA
GTACATCTGATGAAGTATGAGTAAGTGAAGAACATTTTTAATTCTTTAGGAATCTGCAATGAG
TGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTGAG
TATTTCTGTCTTTTACAGAAAAACATTGGGTTTCTCTCTGGGTTTGGACATGAAATGTAAGA
AAAGATTTTTCAGTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGC
CCTGCAAATGTTTACAGAAATGAAATTCTTCTACTTATATAAGAAATCTCACACTGAGATAG
AATTGTGATTTTATAATAACACTTGAAAAGTGCTGGAGTAACAAATATCTCAGTTGGACCAT
CCTTAACCTGATTGAAGTGTCTAGGAACCTTACAGATTGTTCTGCAGTTCTCTCTTTTCC
TCAGGTAGGACAGCTCTAGCATTCTTCTAATCAGGAATATTGTGGTAAGCTGGGAGTATCACT
CTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAACAGAGTGTGTAAAAGGAC
ACCTTCACTGAAGCAAGTCGGAAGTACAATGAAAATAAATATTTTTGGTATTTATTTATGAA
ATATTTGAACATTTTTTCAATAATTCCTTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAA
ATTATTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCC
ATTGCTTAGCTAACTTTTTTCACTTCTGTCACCTGGCTTCGATTTTTATATTTTCTATTATATG
AAATGTATCTTTTGGTTGTTTGATTTTTCTTTCTTTGTAATAGTTCTGAGTTCTGTCA
AATGCCGTGAAAGTATTTGCTATAATAAGAAATTCCTGTGACTTTAAAAA

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FIGURE 528

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPLYFGTKTRYEDVNPVLLSG
PEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGSRD
LGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD
SSAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF
KTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEFDLAIKGVKSPWCDVFDIDDAKVLEY
LNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL
SLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEK
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:**Signal sequence**

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

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FIGURE 529

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTGG
CGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGA
CGCGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGGGCG
GTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTGGGCTC
TTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAAATGGT
ACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTC
TCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTCCCAAGGG
CAAGTGTACCTTGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAGACCTTGAC
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACCTATATCTGT
GATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTATGTCGTAGAA
AAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGGTCTTA
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAAACTCTAAACGG
GATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGCTCCTCGGAAGTCC
CCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACCAGGGCCCAGTCATA
TATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG
GTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATCCTCAGCAAGAAACAAA
ACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGTAGCCTTGGAGACCCAGG
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAA
TATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGATGAAAAGATGGTATGATTC
TACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTCAGGTCATTTACAATTGGGAG
ATTTTCAGAAACATTCCTTTACCATCATTTAGAAATGGTTTGCCTTAATGGAGACAATAGCAG
ATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATACCCAGGGTGGCCTTTAGC
ACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTG
AAAACAATTTGAGAAGTTTTTTTTGAAGTTTTTCTCACTAAAATATGGGGCAATTGTTAGCCTT
ACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTGAAATGTGTATATCAATTTCTGGATT
CATAATAGCAAGATTAGCAAAGGATAAATGCCGAAGGTCATTCTGACACAGTTGGAT
CAATACTGATTAAAGTAGAAAATCCAAGCTTTGCTTGAGAACTTTTGTAACGTGGAGAGTAAAA
AGTATCGGTTTTA

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FIGURE 530

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIENMQ
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMILAV
LYRRKNSKRDTGCTSESLSPVKQAPRKSPDTEGLVKSLPSGSHQGPVIYAQLDHSGGHHS
DKINKSESVVYADIRKN

Important features:**Signal peptide:**

amino acids 1-37

Transmembrane domain:

amino acids 161-183

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FIGURE 531

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCGA
GGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGCTC
TTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCGGGACTGGT
GCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCTGCTG
GAGCACTCATTTGAGATCGATGACAGTGCCAACCTCCGGAAGCGGGGCTCACTGCTCTGGAAC
CAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGCCGACTC
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGGGGCCCTG
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGGTGGAGTCG
CACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGCGTGTCCGTG
GTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTCAAC
ACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGGCCTTCATTGAG
CGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAGTCCTTCTTCGCC
AAATACTGGATGTACATCATTCCCGTCGTCTCTGTTCCCTCATGATGTCAGGAGCGCCAGACACC
GGGGGCCAGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCCTTTGCTGTGTGCCA
CCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTAAAA
GCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGGTCCTGATGTACAAGCT
TGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCAAGGAATGGCTGTCCCCATC
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAAACTGTCCCCAGATC
GACACGCAAAAAAAA

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FIGURE 532

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEID
DSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIIPRRPGALDGLEAGG
YVSSFVPACSLVESHLSDDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQLQP
PTTAPGPETAAFIERLEMEQAQKAKNPQEKSFFAKYWMYIIPVVLFLMMSGAPDTGGQGGGG
GGGGGGGSGLCCVPPSL

Important features:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 226-243

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FIGURE 534

MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWC
CQTHDCCYDHLKTQGCgiYKDNNKSSIHCMdLSQRYCLMAVFNViiYLENEdSE

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

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FIGURE 535

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTG
AACTGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC
CCAAATTGCGTGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTT
TTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGCTGTAAAGATGCAAAAACGTAATATCCAT
GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTT
GTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG
GGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGG
CTGTCATGCAACTGGCCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAA
AGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCC
ACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA
GGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGT
TGCTTAGGTTTGTCCTTCGCTATAACAGCCTTCAAAAAGCTAAGTATAATCAATTTAAAGGG
CTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT
TTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTT
AACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCTTATAATCAGCTGCAT
TCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTTACATTTACGGTCTAAC
TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAACCTTTTGACCTG
GGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGCATGATCAGACTCAAAGAA
CTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCTTTTTTCCAAGGTTGGTCAGC
CTTCAGAACCTTTACTTGCAGTGGAAATAAAATCAGTGTATAGGACAGACCATGTCTGGACC
TGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT
GTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAAGCTCACATTTATT
GGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG
GAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG
AATAAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG
AACTACAGCATCTGTGGCAAAGTACTACAGAGAGGTTTGATCTGGCCAGGGCTCTCCCAAAG
CCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCCCTTTGCCCCCGACG
GTGGGAGCCACAGAGCCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCTTTCCATAAA
ATCATCGCGGGCAGCGTGGCGCTTTTCCTGTCCGTGCTCGTCATCCTGCTGGTTATCTACGTG
TCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAAGGCAC
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTAGAT
TATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCTGCACCTAT
AACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAGC
TGGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTC
CCCTTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCGTTTTAGTGCATTCATA
ATACTGGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGT
GAAGCTTGAACCTCCGTTTAAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAAT
GTCGCATTTGTTTTAAGATAAACTTCTTTCATAGGTAAAAA

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FIGURE 536

MGFNVIRLLSGSAVALVIAPTIVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGC
LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLN
NTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELLDLG
YNRIRSLARNVFAGMIRLKLHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTMSWTW
SSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIQEILDSWISLNDISLAGNIWE
CSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKP
TFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKI IAGSVALFLSVLVILLVIYVS
WKRYPASMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTTETSEMLLNGTGPCTYN
KSGSRECEV

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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FIGURE 537

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGGAAGTGTCTTGCATCATTACGGATTTCGC
AGACAAGTGACCCAGGATCGAGTGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACCTTGGTGTTCACTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGTTGTCTTGTCTGACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTCTGGCCTGATTCGCCCATGAGTATTAGG
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCCGTGCTGGGCCCCGTGTGAAGCCAGCATGTTTACCACCTGGTCTG
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGAAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCACTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCTGCTTGCCAACAGGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGAAAAATATCAATAATTAAGAGTATTTTACCAAGGAATCCTCATGGAAGTTTACTGTGATGTTCTTCTTTCT
CACACAAGTTTTAGCCTTTTTTACAAAGGGAATCATACTGTCTACACATCAGACCATAAGTTGCTTAGGAAACCTT
TAAAAATCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAAATTTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCAGTGTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAAGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGAGACACTGCTCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTATACTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGATGGCTCCCCACCCTCAGCGTTGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTATAGTATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTAACACACCGTAATTTGGCATTGTTTAAAC
CTCATTTATAAAAGCTTCAAAAAACCCA

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FIGURE 538

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS DP
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVARNDRKEI
DEIVIELTVQVKPVT PVC RVPKAVPVGKMATLHCQESEGHPRPHY SWYRNDVPLPTDSRANPR
FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDL NIGGIIGGVLVV
LAVLALITLGICCA YRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features:**Signal peptide:**

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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FIGURE 539

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGGAAGAGAAGCAAAGC
GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAA
CTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGG
CACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGG
GCTCGGGCGGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTAGAGTCGCGGG
CTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCGCA
TGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCC
GCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG
CCTACTTCCATGAAGTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTG
AGGGAGGAGTCTCTCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGC
AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTCTGGATAGGGCTTTGGAGGA
ATGGAGATGGGCAAACATCTGGTGCTGCCAGATCTCTACCAGTGGTCTGATGGAAGCAATT
CCCAGTACCGAACTGGTACACAGATGAACCTTCTGCGGAAGTGAAGAGTGTGTTGTGATGT
ATCACCACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCAGTGGAAATGATGACA
GGTGTAAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTAATCCAACAGCCCCCTG
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTGTTACTGAAG
CAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACCCCTGCTCTTACTGATAC
TGGTTGCTTTTGGAACCTGTTGTTTCCAGATGCTGCATAAAAGTAAAGGAAGAACAAAACTA
GTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAGTAT
AATAACTCATTGACTTGGTTCAGAATTTTGTAATCTGGATCTGTATAAGGAATGGCATCAG
AACAATAGCTTGAATGGCTTGAAATCACAAAGGATCTGCAAGATGAACTGTAAGCTCCCCCT
TGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTTCAATTAAGAATATGCTGTGCTA
ATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAACTTCAAACCTCAAGCAAA
TGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT
TCCTTTTTATTTCTTTACCTTTTCATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATTGA
AATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAAATGAACTGTTCTA
ATATTTATTTTTATGGCATCTCATTTTTCAATACATGCTCTTTTGATTAAAGAACTTATTAC
TGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAGTTTGTCTCTCGAA
ATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA
AGCTATTTTCATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATTGTCT
AATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTCTAGCTTAAAATTAAACAGATTTTG
TAATAATGTAACCTTGTAAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAGT
GACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTG
AGGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTT
GGGATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGC
CTCTGACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAG
TGTGGAGACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACCTACGAAATCGTGTGAAA
ATGGGTTGGAACCCATCAGTGATCGCATATTCATTGATGAAGGTTTGCTTGAGATAGAAAATG
GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTTCTCAAGAGA
AAGTTGTAACCTCTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTG
TTTCTGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 540

MSRVVSLLLGAALLCGHGAFRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACES
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSACPDLYQWSDGSN
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP
VEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKT
SPNQSTLWISKSTRKESGMEV

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

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FIGURE 541

GGAGAAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG
CCACAGCCACTGGGCCCCAAGTTGCTCAGCCTGAAGTAGACACCACCTGGGTCGTGTGCGAGGCCGGCAGGTGG
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACC
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGAGGACT
GCCTGGTCTCAACGTCTATAGCCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGTG
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAAGTGGAGATGAGCATGCACCTGGCAACCAGGGCT
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTC
ACAGAGCCATCACACAGAGTGGGGTCAACACCCAGGGATCATCGACTCTCACCCTTGGCCCCCTAGCTCAGA
AAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCCTTGATGGCACTGTCTTCCCCAAAA
GCCCCAAGGAACCTTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA
GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT
CAACACCCGTCTTGACCAGTCTGGATGTGCCCCCTGAGATGATGCCACCCGTATAGATGAATACCTAGGAAGCA
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTCATCAATGTTCCACCGTCA
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGTCTTTGTGTTGCGAGGTCCCTTCTCA
TGGACGAGAGCTCCCGCTGGCCTTTCCAGAGCCACAGAGGAGAGAAGCAGCTAAGCCTCACCATGATGGCCC
AGTGGACCCACTTTGCCCCGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGCCCCCAATTCAACCAGGCGG
AACAATATCTGGAGATCAACCCAGTGCCACGGGCCGACAGAAGTTAGGGAGGCCTGGATGCAGTTCTGGTCAG
AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCCAGGAGGACCTCTGAGGCC
AGGCCTGAACCTTCTTGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCGCCTCTC
CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGGGCCCTCTGTGACTGGAGTTATGCTCTTTTGAA
ATGTCAACAAGCCGCTCCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCCTGCTTT
CTTCGTGGTAGGTTCTAGCACATTTCTTAGCTTCTCTGGAGGACTCACTCCCAGGAAGCCTTCCCTGCCTTCTC
TGGGCTGTGCGGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT
CCCCCTCAGAGGAGCTCTCTCAAATGGGGATTAGCTAACCCCACTCTGTACCCACACCAGGATCGGGTGGGA
CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACTTGAAC
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC
AATGGCAGAGACCTGGGATGGGAGAAGTCTTGGGGAGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCGTGAC
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTTGGCCCCCTGCACAAGACAACAGA
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCTCACCAATTCCAGCCCCCTGACCTCAGGACGCTGGATG
CCAGCTCCCAGCCCCAGTGCCGGGTCTCCTCCTCCTTCTGCTTGGGGAGACCAGTTCTGGGGAGCTTCCAAG
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTCCGGGCTATTGTACA
GAGAAAAGAAGAGACCCACCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGTTTTCAGATGGAAGTGAGAG
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGTTGCTCTCCTGCCGCCCTCTGCCTGGGCTCCCCTTTGGCA
GCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGAGCCAGCT
CCCTCAGCTTGGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGGGGGCCAG
AGTGAGTTCGGGTGGCGTGGGCTCGGGCGGGGCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGAGGGCTCGG
GACCTGCAGCCCTCCATGCCTGACCTCCCCCACCCTGGGCTCCTGTGCGGCCGAGCCTCCCCAAGGAG
CGCCGCCCCCTGTCCACAGCGCCCACTCCATCGACCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG
GGACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT
TGTAACACACCAATCAGCACCCCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT
ACTCTGGTGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT
TTGACTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCTGTCAAACAGACCACTGACTCTCTGTAAAAAT
GGGCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC
CCCTCGGGTCCCCCTCCACGCGCTGGAAGCTTTGTTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCAAAAA

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FIGURE 542

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQVGVKGTDRLVNVFLGI
PFAQPPLGPDREFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV
LNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAAYGDVVVVTVQYRLGVLGFFSTG
DEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLS PVAAGLFHRAI
TQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNTIYPLT
VDGTVFPKSPKELLKEKPFHSPFLMGVNNHEFSWLI PRGWGLLD TMEQMSREDMLAISTPVL
TSLDVPPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEF
QHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTMM AQWTHFA
RTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKA
QEDL

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

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FIGURE 543

TGTCGCCTGGCCCTCGCCATGACAGACCCCGCGAGCGTCCCCTCCCCGCCCCGCCCTCCTGCTTCTGCTGCTGCTA
CTGGGGGGCGCCACGGCCTCTTTCTGAGGAGCGCCCGCGCTTAGCGTGGCCCCAGGGACTACCTGAACCAC
TATCCCGTGTTTGTGGGCAGCGGGCCCGGACGCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA
GTCCTGCGGGTCAACAGGACGCTGTTCATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGCGATGAAG
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC
GGTTCCAACGCCCTCAACCCGGTGTGCGCCAATAACAGCATAGACACCCCTGCAGCCCGTGGAGACAACATCAGC
GGTATGGCCCGCTGCCCGTACGACCCCAAGCAGCCTAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT
ACTGTTACCGACTTCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCACCCCTGCGCACCGTG
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCGCGTGGCCCGAGTGTGCAAGAAC
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCCTTCTGAAGGCGCGGCTCAACTGCTCTGTA
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAAGCTCGGGGGCGGGCCGTG
GTCTTGGCCGTTTTCACGCGCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCGCGGTGCCGGAGGATCAG
GTGCTCGACCCCGGGCGGGTGTGCGCAGCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGGCGGATGAC
ATCCTCAACTTTGTCAAGACCCACCCCTCTGATGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG
CGGACCCGTATGAGGACACGAGTGAAGTGGCTGTGGACGTGGGAGCGCGCCCTGGGGCAACCAGACCGTT
GTCTTCTGGGTTCTGAGGCGGGGACGGTCCCAAGTTCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT
GGGCTCAGTGTCTTCTGGAGGAGTTTGAAGCTACCGGCCGGACAGGTGTGGACGGCCCGGGCGGTGGCGAGACA
GGGACGCGGCTGTGAGCTTGGAGCTGGACGCGAGCTTCCGGGGGCGCTGCTGGCTGCCTTCCCCCGTGCCTGGTC
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC
GGGTGGGGCCCCGACGGCTCCTGCATCTTCTCAGCCCGGGCACCAGAGCCGCTTTGAGCAGGACGTGTCCGGG
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG
TCGGTGAACCTGCTGGTAACGTGCTCGGTGGCGGCCTTCTGGTGGGAGCCGTGGTGTCCGGCTTACCGTGGGC
TGGTTCTGGGCCCTCCGTGAGCGGGCGGGAGTGGCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG
GGGAGGGCGGTGCTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGGGCGGAGGCGGT
GGCGGTGGCGCCGGGGTTCCCCCGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG
CTGCAGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCACGCGCCAGCAGACGCGCTGCCGCGAAGCGC
CTGCCACTCCGACCCCGCACCCCCACGCCCTGGGCCCCCGCGCTGGGACCACGGCCACCCCTGCTCCCCGCC
TCCGCTTCATCTCCTCCTGCTGCTGGCGCCCGCCGGGCCCCCGAGCAGCCCCCGCGCTGGGGAGCCGACC
CCCGACGGCCGCTCTATGCTGCCCGCCCGCGCTCCACCGCGACTTCCCGCTACCCCCCAGCCAGC
CCGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCCCTTGGACCCAGCCTCAGCCGCGGATGGCTCCCCGGG
CCCTGGAGCCCGCCCCGACGGGCGCCTGAGGAGGCCACTGGGCCCCACGCCCCCTCCGGCCGCCACCCCTGCGC
CGCACCCACAGTTCAACAGCGCGAGGCCCGGCTGGGGACCGCCACCGCGGCTGCCACGCGCGCGGGGACA
GACTTGGCCACCTCCTCCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGGCCCTAGGCGGGGGCCCCCG
ATGCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGACGGTGCCAGAACGCGGGGGCCCGGGCAACTCCG
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAACCAG
CTCGCCCTCCCCCTACCCGGGGCGCAGGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG
GATTTGAGGTTGACCTTATGCGGTAGGTTTGGTTTTTTTTTGCAGTTTGGTTTCTTTTGGGTTTCTAACC
AATTGCACAACTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGACGCGCGGTGGGGAATGGGGGGCCACAG
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCCCTGGCGTGTGTGGGTGTGCG
TGCGTGTGCGTGCCGTGTTCTGTGTCAAGGGGCCGGGAGGTGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG
TGGGCGTGTGTCAAGTGGGCCACGCGTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC
TGGGCGTGTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCGGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC
CCCCCCTCTGACAGAGGAAGCGGGGACAATGCCGGGTTTTCAGGACGAGACACGAGGAGGGCTGCCCGGA
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCGCGGAAGGTGGGTGGGGCCCTCTGTAA
ATACGGCCCCAGGGTGGTGAAGAGTCCCATGCCACCCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA
CCATGCATGCCACGTGGCTGGCTGGTCTCTGCCCTCTTGGAGTTTGCCTCCCCAGCCCCCTCCCATCAAT
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 544

MQTPRASPPRPALLLLLLLLGGAHGLFPEEPPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGAD
DLNIQRLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGEC
RNFVKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALFSDG
MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFREIAMEF
NYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTGVVSLG
GRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPVPEDQVPRPRPGCC
AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDVGAGPWGN
QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQRLLSLELD
AASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPGTRAAFEQDV
SGASTSGLGDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGWVGLRERREL
ARRKDKEAILAHGAGEAVLSVSRLEGERRAQGPGRGGGGGGGAGVPPEALLAPLMQNGWAKAT
LLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLPASASSLLLLAPA
RAPEQPPAPGEPTPDGRLYAARPPGRASHGDFPLTPHASPDRRRVVSAPTGPLDPASAADGLPR
PWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPGTDLAHL LPYGGADR
TAPPVP

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466**Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

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FIGURE 545

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 546

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSELRPE
IFSSREAWQFFLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHY
TLRKISSLANSF LTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQA AAVVKALGELDI
LLQWMEETE

Important features:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

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FIGURE 547

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGCA
GAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCGCG
GAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTGCGA
TCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTCATTT
ATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATTGCTTC
TTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCGGAGAAG
AGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCTTCCCGCCCGCTATTTCTATATT
CAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCTTCCAGGTG
AAAGTCTCAGCACCAGAGGAGCAATTCAGTAGAGTTGGAGTCCAGGTTTTAGACCGAAAAGAT
GGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGTGGAAATTTAA
TTCCAAGGGCAACATGTGGCCAAATCCCATATATTTTAAAAGGGCCGGTTTACCATGAGAAC
TGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGCCCTGAAACCATT
GCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAAGATTGCAGTAGAA
ATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAAAGGATAACAAGGTT
TATATCAAGACTCATGGTGAACATGTAGGTTTTAGAAATTTTCATGGATGCCATACTACTTTCT
TTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTTGGGAGACTGGCCTTTG
GAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCTGGTGTGGCTCCACAGATTCC
AAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTGGAAACCATGGGCCGGGTA
AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTGGGAAAGCAAAAATCCACT
GCCGTCTGGAGAGGGGCGAGACAGCCGCAAAGAGAGACTCGAGCTGGTTAAACTCAGTAGAAAA
CACCCAGAACTCATAGACGCTGCTTTACCAACTTTTTCTTCTTTAAACACGATGAAAACCTG
TATGGTCCCATTTGTGAAACATATTTTCATTTTTTTGATTTCTTCAAGCATAAGTATCAAATAAAT
ATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGCTAGTTGGTGACAGTGTTGTGCTG
AAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAGCTGCAGCCCTGGAAACACTACATT
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACTTAAATGGGCGAAAGATCACGATGAA
GAGGCCAAAAGATAGCAAAAGCAGGACAAGAATTTGCAAGAAATAATCTCATGGGCGATGAC
ATATTCTGTTATTATTTCAAACCTTTTCCAGGAATATGCCAATTTACAAGTGAGTGAGCCCCAA
ATCCGAGAGGGCATGAAAAGGTAGAACCACAGACTGAGGACGACCTCTTCCCTTGTAATTGC
CATAGGAAAAAGACCAAAGATGAACTTGAATGCAAAATAACTTCTATTAGAATAATGGTGC
TCTGAAGACTCTTCTTAACTAAAAAGAAGAATTTTTTTAAGTATTAATTCCATGGACAATATA
AAATCTGTGTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTG
TACTTTAAAGTACATTTTTTAGAATTTTATAATAAAACCACCTTTATTTTAAAGGAAAAAA

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FIGURE 548

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKFT
SSPGEKVFQVKVSAPEEQFTRVGVQVLDRKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKSPY
ILKGPVYHENCDCPLQDSAOWLREMNCPETIAQIQRDLAHFPADVPEKIAVEIPKRFGQRQSL
CHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNSNIHP
IFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGRDSRKE
RLELVKLSRKHPOLIDAAFTNFFFFKH DENLYGPIVKHISFFDFFKHKYQINIDGTVAAYRLP
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKS NLSDLLEKLKWAKDHDEEAKKIAKAGQE
FARNNLMGDDIFCYFYLKFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

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FIGURE 549

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGGCCGTCACCCGCACCGCTGC
CTGCTTGCGGTTGGAGAAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGGGC
GTGGCCGAGGCCGGGGTGACCCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAATTC
AGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCAAAAA
AGGACTCACCTCCCAAAAATTCCGTGAAGGTTGATGAGCTTTCACCTCTACTCAGTTCCTGAGG
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGCTCCGAC
ACTATTGCGAGCCATACACAACCTGGTGTCAGGAAACGTACTCCCAAACCTAAGCCCCAAGATGC
AAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCCTGGATTTT
TTCCGAGACTTGGTGTTATTGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTAGAGGTTCAA
AAATAAAGAAGCTAGTGTATCCGCCTGGTTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC
AACAAGCCATCGTGTTTGGCCAGGTCAGTGGGGAGAGATTATATGACTGGGGTTTACGAGGAT
ATATAGTCATAGAAGATTTGTGGAAGGAGAAGTTTCAAAGCCAGGAAATGTGAAGAATTCAC
CTGGAACCTAAGTAGAAAACTCCATGCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAA
CTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTA
AATTGGCTTTCTTCTTCAGGAAAACTAGACCAGACCTCTGTTATCTTCTGTGAAATCATCCT
ACAAGCAAACCTAACCTGGAATCCCTTCACCTAGAGATAATGTACAAGCCTTAGAACTCCTCAT
TCTCATGTTGCTATTTATGTACCTAATTAAACCCCAAGTTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 550

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEES
ISQLRHYCEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL
LARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG
NVKNSPGTK

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 111-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 36-44

N-myristoylation sites:

Amino acids 124-130;144-150;189-195